Theoretical Prevision of Physical-Chemical Properties of Amino Acids from Genetic Code

L. Frappat\textsuperscript{a}, A. Sciarrino\textsuperscript{b}, P. Sorba\textsuperscript{a}

\textsuperscript{a} Laboratoire d’Annecy-le-Vieux de Physique Théorique LAPTH
CNRS, UMR 5108, associée à l’Université de Savoie
BP 110, F-74941 Annecy-le-Vieux Cedex, France

\textsuperscript{b} Dipartimento di Scienze Fisiche, Università di Napoli “Federico II”
and I.N.F.N., Sezione di Napoli
Complesso Universitario di Monte S. Angelo, Via Cintia, I-80126 Napoli, Italy

Abstract

Using the crystal basis model of the genetic code, a set of relations between the physical-chemical properties of the amino acids are derived and compared with the experimental data. A prevision for the not yet measured thermodynamical parameters of three amino acids is done.
1 Introduction

It is a known observation [1] that a relationship exists between the codons and the physical-chemical properties (PCP) of the coded amino acids (a.a.). The observed pattern is read either as a relic of some kind of interaction between the a.a. and the nucleotides at an early stage of evolution or as the existence of a mechanism relating the properties of codons with those of a.a.. In particular it is observed that the relationship depends essentially on the nature of the second nucleotide in the codons and it holds when the second nucleotide is adenine (A), uracil (U) or cytosine (C), not when it is guanine (G). To our knowledge neither the anomalous behaviour of G nor the existence of a closest relationship between some of the a.a. is understood. It is the aim of this paper to provide an explanation of both these facts in the framework of the model of genetic code we have discussed in a previous paper [2], called crystal basis model, as it is heavily based on the mathematical structure of the modules of the irreducible representations (IR) of $U_q[sl(2) \oplus sl(2)]$, known in the mathematical literature as crystal basis [3]. After recalling briefly the model in Sect. 2, we derive in Sect. 3 a set of relations between the PCP of the amino acids, based on the content of the IRs of the dinucleotides and of the codons coding for the amino acids. Finally we compare our predictions with the experimental data.

2 The Model

The four nucleotides A, C, G, U are considered as basic states of the $(\frac{1}{2}, \frac{1}{2})$ irreducible representation of the quantum enveloping algebra $U_q[sl(2) \oplus sl(2)]$ in the limit $q \to 0$, with the following assignment of quantum numbers:

$$C \equiv (+\frac{1}{2}, +\frac{1}{2}) \quad U \equiv (-\frac{1}{2}, +\frac{1}{2}) \quad G \equiv (+\frac{1}{2}, -\frac{1}{2}) \quad A \equiv (-\frac{1}{2}, -\frac{1}{2})$$

In this framework, the codons are built as composite states of the nucleotide states by tensoring three such $(\frac{1}{2}, \frac{1}{2})$ representations. Note that the crystal basis, which exists in the limit $q \to 0$ of the $q$-deformed universal enveloping algebra $U_q(G)$ for any semi-simple Lie algebra $G$, is the only way to provide such composite states as pure states, and to ensure the existence of an order in the tensoring procedure.

However, it is well-known (see Table 1) that in a multiplet of codons relative to a specific amino acid, the first two bases constituent of a codon are "relatively stable", the degeneracy being mainly generated by the third nucleotide. Considering the tensor product

$$(\frac{1}{2}, \frac{1}{2}) \otimes (\frac{1}{2}, \frac{1}{2}) = (1, 1) \oplus (1, 0) \oplus (0, 1) \oplus (0, 0)$$

we get, using Kashiwara’s theorem [3], the following tableau:

