I'm not a robot

L amino asitin d amino asite dönüşmesi

Of the 20 common amino acids in the human body that build our proteins, each of them (except for glycine) occur in two isomeric forms: L-forms and D-forms. This means that the same components of the molecules can be arranged in two different orders, a tad like how a palindrome is the same word backwards as forwards (like "radar" and "kayak"). Actually with L- vs. D-amino acids, it's more like the playful term for a word that backwards becomes a different word, a "Semordnilap" (which is "palindromes" spelled backwards). As Oprah Winfrey named her company Harpo Studios, or the town of Retsof, New York, was named for salt mine owner William Foster. Wolf vs. flow, room vs. moor, star vs. rats: the same letters, arranged exactly backwards, that then come to hold a whole new meaning. That is the basic difference between L- and D-form amino acids. The rest of this article will provide more detail and context. What Do the L and the D Stand For? It's easy to assume that if something is called L-form, that must mean it's in the form of an L, like a sectional sofa, or that D-form would refer to a half-moon shape, like a semi-circular booth in a restaurant, but that's not what those letters stand for here. In this context, the L and the D are referring to the order the side chain structures attach to an amino acid's central carbon atom (also known as the chiral carbon or alpha carbon). Those groups are: a single hydrogen atom (H); a carboxyl group (or COOH group); an amine group (or NH2 group); and the distinguishing R group which mostly differentiates one amino acid from another. Picture a pair of pinwheels with four color petals (the four functional groups) attached to the centers (the alpha carbon or chiral molecules). The L-form's colors follow the alphabet and go blue, green, red, yellow if your eyes read it like a clock; your eyes read clockwise, while the wheel spins counterclockwise. The D-form goes the opposite way: to read it in the order of blue, green, red, then yellow, D-form will have to spin clockwise, while you read it backwards, eyes traveling in the counterclockwise direction. "L" Stands for "Levorotation" In order for your eyes to read the amino acid correctly (in alphabetical color order) the molecule itself must rotate counterclockwise, or to the left. Levorotation refers specifically to that counterclockwise rotation. "D" Stands for "Dextrorotation" In order for your eyes to read the amino acid in alphabetical color order, the molecule must spin clockwise, or to the right. The prefix of dextrorotation comes from the Latin, dextro, meaning "to the right." Your right hand is your dexterous one, and the left hand in the Latin would be your sinister one (many apologies to the left-handed among us; like right-handed writing desks and scissors weren't enough, you are also designated sinister as well). How to Remember Which Is Which If you know you're not going to remember the Latin, just remember this: L stands for left-moving: The molecule rotates left so you can read its structure forward, towards the right. D stands for your dextrous right hand: The molecule spins right so that you're reading its structure counterclockwise, backwards towards the left. L- vs. D-Amino Acids: What Do They Do? This section will attempt to clarify the properties of L- and D-form amino acids, what makes them different, and what they have in common. L-Amino Acids L-amino acids are the molecules used to produce proteins in the human body and are divided into nonessential amino acids and essential amino acids (which we must get from consuming our food). In fact, L-amino acids occur in all proteins made by animals (including humans), plants, bacteria, and fungi. They serve as both hormones and enzymes, regulating the functions in the body. L-amino acids are also the ones that can be produced by lightning reactions, possibly the origin of the organic compounds of life on Earth, and the building blocks of our proteins. D-Amino Acids The D-forms of amino acids are mirror images of the L-form amino acids. D-amino acids are not incorporated into proteins; however, D-serine acts as a neurotransmitter in the brain. Some D-amino acids can be found in bacterial cell walls, but again, not in bacterial proteins. The Similarity They are each one of the two forms that amino acids can take in nature. Normal chemical synthesis of amino acids