**Table 1**. SO type <-> GenBank feature type <-> SBOL Visual type <-> Pigeon type

|  |  |  |  |
| --- | --- | --- | --- |
| **SO type** | **GenBank feature type** | **SBOL Visual type** | **Pigeon type**  **(ICE color)** |
| ***SO\_0000001*** | ***misc\_feature*** | ***User Defined*** | ***s (2)*** |
| *SO\_0000001* | *misc\_feature* | *User Defined* | - (13) |
| *SO\_0000001* | *misc\_feature* | *User Defined* | > (1) |
| *SO\_0000001* | *misc\_feature* | 3’ Sticky Restriction Site | *s (2)* |
| *SO\_0000001* | *misc\_feature* | 5’ Sticky Restriction Site | *s (2)* |
| *SO\_0000001* | *misc\_feature* | Ribonuclease Site | *s (2)* |
| *SO\_0000001* | *misc\_feature* | Signature | *s (2)* |
| SO\_0000002 | misc\_structure | *User Defined* | *s (2)* |
| SO\_0000005 | satellite | *User Defined* | *s (2)* |
| SO\_0000013 | scRNA | *User Defined* | *s (2)* |
| **SO\_0000019** | *stem\_loop* | *User Defined* | *s (2)* |
| SO\_0000057 | operator | Operator | o (13) |
| SO\_0000104 | protein | *User Defined* | *s (2)* |
| **SO\_0000109** | *variation* | *User Defined* | *s (2)* |
| SO\_0000110 | *misc\_feature* | *User Defined* | *s (2)* |
| SO\_0000112 | primer | *User Defined* | *s (2)* |
| SO\_0000139 | RBS | Ribosome Entry Site | r (13) |
| SO\_0000140 | attenuator | *User Defined* | *s (2)* |
| *SO\_0000141* | *terminator* | *Terminator* | **t (6)** |
| *SO\_0000141* | *terminator* | *Terminator* | T (6) |
| SO\_0000147 | exon | *User Defined* | *s (2)* |
| **SO\_0000149** | *source* | *User Defined* | *s (2)* |
| SO\_0000155 | plasmid | *User Defined* | *s (2)* |
| SO\_0000165 | enhancer | *User Defined* | *s (2)* |
| *SO\_0000167* | *promoter* | *Promoter* | **p (4)** |
| *SO\_0000167* | *promoter* | *Promoter* | P (4) |
| SO\_0000172 | CAAT\_signal | *User Defined* | *s (2)* |
| SO\_0000173 | GC\_signal | *User Defined* | *s (2)* |
| SO\_0000174 | TATA\_signal | *User Defined* | *s (2)* |
| SO\_0000175 | -10\_signal | *User Defined* | *s (2)* |
| SO\_0000176 | -35\_signal | *User Defined* | *s (2)* |
| SO\_0000178 | operon | *User Defined* | *s (2)* |
| *SO\_0000185* | **precursor\_RNA** | *User Defined* | *s (2)* |
| *SO\_0000185* | prim\_transcript | *User Defined* | *s (2)* |
| SO\_0000188 | intron | *User Defined* | *s (2)* |
| SO\_0000204 | 5'UTR | *User Defined* | *s (2)* |
| SO\_0000205 | 3'UTR | *User Defined* | *s (2)* |
| **SO\_0000233** | *misc\_RNA* | *User Defined* | *s (2)* |
| SO\_0000234 | mRNA | *User Defined* | *s (2)* |
| SO\_0000252 | rRNA | *User Defined* | *s (2)* |
| SO\_0000253 | tRNA | *User Defined* | *s (2)* |
| SO\_0000274 | snRNA | *User Defined* | *s (2)* |
| SO\_0000275 | snoRNA | *User Defined* | *s (2)* |
| SO\_0000286 | LTR | *User Defined* | *s (2)* |
| SO\_0000296 | rep\_origin | Origin of Replication | z (13) |
| SO\_0000297 | D-loop | *User Defined* | *s (2)* |
| SO\_0000298 | misc\_recomb | *User Defined* | *s (2)* |
| SO\_0000305 | modified\_base | *User Defined* | *s (2)* |
| SO\_0000313 | *stem\_loop* | *User Defined* | *s (2)* |
| SO\_0000316 | CDS | CDS | c (8) |
| SO\_0000323 | start | *User Defined* | *s (2)* |
| SO\_0000324 | tag | *User Defined* | *s (2)* |