$$\begin{array}{ccc}
\rightarrow & sl(2)_H & (0,0) \\
\downarrow \\
sl(2)_V & (0,1) & \begin{pmatrix}
\text{CA} \\
\text{CU} \\
\text{GU} \\
\text{GA}
\end{pmatrix}
\end{array} \begin{array}{c}
(1,0) \\
(1,1)
\end{array} \begin{array}{c}
\text{CG} \\
\text{UC}
\end{array} \begin{array}{c}
\text{UG} \\
\text{AU}
\end{array} \begin{array}{c}
\text{GC} \\
\text{AC}
\end{array} \begin{array}{c}
\text{GU} \\
\text{AG}
\end{array} \begin{array}{c}
\text{AA}
\end{array}$$
where the subscripts $H$ (:= horizontal) and $V$ (:= vertical) specify the two $sl(2)$.

From Table 1, the dinucleotide states formed by the first two nucleotides in a codon can be put in correspondence with quadruplets, doublets or singlets of codons relative to an amino acid, the sextets (resp. triplets) being viewed as the sum of a quadruplet and a doublet (resp. a doublet and a singlet). We define in our model the “charge” $Q$ of a dinucleotide state by

$$Q = J_{3,H} + \frac{1}{4} C_V (J_{3,V} + 1) - \frac{1}{4}$$

(3)

The dinucleotide states are then split into two octets with respect to the charge $Q$: the eight strong dinucleotides CC, GC, CG, GG, CU, GU, UC, AC associated to the quadruplets (as well as those included in the sextets) of codons satisfy $Q > 0$, while the eight weak dinucleotides AA, AU, UA, UU, UG, AG, CA, GA associated to the doublets (as well as those included in the triplets) and eventually to the singlets of codons satisfy $Q < 0$. Let us remark that by the change $C \leftrightarrow A$ and $U \leftrightarrow G$, which is equivalent to the change of the sign of $J_{3,\alpha}$ or to reflexion with respect to the diagonals of the eq. (1), the 8 strong dinucleotides are transformed into weak ones and vice-versa. Note that a first attempt to differentiate between strong and weak dinucleotides is contained in ref. [4].

The irreducible representations of the tensor product of $(\frac{1}{2}, \frac{1}{2}) \otimes^3$ as well as the correspondence codons/amino acids for the eukariotic code is reported in Table 1. The upper labels denote different IRs.

3 Relationship between the PCP of Amino Acids

We assume that some PCP of a given amino acid are related to the nature of the codons, in particular they depend on the following mathematical features, written in hierarchical order:

1. the IR of the dinucleotide formed by the first two nucleotides;
2. the sign of the charge $Q$, eq. (3), on the dinucleotide state;
3. the value of the third component of $J_{3,V}$ inside a fixed IR for the dinucleotides;
4. the upper label(s) of the codon IR(s);

Not all the PCP are supposed to follow the scheme above; some of them are essentially given by the specific chemical structure of the amino acid itself.

In the following, we analyze the PCP of the amino acids in the light of the dinucleotide content of the irreducible representations of eq. (2).

– representation $(0,0)$

The codons of the form CAN ($N = C, U, G, A$) all belong to the IR $(\frac{1}{2}, \frac{1}{2})^4$ and code for His and Gln, both being coded by doublets and differing by the value of $J_{3,V}$. Then we expect that the PCP of His and Gln are very close.
We analyse now the codons built up by the dinucleotide IR (1, 0). i.e. CG ($Q > 0$), UG, UA (both $Q < 0$). The codons CGS ($S = C, G$), resp. CGW ($W = U, A$), belonging to IR ($3/2, 1/2$), resp. ($1/2, 1/2$), all code for Arg, so we do not have any relation. The codons UGS, resp. UGW, belonging to IR ($3/2, 1/2$), resp. ($1/2, 1/2$), code for Cys (which is a doublet) and Trp (singlet), resp. the other Cys and Ter (triplets). So we expect the PCP of Cys not very different from those of Trp. The codons UAN, belonging to the IR ($3/2, 1/2$), code for Tyr and Ter. So we expect some affinity between the a.a. coded by UGN and UAN, in particular between Cys and Tyr both being coded by doublets.