always creates a racemic mixture, which is a mixture of equal parts L- and D-amino acids. They are mirror images of one another, and each contain a central carbon atom, a hydrogen atom, a carboxylic acid group, an amine group, and an R group carbon chain. They are like identical twins born to be the reverse of one another, as in this real case of twin boys who were nearly conjoined, but instead were born with their livers, hearts, and spleens on opposite corresponding sides of their bodies. That means one twin has a condition called dextrocardia, where his heart points towards the dextrous or right side of his body, instead of the left side. They are identical, but with opposite features, as in one of the boys is right-handed, and the other, left-handed. (Interestingly enough, there is a chance that as many as a quarter of all identical twins could be mirror twins.) The Difference The main difference between these two formations is the location of the amine group in their structure, which designates how the amino acid will be used. L-amino acids are used in protein synthesis, while D-amino acids are not. L-aminos rotate counterclockwise or left in a process known as levorotation, while D-amino acids rotate clockwise to the right, in what's known as dextrorotation. Usage-wise, L-amino acids are used to produce proteins, making them vitally important to our healthy functioning, while D-amino acids are found instead in the cell walls of bacteria. Conclusion: L vs. D Hopefully the explanation and comparison of the L- and D-form amino acids has enlightened the subject and shown you their similarities and their differences: less like dexter vs. sinister, and more like brother-to-brother twins. Now that you know the science, how about you explore the benefits? Check out our premium amino acid supplements here. Share — copy and redistribute the material in any medium or format for any purpose, even commercially. Adapt — remix, transform, and build upon the material for any purpose, even commercially. The licensor cannot revoke these freedoms as long as you follow the license terms. Attribution — You must give appropriate credit , provide a link to the license, and indicate if changes were made . You may do so in any reasonable manner, but not in any way that suggests the licensor endorses you or your use. ShareAlike — If you remix, transform, or build upon the material, you must distribute your contributions under the same license as the original. No additional restrictions — You may not apply legal terms or technological measures that legally restrict others from doing anything the license permits. You do not have to comply with the license for elements of the material in the public domain or where your use is permitted by an applicable exception or limitation . No warranties are given. The license may not give you all of the permissions necessary for your intended use. For example, other rights such as publicity, privacy, or moral rights may limit how you use the material. Resim aminoasitlerin oluşturduğu bir polipeptid zincirini göstermektedir. Amino asitler (bazı kaynaklardaki yazılışıyla aminoasitler), proteinleri oluşturan temel yapı taşlarıdır. Proteinojenik amino asit, temel amino asit, Proteinojenik amino asit, Proteinojenik amino asit, proteinojenik olmayan amino asit, dallanmış zincirli aminoasit, ketojenik amino asit, glukojenik amino asit, glukojenik amino asit, ikincil amino asit, imino asit, D-Amino asit, dehidroamino asit türlerine bölünür. Kimyada bir aminoasit hem amin hem de karboksil fonksiyonel gruplar içeren bir moleküldür. Aminoasitlerin peptit bağlarıyla uç uca eklenmesiyle oluşturdukları kısa polimer zincirler "peptit", uzun polimer zincirler ise "polipeptit" veya "protein" olarak adlandırılırlar. Hücre içerisinde ribozomlar, mRNA moleküllerini kalıp olarak kullanarak amino asitleri uç uca ekleyerek proteinleri sentezlerler. Bu işleme translasyon (okuma) denir. Bahsedilen amino asitlerin hepsinin aynı anda herhangi bir proteinin yapıtaşında bulunması gerekmez. Ayrıca hepsi eşit miktarda da değildir. Proteinlerde bunlardan çok daha farklı amino asitler de bulunabilir. Proteinlerin toplam amino asit sayısı, içerdiği amino asit çeşidi sayısı ve sıralaması DNA'dan gelen komutlar sayesinde belirlenir. Farklı proteinler, 20 temel amino asitle oluşturulmuş polipeptitlerin daha sonra "farklılaşmaları" ile oluşur. Bu tür amino asit farklılaşmaları, proteinin