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| **Algorithm used for MHC I and II** |
| import csv  f = open("test.csv")  fw = open("result.csv",'w')  fieldnames = ['Start Point', 'Lowest IC50', "Unique Allele"]  writer = csv.DictWriter(fw, fieldnames=fieldnames)  writer.writeheader()  csvF = csv.DictReader(f)  rowList = []  for row in csvF:  t = (row['allele'],row['start'],row['end'],row['mhc\_ic50'])  # print(t)  rowList.append(t)  num1 = 0  print(num1)  num2 = rowList[len(rowList)-1]  num2=int(num2[2])  print(num2)  resultRange = list(range(num1,num2+1))  print(resultRange)  for i in resultRange:  allele = []  ic50 = []  empty = 0  for j in rowList:  start = int(j[1])  end = int(j[2])  if i>=start and i<=end:  ic50.append(int(j[3]))  if allele.count(j[0])==0:  allele.append(j[0])  else:  empty=1  if len(ic50) != 0:  print(str(i)+" "+str(min(ic50))+" " +str(len(allele))+"\n")  writer.writerow({'Start Point':i, "Lowest IC50":min(ic50), "Unique Allele":len(allele)})  else:  writer.writerow({'Start Point': i, "Lowest IC50": 0, "Unique Allele": 0})  f.close()  fw.close() |