

Table S1. Predicted proteins from HBV encoded reading frames based on reliability of AUG initiation codons¹.

mRNA ²	Viral protein ³	Identity to Kozak rule A/GXXATGG	Reliability ⁴	ORF length (Aa)	Predicted molecular weight (kDa)	Sequence ⁵
pg RNA	canonical core protein	GXXATGG	0.36	183	21	H ₂ N- M1 -X64- M2 -X26- M3 -X90-COOH
	core isoform 1	tXXATGa	0.11	118	13.6	H ₂ N- M2 -X26- M3 -X90-COOH
	core isoform 2	AXXATGG	0.07	91	10.6	H ₂ N- M3 -X90-COOH
pg RNA	canonical P protein	cXXATGc	0.91	843	94.2	H ₂ N- M1 -X473- M2 -X179- M3 -X188-COOH
	P protein isoform 1	AXXATGc	0.31	369	41	H ₂ N- M2 -X179- M3 -X188-COOH
	P protein isoform 2	cXXATGc	0.29	189	20.8	H ₂ N- M3 -X188-COOH
preC/C	precore/core protein	AXXATGc	0.56	212	24.2	H ₂ N- M1 '-X28- M1 -X64- M2 -X26- M3 -X90-COOH
	core isoform 1	tXXATGa	0.11	118	13.6	H ₂ N- M2 -X26- M3 -X90-COOH
	canonical core protein	GXXATGG	0.09	183	21	H ₂ N- M1 -X64- M2 -X26- M3 -X90-COOH
	core isoform 2	AXXATGG	0.07	91	10.6	H ₂ N- M3 -X90-COOH
PreS1	canonical LS protein	AXXATGG	0.95	400	43.7	H ₂ N- M1 -X118- M2 -X54- M3 -X225-COOH
	MS protein isoform	GXXATGc	0.24	281	31	H ₂ N- M2 -X54- M3 -X225-COOH
	S protein isoform	AXXATGG	0.18	226	25.1	H ₂ N- M3 -X225-COOH
S	MS protein isoform	GXXATGc	0.54	281	31	H ₂ N- M2 -X54- M3 -X73- M3 '-X151-COOH
	S protein isoform	AXXATGG	0.18	226	25.1	H ₂ N- M3 -X73- M3 '-X151-COOH
	S-smaller protein isoform	tXXATGt	0.09	152	17.2	H ₂ N- M3 '-X151-COOH
XI	canonical HBx protein	cXXATGG	0.53	154	16.5	H ₂ N- M1 -X77- M2 -X25- M3 -X49-COOH
	middle HBx isoform	cXXATGG	0.08	76	8.6	H ₂ N- M2 -X25- M3 -X49-COOH
	smaller/Mini HBx isoform	tXXATGa	0.04	50	5.8	H ₂ N- M3 -X49-COOH
XII	middle HBx Isoform	cXXATGG	0.16	76	8.6	H ₂ N- M2 -X25- M3 -X49-COOH
	smaller/Mini HBx isoform	tXXATGa	0.04	50	5.8	H ₂ N- M3 -X49-COOH

¹ <https://atgpr.dbcls.jp/>, [33].

² mRNA considering each individual viral canonical reading frame.

³ In bold, each viral canonical reading frame.

⁴ Reliability is the likelihood that the estimate will be achieved accurately.

⁵ Canonical Met are in red, and potential Met isoforms are in bold.

Table S2. Main characteristics of the Canonical and HBx isoform proteins.

	Name ¹	Amino acids ²	Molecular weight, (kDa) ²	Isoelectric point, (pI) ²	Subcellular Location ¹		Individual effect on HBV replication ^{1,3}
					High abundance	Low abundance	
Canonical HBx	Wildtype	154	16.6	8.91	Cytoplasmic	Nuclear	Activating
HBx XF	Full-length	154	16.5	8.91	Nucleocytoplasmic/ Nuclear	Nucleocytoplasmic	Repressing
HBx XM	Middle	76	8.6	8.82	Nuclear	Cytoplasmic	Repressing
HBx XS	Small, mini	50	5.8	6.53	Cytoplasmic	Cytoplasmic	Activating

¹ As established in [142].

² Corresponding to HBx proteins from HBV subgenotype F1b, Genbank KM233681.1, 3215 bp [3, 4].

³ As established in [159].