özelliklerini ve işlevlerini oldukça fazla değiştirir. Örneğin çözünürlüklerini arttırabilir veya azaltabilir ya da diğer molekülerle etkileşmelerini düzenleyebilir. Amino asitlere ek olarak proteinler, çok daha farklı gruplar da barındırabilirler. Amino asit dışında, yapısında farklı türler barındıran proteinlere, "konjuge proteinler" denir. Konjuge proteinler, kovalent veya kovalent olmayan bağlarla, nükleik asitlerle nükleoproteinleri, lipitlerle lipoproteinleri, karbonhidratlarla glikoproteinleri ve daha birçok küçük molekül kütleli maddelerle, metallerle ve metal içeren gruplarla kompleks yapılar oluşturabilirler. Amino asitler aynı zamanda sadece sitoplazmada üretilirler.[kaynak belirtilmeli] Her amino asitin, bir karboksil ve bir de amino grubu vardır. Bu gruplar birbirlerinden α-karbon adı verilen tek bir C atomuyla ayrılırlar. Nötral sulu çözeltilerde α-karboksil grubu bir protonunu kaybeder ve eksi (-) yüklü hale geçer (− COO −) {\displaystyle {\ce {(-COO^-)}}} . Aynı şekilde α-amino grubuysa bir elektron kaybederek artı (+) yüklü olur − NH 3 + {\displaystyle {\ce {-NH3^+}}} . Amino asitlerin asimetrik merkezleri (kiral karbonları) vardır. Örneğin Glisin'de, amino asitin α-karbonu dört farklı gruba bağlanabilir. Bu sebepten her amino asit D veya L formunda bulunabilir. Ribozomlar üzerinde amino asit sentezinde her zaman L amino asit kullanılır. Sadece mikroorganizmalar, belli küçük peptitlerin sentezinde D amino asitlerini kullanırlar. İlginç bir örnek olarak, Güney Amerika ağaç kurbağasının derisinde sentezlenen bazı peptidler verilebilir. Bu peptidlerde D amino asitleri bulunmuştur. Bu peptitlerden "dermorphin", sıçan beyindeki opiate reseptörleri (beyindeki uyuşturucu madde reseptörleri) ile etkileşime girerek oldukça güçlü bir ağrı kesici etki göstermiştir. Bu kurbağaların sentezlediği peptitlerdeki D amino asitleri, peptitte daha önceden bulunan L amino asitleri ile birleşerek enzimleri aktive edebilmektedir. Polipeptidin ana zinciri, her amino asit için aynı olan grupların birleşimidir. Yan zincir veya R grubu ise, α-karbonuna bağlıdır ve 20 amino asitin her birinde farklıdır. Bu farklılık, proteinin kendine özgü oldukça değişik yapıları ve aktiviteleri kazandırır. Tüm amino asit yan zincirleri bir arada düşünüldüğünde, artı veya eksi yüklüden hidrofobiğe kadar oldukça fazla çeşitli yapısal özellikler gösterirler. Ayrıca bu yan zincirler, oldukça farklı çeşitlilikte kovalent ve nonkovalent bağların yapısına katılabilirler. Bir enzimin "aktif bölgesi", birçok farklı organik reaksiyonu katalizleyebilir. Yan zincirlerin çeşitli karakteristiği, molekülün yapısını ve aktivitesini belirleyen molekül içi (intramoleküler) etkileşimlerden, peptitin diğer polipeptitler gibi moleküllerle aralarındaki ilişkiyi belirleleyen moleküller arası etkileşimlere kadar birçok şeyi etkiler. Apolar aminoasitler, yan zincirlerinde hidrofobik özellik gösteren radikal grup bulundururlar. Elektrostatik bağlar yapamayan amino asitlerdir. Yan zincirlerinde, genellikle oksijen veya azot yoktur. Öncelikli olarak (bir proteindeki özel bir boşluğa hangi amino asitin en iyi şekilde uyabileceğini belirleyen) büyüklük ve şekillerine göre ayrılırlar. Van der Waals kuvvetleri ve hidrofobik etkileşimler sayesinde bir arada tutunurlar. Glisin Alanin Valin Lösin İzolösin Fenilalanin Triptofan Metiyonin Prolin Prolin bir iminoasittir, yani amino grubu değil imino grup taşır. Bunu kâğıt kromatografisinde farklı renge boyandığından da anlayabiliriz. Polar yüksüz aminoasitler, nötral pH'da yüksüzdürler. Bu gruptaki amino asitlerin yan zincirleri zayıf asit ve bazlardır. Fizyolojik pH'da tamamen yüklü değildirler, ancak kısmi artı (+) ve eksi (-) yükler içerirler. Bu sebeple, su da dahil olmak üzere, diğer moleküllerle H-bağı yapabilirler. Genelde oldukça reaktif amino asitlerdir. Serin Treonin Asparajin Sistein Glütamin Tirozin Ayrıca, iki Sisteinin disülfit bağı ile birleşmesiyle oluşan dipeptite sistin denir. Polar asidik aminoasitler, fizyolojik pH'da negatif yüklüdürler ve asidik özellik gösterirler. Aspartik asit Polar bazik aminoasitler, yan zincirlerinde proton alıcı moleküller taşırlar. Lizin Arjinin Histidin Aminoasit 3-Harf 1-Harf Yan zincir polaritesi Yan zincir asidite veya bazisite Hidropati endeksi[1] alanin ala A apolar nötr 1.8 arjinin arg R polar kuvvetli bazik -4.5 asparajin asn N polar nötr -3.5 aspartik asit asp D polar asidik -3.5 sistein cys C polar nötr 2.5 glütamik