The codons built up by the dinucleotide IR (0, 1) are CU, GU (both $Q > 0$) and GA ($Q < 0$). The codons CUY and GUY ($Y = C, U$), resp. CUR and GUR ($R = G, A$), belonging to IR ($1/2, 3/2$), resp. ($1/2, 1/2$), code for Leu and Val. Therefore we do not have any relation between a.a. coded by the same dinucleotide, but we expect that the PCP of Leu and Val are close since CU and GU both belong to the same IR and are both strong. The codons GAN belong to the IR ($1/2, 3/2$) and they code Asp and Glu (both doublets). Then we expect the PCP of Asp and Glu to be very close.

The dinucleotide IR (1, 1) contains five states with $Q > 0$ (CC, UC, GC, AC, GG). The codons CCN, resp. UCN, belong to four different IRs and code for Pro (quartet), resp. Ser (sextets). We expect an affinity between the PCP of these a.a.. The codons GCN, resp. ACN, belong to four different IRs and code for Ala (quartet), resp. Thr (quartets). We expect a strong affinity between the PCP of Ala and Thr. The codons GGN belong to two different IRs and code for Gly, so we expect an affinity of PCP of Gly with those of Pro, Ser, Ala, Thr. Now let us look at the four states with $Q < 0$ (UU, AU, AG, AA). The codons UUN belong to two different IRs and code for Leu, the doublet subpart of the sextet, and for Phe (doublet). An affinity is expected between the PCP of these two a.a.. The codons AUN belong to two different IRs and code Ile (triplet) and Met (singlet) and, in fact, the values of PCP of these two a.a. are not very different. The codons AGN belong to two different IRs and code for Ser and Arg, the doublet subpart of the sextet, so an affinity between the PCP of these codons is expected. The codons AAN belong to the same IR ($3/2, 3/2$) and code for Asn and Lys, so the values of the PCP of these a.a. should be close.

Note that for the three sextets (Arg, Leu, Ser) the quartet (doublet) subpart is coded by a codon with a strong (weak) dinucleotide.

In conclusion we predict the following relations between the values of the PCP of the amino acids ($\cong$ means strong affinity, $\approx$ affinity, $\sim$ weak affinity):

1. His $\cong$ Gln
2. Asp $\cong$ Glu
3. Asn ≡ Lys ~ Arg, Ser
4. Cys ≡ Tyr ≈ Trp
5. Leu ≡ Val
6. Pro ≡ Ser ≈ Gly
7. Ala ≡ Thr ≈ Gly, Pro, Ser
8. Ile ≡ Met ≈ Phe

4 Discussion

We have compared our theoretical previsions with 10 physical-chemical properties:

1. the Chou-Fasman conformational parameters \( P_\alpha, P_\beta \) and \( P_\tau \) which gives a measure of the probability of the a.a. to form respectively a helix, a sheet and a turn. However it has been suggested in [4] that the sum \( P_\alpha + P_\beta \) is a more appropriate parameter to characterize the generic structure forming potential while the difference \( P_\alpha - P_\beta \) is a more appropriate parameter for the helix forming potential, which is a quantity more depending on the particular a.a.. So we compare with \( P_\alpha + P_\beta \) and \( P_\tau \);

2. the Grantham polarity \( P_G \) [7];

3. the relative hydrophilicity \( R_f \) as computed by Weber and Lacey [8];

4. the thermodynamic activation parameters at 298 K: \( \Delta H \) (enthalpy, in kJ/mol), \( \Delta G \) (free energy, in kJ/mol) and \( \Delta S \) (entropy, in J/mole/K) as obtained by Siemion and Stefanowicz [9];

5. the negative of the logarithm of the dissociation constants at 298 K: \( pK_a \) for the \( \alpha\)-COOH group and \( pK_b \) for the \( \alpha\)-NH\(^+_3\) group [10];

6. the isoelectronic point \( pI \) [11], i.e. the \( p\)H value at which no electrophoresis occurs.