| SO\_0000327 | stop | *User Defined* | *s (2)* |
| SO\_0000331 | STS | *User Defined* | *s (2)* |
| SO\_0000409 | misc\_binding | *User Defined* | *s (2)* |
| SO\_0000410 | protein\_bind | *User Defined* | *s (2)* |
| SO\_0000413 | misc\_difference | *User Defined* | *s (2)* |
| SO\_0000417 | protein\_domain | *User Defined* | *s (2)* |
| SO\_0000418 | sig\_peptide | *User Defined* | *s (2)* |
| SO\_0000419 | mat\_peptide | *User Defined* | *s (2)* |
| SO\_0000458 | D\_segment | *User Defined* | *s (2)* |
| SO\_0000470 | J\_region | *User Defined* | *s (2)* |
| SO\_0000551 | polyA\_signal | *User Defined* | *s (2)* |
| SO\_0000553 | polyA\_site | *User Defined* | *s (2)* |
| SO\_0000555 | 5'clip | *User Defined* | *s (2)* |
| SO\_0000557 | 3'clip | *User Defined* | *s (2)* |
| SO\_0000627 | *misc\_feature* | Insulator | | (2) |
| SO\_0000657 | repeat\_region | *User Defined* | *s (2)* |
| SO\_0000673 | *misc\_RNA* | *User Defined* | *s (2)* |
| SO\_0000704 | gene | *User Defined* | *s (2)* |
| SO\_0000723 | iDNA | *User Defined* | *s (2)* |
| SO\_0000724 | oriT | *User Defined* | *s (2)* |
| SO\_0000725 | transit\_peptide | *User Defined* | *s (2)* |
| SO\_0000726 | repeat\_unit | *User Defined* | *s (2)* |
| SO\_0000730 | gap | *User Defined* | *s (2)* |
| SO\_0000856 | conserved | *User Defined* | *s (2)* |
| SO\_0001017 | s\_mutation | *User Defined* | *s (2)* |
| SO\_0001023 | allele | *User Defined* | *s (2)* |
| SO\_0001054 | transposon | *User Defined* | *s (2)* |
| SO\_0001060 | *variation* | *User Defined* | *s (2)* |
| SO\_0001645 | misc\_marker | *User Defined* | *s (2)* |
| SO\_0001687 | *misc\_feature* | Restriction Enzyme  Recognition  Site | x (2) |
| SO\_0001691 | *misc\_feature* | Blunt Restriction Site | *s (2)* |
| SO\_0001833 | V\_region | *User Defined* | *s (2)* |
| SO\_0001834 | C\_region | *User Defined* | *s (2)* |
| SO\_0001835 | N\_region | *User Defined* | *s (2)* |
| SO\_0001836 | S\_region | *User Defined* | *s (2)* |
| SO\_0001932 | *misc\_feature* | 3’ Overhang | *s (2)* |
| SO\_0001933 | *misc\_feature* | 5’ Overhang | *s (2)* |
| SO\_0001953 | *misc\_feature* | Assembly Scar | *s (2)* |
| SO\_0001955 | *misc\_feature* | Protein Stability Element | *s (2)* |
| SO\_0001956 | *misc\_feature* | Protease Site | *s (2)* |
| SO\_0001957 | *misc\_feature* | RNA Stability Element | *s (2)* |
| SO\_0005836 | misc\_signal | *User Defined* | *s (2)* |
| SO\_0005850 | primer\_bind | Primer Binding Site | *s (2)* |
| SO\_2000061 | *source* | *User Defined* | *s (2)* |

NOTE: SO type “SO\_0000185” is associated with both GenBank feature types “precursor\_RNA” and “prim\_transcript”. When mapping SO type -> GenBank type, the suggested GenBank type is “precursor\_RNA”.

NOTE: Any type (e.g., “*SO\_0000001*”) that is set in italic typeface indicates that that type is repeated more than once in the table. As such, types (e.g., “***misc\_feature***”) set in bold indicate the destination type to map two if there is ambiguity. If there are two conflicting types in bold, the default value (e.g., “***misc\_feature***”) should be mapped to.

NOTE: Any unlisted types should be associated the default values for the other categories.