asit glu E polar asidik -3.111 glütamin gln Q polar nötr -3.5 glisin gly G apolar nötr -.4 histidin his H polar hafif bazik -3.2 izolösin ile I apolar nötr 4.5 lösin leu L apolar nötr 3.8 lizin lys K polar bazik -3.9 metiyonin met M apolar nötr 1.9 fenilalanin phe F apolar nötr 2.8 prolin pro P apolar nötr serin ser S polar nötr -.8 treonin thr T polar nötr -.7 triptofan trp W apolar nötr -.9 tirozin tyr Y polar nötr -1.3 valin val V apolar nötr 4.2 Yukarıdaki tabloda gösterilen 3-harfli ve 1-harfli aminoasit koduna ek olarak, kimyasal veya kristalografik analizler sonucunda bir proteinin belli bir pozisyonundaki aminoasit kesin olarak belirlenemediğinde, aşağıdaki tablodaki kısaltmalar da kullanılabilmektedir. Dejeneresite kodu 3-Harf 1-Harf asparajin veya aspartat asx B glütamin veya glütamat glx Z herhangi bir veya bilinmeyen unk X Proteinlerin yapısını oluşturan 20 çeşit amino asit arasında 10 tanesi temel amino asitler olarak adlandırılır. Bu amino asitler insan vücudu tarafından ihtiyacı karşılayacak düzeyde sentezlenemedikleri için dışarıdan beslenme yoluyla alımları zorunludur. Sistein, tirozin, histidin ve arjinin çocuklar için yarı zaruri aminoasitler olarak kabul edilmektedirler çünkü bunların sentezlenmesini yürüten metabolik reaksiyonlar çocuklarda tam olarak gelişmemiştir.[2] Temel aminoasitler Diğerleri İzolösin Alanin Lösin Asparajin Lizin Aspartik asit Metionin Sistein Fenilalanin Glutamik asit Treonin Glutamin Triptofan Glisin Valin Prolin Arjinin* Serin Histidin* Tirozin (*) Sadece özel durumlarda beslenme açısından dışarıdan alımı zaruridir. (Yenidoğanlarda ve üremili hastalarda) Prolin eskiden ikinci amin grubu yüzünden iminoasitler altında inceleniyordu, fakat bu tanımlama eskimiştir.[3] Artık non.esensiyel glutamik asitten oluşan bir aminoasit olarak değerlendirilmektedir.[4] Histidin kanda tamponlama görevinde kullanılır. Tirozin; vücudun rengini veren melanin pigmentinin yapımında, katekolaminlerin sentezinde kullanılır. Triptofan serotonin sentezinde rol oynar. Aspartat üre döngüsünde ürenin azotlarından birine kaynaklık eder. Glütamin toksik amonyağın toksik olmayan depo şeklidir. Protein yapısına sadece L-alfa amino asitler katılır. Glisin en küçük ve en iyi sığan amino asittir. Metiyonin Metilasyon reaksiyonlarında metil vericisidir. Komşu 2 sistein aminoasitleri arasında disülfit bağı oluşur. Adolph Strecker tarafından bulunan Strecker amino asit sentezi bir aldehit (ya da keton)dan bir dizi kimyasal reaksiyonla bir amino asit sentezlenmesidir.[5][6][7] Aldehit potasyum siyanür eşliğinde amonyum klorür ile bir α-aminonitril oluşturacak şekilde reaksiyona sokulur. Daha sonra bu α-aminonitril hidrolize edilerek istenilen amino asit elde edilir.[8][9] Orijinal Strecker reaksiyonunda asetaldehit, amonyak ve hidrojen siyanür ün verdiği reaksiyon ürünü, hidrolizlenerek alanin elde edilmiştir. Strecker amino asit sentezi Amonyum tuzlarının kullanımı ornatılmamış amino asitleri verirken, primer ve sekonder aminlerin kullanımı da ornatılmış amino asitleri verir. Aynı şekilde, aldehitlerin yerine ketonların kullanımı α,α-disubstitüe amino asitleri verir.[10] Adolph Strecker'in 1850 yılından beri uygulanan geleneksel sentezi rasemik α-amino nitrilleri verir iken son zamanlarda asimetrik yardımcı maddeler[11] ya da asimetrik katalizörler[12][13] kullanılarak değişik yöntemler geliştirilmiştir.[14] Strecker sentezinin günümüzde kullanıldığı bir örnek 3-metil-2-bütanon'dan başlayarak bir L-valin türevinin çok miktarda sentezlenmesidir:[15][16] Lippincott Illustrated Reviews Biochemistry Harper's Biochemistry S. Karp, Molecular Biology and Cell, Wiley & Sons., 1998. D. L. Nelson, M. M. Cox, Lehninger Principles of Biochemistry, Freeman and Co., 2005. ^ Kyte J & RF Doolittle (1982). "A simple method for displaying the hydropathic character of a protein". J. Mol. Biol., 157. ss. 105-132. PMID 7108955. ^ Imura K, Okada A (1998). "Amino acid metabolism in pediatric patients". Nutrition. 14 (1). ss. 143-8. 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" sayfasından alınmıştır 0 ratings0% found this document useful (0 votes)22 viewsSaveSave Amino Asit Ve Protein Metabolizması (PDFDrive) For Later0%0% found this document useful, undefined Organic compounds containing amine and carboxylic groups This article is about the class of chemicals. For the structures and properties of the standard proteinogenic amino acids, see Proteinogenic amino acid. Structure of a typical L-alpha-amino acid in the "neutral" form Amino acids are organic compounds that contain both amino and carboxylic acid functional groups.