```perl
#!/usr/local/bin/perl

############################################################################
#                                                                          #
# Hydropathy-Analyis: (C) Ulrich Krauss(2012)                              #
#                                                                          #
# Reads in txt-file in fasta format containing unaligned amino acid  sequences#
# Assigns a hydropathy "value" according to the Kyte-Doolittle scale to each  #
# amino acid and writes a "out-file.txt" that contains an ordered space     #
# separated list of hydropathy values for each sequence in the fasta file   #
#                                                  #
# The outfile can easily be imported into any data analysis software such as  #
# MS excel, Origin, GraphPadprism                                          #
#                                            #
#                                            #
# FASTA FORMAT:                                     #
# >Sequence 1                                           #
# AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA                     #
#                                             #
# >Sequence 2                                         #
# CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC                     #
#                                          #
############################################################################
#                                            #
# NOTE:Supply a gap-free sequence alignment in fasta format to allow easy    #
#      plotting and visualization                            #
#                                            #
# NOTE:Input Fasta file has to be located in the same directory as the script #
#                                          #
# SYNTAX: HPLOT_v1.pl fasta-input-file.txt                      #
#                                            #
############################################################################

$/ = '\777'; # entire input to be read in one slurp
$seqs = <>;  # read input, assigning to single string

while ($seqs =~ m/^(>[^>]+)/mg) { # match indiv. sequences by '>'s = Fasta Format
    push(@seqs,$1);             # and store in array
}

for (@seqs) {
# only allow characters A-Z,a-z,0-9,'_','-', and '.' in names;
    /^> *([\w\-\.]+)/ && ($seq_name = $1);

    if ($seq_name) {

        my $seqI = $_;
        $seqI =~ s/^>.+\n//;   # remove FASTA header
        $seqI =~ s/\n//g;  # remove endlines

            my $value = '';
            my $codon = '';

                for (my $i=0; $i < (length($seqI)) ; $i +=1) {
                    $codon = substr($seqI,$i,1);
                    $value .= seq2value ($codon);
                }
```

```perl
# write out-file
            open (MYFILE, '>>out-file.txt');
            printf MYFILE ('%1$6s %2$6s %3$6s', $seq_name, $seqI, $value);
            print MYFILE "\n";
            close (MYFILE);


# on-screen output
print "  \n\n$seq_name $value\n\n";



    }
    else {
        warn "couldn't recognise the sequence name in \n$_";
    }
}


exit;




#sub hydropathy-scale - kyte-doolittle

sub seq2value {

my($codon) = @_;
$codon = uc $codon;


my(%scale) = (

    'A' => '1.80 ',
    'R' => '-4.50 ',
    'N' => '-3.50 ',
    'C' => '2.50 ',
    'D' => '-3.50 ',
    'E' => '-3.50 ',
    'F' => '2.80 ',
    'G' => '-0.40 ',
    'H' => '-3.29 ',
    'I' => '4.50 ',
    'K' => '-3.90 ',
    'L' => '3.80 ',
    'M' => '1.90 ',
    'P' => '-1.60 ',
    'Q' => '-3.50 ',
    'S' => '-0.80 ',
    'T' => '-0.70 ',
    'V' => '4.20 ',
    'W' => '-0.90 ',
    'Y' => '-130 ',
);
if (exists $scale{$codon}) {
return $scale{$codon};
} else {
    print STDERR "bad amino acid ";
    exit;
```

```
}
}
exit;
```