The comparison between the theoretical relations and the experimental values shows (see Tables 2 and 4):

1. His ≡ Gln – The agreement, except for \( pI \), is very good.
2. Asp ≡ Glu – The agreement, except for \( P_\tau \), is very good.
3. Asn ≡ Lys ~ Arg, Ser – The agreement, except for \( pI \) and \( P_\tau \) is very good. The comparison with the values of PCP of Ser and Arg is satisfactory.
4. Cys ≈ Tyr ≈ Trp – Except for $R_f$, the agreement between the first two a.a. is very good, while with Trp is satisfactory.

5. Leu ≈ Val – The agreement is very good.

6. Pro ≈ Ser ≈ Gly – The agreement is very good, except for $P_\alpha + P_\beta$ and $\Delta H$, and with Gly more than satisfactory.

7. Ala ≈ Thr ≈ Gly, Pro, Ser – The agreement is very good between the first two a.a. except for $P_\tau$ and satisfactory with the others except for the conformational parameters.

8. Ile ≈ Met ≈ Phe – The agreement is very good between the first two a.a. and satisfactory with Phe.

In order to have a more quantitative evaluation of the agreement between the data and the theoretical model we compute the mean value and the standard deviation of the whole population (i.e. the twenty amino-acids) for each generic PCP $x$

$$\bar{x} = \frac{1}{n} \sum_{i} x_i \quad \text{and} \quad \sigma_x = \sqrt{\frac{1}{n} \sum_{i} (x_i - \bar{x})^2} \quad (4)$$

in 3 different cases:

1. considering all the amino acids, i.e. summing over the whole set of amino acids ($n = 20$);
2. considering the amino acids coded by the codons with the same second nucleotide ($n = 4$ for C, $n = 5$ for U and G, $n = 7$ for A);
3. considering the couples ($n = 2$) of amino acids given by our 8 relations.

The results are reported in Tables 2 to 4.

As an estimate of the accuracy of our predictions, we compute the sum of the adimensional quantities given for any PCP by the ratios $\sigma_x/\bar{x}$ of the standard deviation to the average value, in the three different cases considered above.

|         | A 1.82 | C 1.13 | G 1.82 | U 0.70 |
|---------|--------|--------|--------|--------|
| Gln/His | 0.35   |        |        |        |
| Asp/Glu | 0.63   |        |        |        |
| Asn/Lys | 0.72   |        |        |        |
| Cys/Tyr | 0.80   |        |        |        |
| Pro/Ser | 0.77   |        |        |        |
| Ala/Thr | 0.48   |        |        |        |
| Ile/Met | 0.39   |        |        |        |
| Leu/Val | 0.38   |        |        |        |

Values of $\eta = \sum \sigma_x/\bar{x}$

Looking to the table above, we remark that the characterization of the PCP from the nature of the second nucleotide in the codons is, except for U, indeed not really discriminatory. On the contrary, the relations derived by our model reduces dramatically the values of our estimate parameter $\eta = \sum_i \sigma_x/\bar{x}$. 

5
From Table 2 we note that the values of the thermodynamical quantities for some amino acids are not yet measured. Our relations predict that the values of $\Delta H$ and $-\Delta S$ for His should be around 60 kJ/mol and 120 kJ/mol/K. For the values of Asp and Glu coded by the unique weak nucleotide GA in the IR (0,1), we do not have any available data to compare with. However, making the further assumption, supported by an inspection of the available data, that the values of the thermodynamical quantities depend slightly on the nature of the charge, we predict that the values of these quantities for Asp and Glu should not be very dissimilar from the values of the analogous quantities for Leu and Val, coded by the strong dinucleotide CU an GU in the IR (0,1). So we predict that for Asp and Glu, one should find $\Delta H \approx 60$ kJ/mol, $-\Delta S \approx 135$ kJ/mol/K and $\Delta G \approx 100$ kJ/mol.