[1] Although over 500 amino acids exist in nature, by far the most important are the 22 α-amino acids incorporated into proteins.[2] Only these 22 appear in the genetic code of life.[3][4] Amino acids can be classified according to the locations of the core structural functional groups (alpha- (α-), beta- (β-), gamma- (γ-) amino acids, etc.); other categories relate to polarity, ionization, and side-chain group type (aliphatic, acyclic, aromatic, polar, etc.). In the form of proteins, amino-acid residues form the second-largest component (water being the largest) of human muscles and other tissues.[5] Beyond their role as residues in proteins, amino acids participate in a number of processes such as neurotransmitter transport and biosynthesis. It is thought that they played a key role in enabling life on Earth and its emergence.[6] Amino acids are formally named by the IUPAC-IUBMB Joint Commission on Biochemical Nomenclature in terms of the fictitious "neutral" structure shown in the illustration. For example, the systematic name of alanine is 2-aminopropanoic acid, based on the formula CH3−CH(NH2)−COOH. The Commission justified this approach as follows:[7] The systematic names and formulas given refer to hypothetical forms in which amino groups are unprotonated and carboxyl groups are undissociated. This convention is useful to avoid various nomenclatural problems but should not be taken to imply that these structures represent an appreciable fraction of the amino-acid molecules. The first few amino acids were discovered in the early 1800s.[8][9] In 1806, French chemists Louis-Nicolas Vauquelin and Pierre Jean Robiquet isolated a compound from asparagus that was subsequently named asparagine, the first amino acid to be discovered.[10][11] Cystine was discovered in 1810,[12] although its monomer, cysteine, remained undiscovered until 1884.[13][11][a] Glycine and leucine were discovered in 1820.[14] The last of the 20 common amino acids to be discovered was threonine in 1935 by William Cumming Rose, who also determined the essential amino acids and established the minimum daily requirements of all amino acids for optimal growth.[15][16] The unity of the chemical category was recognized by Wurtz in 1865, but he gave no particular name to it.[17] The first use of the term "amino acid" in the English language dates from 1898,[18] while the German term, Aminosäure, was used earlier.[19] Proteins were found to yield amino acids after enzymatic digestion or acid hydrolysis. In 1902, Emil Fischer and Franz Hofmeister independently proposed that proteins are formed from many amino acids, whereby bonds are formed between the amino group of one amino acid with the carboxyl group of another, resulting in a linear structure that Fischer termed "peptide".[20] The 21 proteinogenic α-amino acids found in eukaryotes, grouped according to their side chains' pKa values and charges carried at physiological pH (7.4) 2-, alpha-, or α-amino acids[21] have the generic formula H2NCHRCOOH in most cases,[b] where R is an organic substituent known as a "side chain".[22] Of the many hundreds of described amino acids, 22 are proteinogenic ("protein-building").[23][24][25] It is these 22 compounds that combine to give a vast array of peptides and proteins assembled by ribosomes.[26] Non-proteinogenic or modified amino acids may arise from post-translational modification or during nonribosomal peptide synthesis. The carbon atom next to the carboxyl group is called the α-carbon. In proteinogenic amino acids, it bears the amine and the R group or side chain specific to each amino acid, as well as a hydrogen atom. With the exception of glycine, for which the side chain is also a hydrogen atom, the α-carbon is stereogenic. All chiral proteogenic amino acids have the L configuration. They are "left-handed" enantiomers, which refers to the stereoisomers of the alpha carbon. A few D-amino acids ("right-handed") have been found in nature, e.g., in bacterial envelopes, as a neuromodulator (D-serine), and in some antibiotics.[27][28] Rarely, D-amino acid residues are found in proteins, and are converted from the L-amino acid as a post-translational modification.