

```

use Bio::Ensembl::Registry;
my $reg = 'Bio::Ensembl::Registry';

$reg->load_registry_from_db(
    -host => 'ensembl.ensembl.org',    # database host
    -user => 'anonymous'               # database username
);

# get a slice adaptor and slice
my $sa = $reg->get_adaptor("mouse", "core", "slice");
my $slice = $sa->fetch_by_region('chromosome', 4, 136432000, 136434000);

# get a strain slice from the A/J mouse strain
my $strain_name = "A/J";
my $strain_slice = $slice->get_by_strain($strain_name);

# get all strain alleles
foreach my $af (@{$strain_slice->get_all_AlleleFeatures_Slice()}){
    # get the strain's alleles at this locus
    my @strain_alleles = split /\|/, $af->allele_string;

    # work out the genotype class
    my $genotype_class;

    if($strain_alleles[0] ne $strain_alleles[1]) {
        $genotype_class = 'heterozygous';
    }
    elsif($strain_alleles[0] eq $af->ref_allele_string) {
        $genotype_class = 'reference homozygous';
    }
    else {
        $genotype_class = 'non-reference homozygous';
    }

    print
        $af->variation->name, ", a ", $af->variation->var_class, # name and class•
        " at ", $af->seq_region_start, "-", $af->seq_region_end, # location
        " with reference allele ", $af->ref_allele_string, # ref allele
        " has alleles ", $af->allele_string, " in ", $strain_name, # strain alleles
        " (", $genotype_class, ") \n";
}

# print FASTA sequence for this strain and region
print ">A/J|4: 136432000-136434000\n", $strain_slice->seq(), "\n";

```