5 Conclusion

In conclusion, the values of PCP show, with a few exceptions, a pattern of correlations which is expected from the assumptions done in the crystal basis model. Let us emphasize that the assignment of the value of the IRs both for the dinucleotide and for the trinucleotide states or codons is a straightforward consequence of our model. The remarked property that the a.a. coded by codons whose second nucleotide is G do not share similarity in the properties of PCP with other a.a. does find an explication in the model as it is immediate to verify, looking to the table of the tensor product of two $(\frac{1}{2}, \frac{1}{2})$ that that are no two states with G in second position which share simultaneously the properties of belonging to the same IR and being characterized by the same value of $Q$.

A final remark: it has been suggested that the physico-chemical properties of the amino acids have played a fundamental role in the evolution and the organization of the genetic code. In this framework, a measure of the relative distances between amino acids has been defined, see [11] and references therein. The picture which emerges in [11] has some striking confirmations with the predictions of our model. So we argue that the assignment of codons in multiplets, corresponding to irreducible representations, may have a deep connection with the evolutionary organization.

Acknowledgments: We are grateful to M.L. Chiusano for pointing us the interest to analyse the physical-chemical properties in the light of the crystal basis model and for providing us literature on the subject. Partially supported by MURST (Italy) and MAE (France) in the framework of french-italian collaboration Galileo.

References

[1] M. Sjostrom, S. Wold, A Multivariate Study of the Relationship Between the Genetic Code and the Physical-Chemical Properties of Amino Acids, J. Mol. Evol. 22 (1985) 272.
[2] L. Frappat, A. Sciarrino, P. Sorba, A crystal base for the genetic code, Phys. Lett. A 250 (1998) 214.

[3] M. Kashiwara, Crystalizing the $q$-analogue of universal enveloping algebras, Commun. Math. Phys. 133 (1990) 249.

[4] B.G. Konopel’chenko, Yu.B. Rumer, Classification of Codons in the Genetic Code, Translated from Doklady Akademi Nauk SSSR 223, N.2, (1975) 471.

[5] P.Y. Chou, G.D. Fasman, Conformational parameters for amino acids in helical, $\beta$-sheet, and random coil regions calculated from proteins, Biochemistry 13 (1974) 211.

[6] I.Z. Siemion, P.J. Siemion, The informational context of the third base in amino acid codons, BioSystems 33 (1994) 139.

[7] R. Grantham, Amino acid difference formula to help explain protein evolution, Science 185 (1974) 862.

[8] A.L. Weber, J.C. Lacey, Genetic Code Correlations: Amino Acids and Their Anticodon Nucleotides, J. Mol. Evol. 11 (1978) 199.

[9] I.Z. Siemion, P. Stefanowicz Periodical change of amino acid reactivity within the genetic code, BioSystems 27 (1992) 77.

[10] D.R. Lide Ed., Handbook of Chemistry and Physics, 73rd ed., CRC Press (Boca Raton, Florida, USA 1992).

[11] M. Di Giulio, Some aspects of the organization and evolution of the genetic code, J. Mol. Evol. 29 (1989) 191.
Table 1: The eukariotic code. The upper label denotes different irreducible representations.