[29][c] Five amino acids possess a charge at neutral pH. Often these side chains appear at the surfaces on proteins to enable their solubility in water, and side chains with opposite charges form important electrostatic contacts called salt bridges that maintain structures within a single protein or between interfacing proteins.[32] Many proteins bind metal into their structures specifically, and these interactions are commonly mediated by charged side chains such as aspartate, glutamate and histidine. Under certain conditions, each ion-forming group can be charged, forming double salts.[33] The two negatively charged amino acids at neutral pH are aspartate (Asp, D) and glutamate (Glu, E). The anionic carboxylate groups behave as Brønsted bases in most circumstances.[32] Enzymes in very low pH environments, like the aspartic protease pepsin in mammalian stomachs, may have catalytic aspartate or glutamate residues that act as Brønsted acids. Functional groups found in histidine (left), lysine (middle) and arginine (right) There are three amino acids with side chains that are cations at neutral pH: arginine (Arg, R), lysine (Lys, K) and histidine (His, H). Arginine has a charged guanidino group and lysine a charged alkyl amino group, and are fully protonated at pH 7. Histidine's imidazole group has a pKa of 6.0, and is only around 10% protonated at neutral pH. Because histidine is easily found in its basic and conjugate acid forms it often participates in catalytic proton transfers in enzyme reactions.[32] The polar, uncharged amino acids serine (Ser, S), threonine (Thr, T), asparagine (Asn, N) and glutamine (Gln, Q) readily form hydrogen bonds with water and other amino acids.[32] They do not ionize in normal conditions, a prominent exception being the catalytic serine in serine proteases. This is an example of severe perturbation, and is not characteristic of serine residues in general. Threonine has two chiral centers, not only the L (2S) chiral center at the α-carbon shared by all amino acids apart from achiral glycine, but also (3R) at the β-carbon. The full stereochemical specification is (2S,3R)-L-threonine. Nonpolar amino acid interactions are the primary driving force behind the processes that fold proteins into their functional three dimensional structures.[32] None of these amino acids' side chains ionize easily, and therefore do not have pKas, with the exception of tyrosine (Tyr, Y). The hydroxyl of tyrosine can deprotonate at high pH forming the negatively charged phenolate. Because of this one could place tyrosine into the polar, uncharged amino acid category, but its very low solubility in water matches the characteristics of hydrophobic amino acids well. Several side chains are not described well by the charged, polar and hydrophobic categories. Glycine (Gly, G) could be considered a polar amino acid since its small size means that its solubility is largely determined by the amino and carboxylate groups. However, the lack of any side chain provides glycine with a unique flexibility among amino acids with large ramifications to protein folding.[32] Cysteine (Cys, C) can also form hydrogen bonds readily, which would place it in the polar amino acid category, though it can often be found in protein structures forming covalent bonds, called disulphide bonds, with other cysteines. These bonds influence the folding and stability of proteins, and are essential in the formation of antibodies. Proline (Pro, P) has an alkyl side chain and could be considered hydrophobic, but because the side chain joins back onto the alpha amino group it becomes particularly inflexible when incorporated into proteins. Similar to glycine this influences protein structure in a way unique among amino acids. Selenocysteine (Sec, U) is a rare amino acid not directly encoded by DNA, but is incorporated into proteins via the ribosome. Selenocysteine has a lower redox potential compared to the similar cysteine, and participates in several unique enzymatic reactions.[34] Pyrrolysine (Pyl, O) is another amino acid not encoded in DNA, but synthesized into protein by ribosomes.[35] It is found in archaeal species where it participates in the catalytic activity of several methyltransferases. Amino acids with the structure NH+3−CXY−CXY−CO−2, such as β-alanine, a component of carnosine and a few other peptides, are β-amino acids. Ones with the structure NH+3−CXY−CXY−CXY−CO−2 are γ-amino acids, and so on, where X and Y are two substituents (one of which is normally H).