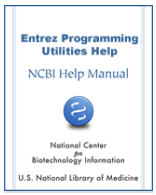
Table 1 – Valid values of &retmode and &rettype for EFetch (null = empty string)

Record Type	&rettype	&retmode
All Databases		
Document summary	docsum	xml, *default*
List of UIDs in XML	uilist	xml
List of UIDs in plain text	uilist	text
db = bioproject		
Full record XML	xml, *default*	xml, *default*
db = biosample		
Full record XML	full, *default*	xml, *default*
Full record text	full, *default*	text
db = biosystems		
Full record XML	xml, *default*	xml, *default*
db = gds		
Summary	summary, *default*	text, *default*
db = gene		
text ASN.1	*null*	asn.1, *default*
XML	*null*	xml
Gene table	gene_table	text
db = homologene		
text ASN.1	*null*	asn.1, *default*
XML	*null*	xml
Alignment scores	alignmentscores	text
FASTA	fasta	text
HomoloGene	homologene	text
db = mesh		
Full record	full, *default*	text, *default*
db = nlmcatalog		
Full record	*null*	text, *default*
XML	*null*	xml
db = nuccore, nucest, nucgss, protein or popset		
text ASN.1	*null*	text, *default*
binary ASN.1	*null*	asn.1
Full record in XML	native	xml
Accession number(s)	acc	text
FASTA	fasta	text
TinySeq XML	fasta	xml
SeqID string	seqid	text
Additional options for db = nuccore, nucest, nucgss or popset		
GenBank flat file	gb	text
GBSeq XML	gb	xml
INSDSeq XML	gbc	xml
Additional option for db = nuccore and protein		
Feature table	ft	text
Additional option for db = nuccore		
GenBank flat file with full sequence (contigs)	gbwithparts	text
CDS nucleotide FASTA	fasta_cds_na	text
CDS protein FASTA	fasta_cds_aa	text
Additional option for db = nucest		
EST report	est	text

Additional option for db = nucgss		
GSS report	gss	text
Additional options for db = protein		
GenPept flat file	gp	text
GBSeq XML	gp	xml
INSDSeq XML	gpc	xml
db = pmc		
XML	*null*	xml, *default*
MEDLINE	medline	text
db = pubmed		
text ASN.1	*null*	asn.1, *default*
XML	*null*	xml
MEDLINE	medline	text
PMID list	uilist	text
Abstract	abstract	text
db = sequences		
text ASN.1	*null*	text, *default*
Accession number(s)	acc	text
FASTA	fasta	text
SeqID string	seqid	text
db = snp		
text ASN.1	*null*	asn.1, *default*
XML	*null*	xml
Flat file	flt	text
FASTA	fasta	text
RS Cluster report	rsr	text
SS Exemplar list	ssexemplar	text
Chromosome report	chr	text
Genotype XML	genxml	xml
Summary	docset	text
UID list	uilist	text or xml
db = sra		
XML	full, *default*	xml, *default*
db = taxonomy		
XML	*null*	xml, *default*
TaxID list	uilist	text or xml

From: The E-utilities In-Depth: Parameters, Syntax and More



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Bethesda (MD): National Center for Biotechnology Information (US); 2010-.

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