| codon | a.a. | $J_H$ | $J_V$ | codon | a.a. | $J_H$ | $J_V$ |
|-------|------|-------|-------|-------|------|-------|-------|
| CCC   | Pro  | 3/2   | 3/2   | UCC   | Ser  | 3/2   | 3/2   |
| CCU   | Pro  | (1/2 3/2)¹ | UCU   | Ser  | (1/2 3/2)¹ | |
| CCG   | Pro  | (3/2 1/2)¹ | UCG   | Ser  | (3/2 1/2)¹ | |
| CCA   | Pro  | (1/2 1/2)¹ | UCA   | Ser  | (1/2 1/2)¹ | |
| CUC   | Leu  | (1/2 3/2)² | UUC   | Phe  | 3/2   | 3/2   |
| CUU   | Leu  | (1/2 3/2)² | UUU   | Phe  | 3/2   | 3/2   |
| CUG   | Leu  | (1/2 1/2)³ | UUG   | Leu  | (3/2 1/2)¹ | |
| CUA   | Leu  | (1/2 1/2)³ | UUA   | Leu  | (3/2 1/2)¹ | |
| CGC   | Arg  | (3/2 1/2)² | UGC   | Cys  | (3/2 1/2)² | |
| CGU   | Arg  | (1/2 1/2)² | UGU   | Cys  | (1/2 1/2)² | |
| CGG   | Arg  | (3/2 1/2)² | UGG   | Trp  | (3/2 1/2)² | |
| CGA   | Arg  | (1/2 1/2)² | UGA   | Ter  | (1/2 1/2)² | |
| CAC   | His  | (1/2 1/2)⁴ | UAC   | Tyr  | (3/2 1/2)² | |
| CAU   | His  | (1/2 1/2)⁴ | UAU   | Tyr  | (3/2 1/2)² | |
| CAG   | Gln  | (1/2 1/2)⁴ | UAG   | Ter  | (3/2 1/2)² | |
| CAA   | Gln  | (1/2 1/2)⁴ | UAA   | Ter  | (3/2 1/2)² | |
| GCC   | Ala  | 3/2   | 3/2   | ACC   | Thr  | 3/2   | 3/2   |
| GCU   | Ala  | (1/2 3/2)¹ | ACU   | Thr  | (1/2 3/2)¹ | |
| GCG   | Ala  | (3/2 1/2)¹ | ACG   | Thr  | (3/2 1/2)¹ | |
| GCA   | Ala  | (1/2 1/2)¹ | ACA   | Thr  | (1/2 1/2)¹ | |
| GUC   | Val  | (1/2 3/2)² | AUC   | Ile  | 3/2   | 3/2   |
| GUU   | Val  | (1/2 3/2)² | AUU   | Ile  | 3/2   | 3/2   |
| GUG   | Val  | (1/2 1/2)³ | AUG   | Met  | (3/2 1/2)¹ | |
| GUA   | Val  | (1/2 1/2)³ | AUA   | Ile  | (3/2 1/2)¹ | |
| GGC   | Gly  | 3/2   | 3/2   | AGC   | Ser  | 3/2   | 3/2   |
| GGU   | Gly  | (1/2 3/2)¹ | AGU   | Ser  | (1/2 3/2)¹ | |
| GGG   | Gly  | 3/2   | 3/2   | AGG   | Arg  | 3/2   | 3/2   |
| GGA   | Gly  | (1/2 3/2)¹ | AGA   | Arg  | (1/2 3/2)¹ | |
| GAC   | Asp  | (1/2 3/2)² | AAC   | Asn  | 3/2   | 3/2   |
| GAU   | Asp  | (1/2 3/2)² | AAU   | Asn  | 3/2   | 3/2   |
| GAG   | Gln  | (1/2 3/2)² | AAG   | Lys  | 3/2   | 3/2   |
| GAA   | Glu  | (1/2 3/2)² | AAA   | Lys  | 3/2   | 3/2   |
Table 3: Table of amino-acid properties

| Amino acid | $P_a + P_b$ | $P_r$ | $P_G$ | $R_f$ | $\Delta H$ | $-\Delta S$ | $\Delta G$ | $pK_a$ | $pK_b$ | $pI$ |
|------------|-------------|-------|-------|-------|------------|-------------|-----------|--------|--------|------|
| Ala        | 2.25        | 0.66  | 8.09  | 0.89  | 50.7       | 147.8       | 94.66     | 2.34   | 9.69   | 6.00 |
| Arg        | 1.91        | 0.95  | 10.50 | 0.88  | 54.8       | 143.2       | 97.5      | 2.17   | 9.04   | 11.15|
| Asn        | 1.60        | 1.56  | 11.5  | 0.89  | 55         | 135.8       | 95.51     | 2.02   | 8.80   | 5.41 |
| Asp        | 1.55        | 1.46  | 13    | 0.87  | -          | -           | -         | 1.88   | 9.60   | 2.77 |
| Cys        | 1.89        | 1.19  | 5.5   | 0.85  | 43.9       | 163.2       | 92.89     | 1.96   | 10.28  | 5.02 |
| Gln        | 2.21        | 0.98  | 10.5  | 0.82  | 61.1       | 121.8       | 97.30     | 2.17   | 9.13   | 5.65 |
| Glu        | 1.88        | 0.74  | 12.2  | 0.84  | -          | -           | -         | 2.19   | 9.67   | 3.22 |
| Gly        | 1.32        | 1.56  | 9     | 0.92  | 49.0       | 140.6       | 91.08     | 2.34   | 9.60   | 5.97 |
| His        | 1.87        | 0.95  | 10.4  | 0.83  | -          | -           | -         | 94.59  | 1.82   | 9.17  | 7.47 |
| Ile        | 2.68        | 0.47  | 5.2   | 0.76  | 57.3       | 152.3       | 102.6     | 2.36   | 9.60   | 5.94 |
| Leu        | 2.51        | 0.59  | 4.9   | 0.73  | 59.4       | 128.1       | 97.70     | 2.36   | 9.60   | 5.98 |
| Lys        | 1.90        | 1.01  | 11.3  | 0.97  | 57.8       | 135.6       | 98.16     | 2.18   | 8.95   | 9.59 |
| Met        | 2.50        | 0.60  | 5.7   | 0.74  | 58.2       | 128.5       | 96.65     | 2.28   | 9.21   | 5.74 |
| Phe        | 2.51        | 0.60  | 5.2   | 0.52  | 48.3       | 156.1       | 94.76     | 1.83   | 9.13   | 5.48 |
| Pro        | 1.12        | 1.52  | 8     | 0.82  | 50.7       | 164.5       | 99.49     | 1.99   | 10.60  | 6.30 |
| Ser        | 1.52        | 1.43  | 9.19  | 0.96  | 36.0       | 180         | 89.98     | 2.21   | 9.15   | 5.68 |
| Thr        | 2.02        | 0.96  | 8.59  | 0.92  | 53.4       | 136.0       | 93.98     | 2.09   | 9.10   | 5.64 |
| Trp        | 2.45        | 0.96  | 5.4   | 0.2   | 51.1       | 151.5       | 96.25     | 2.83   | 9.39   | 5.89 |
| Tyr        | 2.16        | 1.14  | 6.2   | 0.49  | 54.4       | 139.0       | 95.68     | 2.20   | 9.11   | 5.66 |
| Val        | 2.76        | 0.50  | 5.9   | 0.85  | 60.2       | 139.0       | 101.7     | 2.32   | 9.62   | 5.96 |

Table 2: PCP of amino-acids coded by codons with same second nucleotide (written at the left)
\[ P_{\alpha} + P_{\beta} \]
\[ P_{\tau} \]
\[ P_{\tau} \]
\[ R_{f} \]
\[ \Delta H \]
\[ -\Delta S \]
\[ \Delta G \]
\[ pK_{a} \]
\[ pK_{b} \]
\[ pI \]

| Amino Acid Doublet | \( P_{\alpha} + P_{\beta} \) | \( P_{\tau} \) | \( P_{\tau} \) | \( R_{f} \) | \( \Delta H \) | \( -\Delta S \) | \( \Delta G \) | \( pK_{a} \) | \( pK_{b} \) | \( pI \) |
|-------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|
| Glu/His           | 2.04            | 0.97            | 10.45           | 0.83            | 61.10           | 121.80          | 95.95           | 2.00            | 9.15            | 6.56            |
|                   | 0.17            | 0.01            | 0.05            | 0.01            | -               | -               | 1.36            | 0.17            | 0.02            | 0.91            |
|                   | 8 %             | 2 %             | 0 %             | 1 %             | -               | -               | 1 %             | 9 %             | 0 %             | 14 %            |
| Asp/Glu           | 1.72            | 1.10            | 12.60           | 0.86            | 2.04            | 9.64            | 3.00            | 8 %             | 0 %             | 8 %             |
|                   | 0.17            | 0.36            | 0.40            | 0.02            | 0.16            | 0.04            | 0.22            | 8 %             | 0 %             | 8 %             |
| Asn/Lys           | 1.75            | 1.29            | 11.40           | 0.93            | 56.40           | 135.70          | 96.84           | 2.10            | 8.88            | 7.50            |
|                   | 0.15            | 0.28            | 0.10            | 0.04            | 1.40            | 0.10            | 1.32            | 0.08            | 0.08            | 2.09            |
|                   | 9 %             | 21 %            | 1 %             | 4 %             | 2 %             | 0 %             | 1 %             | 4 %             | 1 %             | 28 %            |
| Cys/Tyr           | 2.03            | 1.17            | 5.85            | 0.67            | 49.15           | 151.10          | 94.29           | 2.08            | 9.70            | 5.34            |
|                   | 0.14            | 0.02            | 0.35            | 0.18            | 5.25            | 12.10           | 1.40            | 0.12            | 0.58            | 0.32            |
|                   | 7 %             | 2 %             | 6 %             | 27 %            | 11 %            | 8 %             | 1 %             | 6 %             | 6 %             | 6 %             |
| Pro/Ser           | 1.32            | 1.48            | 8.60            | 0.89            | 43.35           | 172.25          | 94.74           | 2.10            | 8.88            | 5.99            |
|                   | 0.20            | 0.04            | 0.60            | 0.07            | 7.35            | 7.75            | 4.76            | 0.11            | 0.73            | 0.31            |
|                   | 15 %            | 3 %             | 7 %             | 8 %             | 17 %            | 4 %             | 5 %             | 5 %             | 7 %             | 5 %             |
| Ala/Thr           | 2.14            | 0.81            | 8.34            | 0.91            | 52.05           | 141.9           | 94.32           | 2.22            | 9.40            | 5.82            |
|                   | 0.12            | 0.15            | 0.25            | 0.02            | 1.35            | 5.90            | 0.34            | 0.13            | 0.29            | 0.18            |
|                   | 5 %             | 19 %            | 3 %             | 2 %             | 3 %             | 4 %             | 0 %             | 6 %             | 3 %             | 3 %             |
| Ile/Met           | 2.59            | 0.54            | 5.45            | 0.75            | 57.75           | 140.40          | 99.63           | 2.32            | 9.41            | 5.84            |
|                   | 0.09            | 0.07            | 0.25            | 0.01            | 0.45            | 11.90           | 2.97            | 0.04            | 0.19            | 0.10            |
|                   | 3 %             | 12 %            | 5 %             | 1 %             | 1 %             | 8 %             | 3 %             | 2 %             | 2 %             | 2 %             |
| Leu/Val           | 2.64            | 0.55            | 5.40            | 0.79            | 59.80           | 133.55          | 99.70           | 2.34            | 9.61            | 5.97            |
|                   | 0.12            | 0.05            | 0.50            | 0.06            | 0.40            | 5.45            | 2.00            | 0.02            | 0.01            | 0.01            |
|                   | 5 %             | 8 %             | 9 %             | 8 %             | 1 %             | 4 %             | 2 %             | 1 %             | 0 %             | 0 %             |

Table 4: Table of amino-acid doublet properties