[7] Main article: Zwitterion Ionization and Brønsted character of N-terminal amino, C-terminal carboxylate, and side chains of amino acid residues The common natural forms of amino acids have a zwitterionic structure, with −NH+3 (−NH+2− in the case of proline) and −CO−2 functional groups attached to the same C atom, and are thus α-amino acids, and are the only ones found in proteins during translation in the ribosome. In aqueous solution at pH close to neutrality, amino acids exist as zwitterions, i.e. as dipolar ions with both NH+3 and CO−2 in charged states, so the overall structure is NH+3−CHR−CO−2. At physiological pH the so-called "neutral forms" −NH2−CHR−CO2H are not present to any measurable degree.[36] Although the two charges in the zwitterion structure add up to zero it is misleading to call a species with a net charge of zero "uncharged". In strongly acidic conditions (pH below 3), the carboxylate group becomes protonated and the structure becomes an ammonio carboxylic acid, NH+3−CHR−CO2H. This is relevant for enzymes like pepsin that are active in acidic environments such as the mammalian stomach and lysosomes, but does not significantly apply to intracellular enzymes. In highly basic conditions (pH greater than 10, not normally seen in physiological conditions), the ammonio group is deprotonated to give NH2−CHR−CO−2. Although various definitions of acids and bases are used in chemistry, the only one that is useful for chemistry in aqueous solution is that of Brønsted:[37][38] an acid is a species that can donate a proton to another species, and a base is one that can accept a proton. This criterion is used to label the groups in the above illustration. The carboxylate side chains of aspartate and glutamate residues are the principal Brønsted bases in proteins. Likewise, lysine, tyrosine and cysteine will typically act as a Brønsted acid. Histidine under these conditions can act both as a Brønsted acid and a base. Composite of titration curves of twenty proteinogenic amino acids grouped by side chain category For amino acids with uncharged side-chains the zwitterion predominates at pH values between the two pKa values, but coexists in equilibrium with small amounts of net negative and net positive ions. At the midpoint between the two pKa values, the trace amount of net negative and trace of net positive ions balance, so that average net charge of all forms present is zero.[39] This pH is known as the isoelectric point pI, so pI = 1/2(pKa1 + pKa2). For amino acids with charged side chains, the pKa of the side chain is involved. Thus for aspartate or glutamate with negative side chains, the terminal amino group is essentially entirely in the charged form −NH+3, but this positive charge needs to be balanced by the state with just one C-terminal carboxylate group is negatively charged. This occurs halfway between the two carboxylate pKa values: pI = 1/2(pKa1 + pKa(R)), where pKa(R) is the side chain pKa.[38] Similar considerations apply to other amino acids with ionizable side-chains, including not only glutamate (similar to aspartate), but also cysteine, histidine, lysine, tyrosine and arginine with positive side chains. Amino acids have zero mobility in electrophoresis at their isoelectric point, although this behaviour is more usually exploited for peptides and proteins than single amino acids. Zwitterions have minimum solubility at their isoelectric point, and some amino acids (in particular, with nonpolar side chains) can be isolated by precipitation from water by adjusting the pH to the required isoelectric point. The 20 canonical amino acids can be classified according to their properties. Important factors are charge, hydrophilicity or hydrophobicity, size, and functional groups.[28] These properties influence protein structure and protein–protein interactions. The water-soluble proteins tend to have their hydrophobic residues (Leu, Ile, Val, Phe, and Trp) buried in the middle of the protein, whereas hydrophilic side chains are exposed to the aqueous solvent. (In biochemistry, a residue refers to a specific monomer within the polymeric chain of a polysaccharide, protein or nucleic acid.) The integral membrane proteins tend to have outer rings of exposed hydrophobic amino acids that anchor them in the lipid bilayer. Some peripheral membrane proteins have a patch of hydrophobic amino acids on their surface that sticks to the membrane. In a similar fashion, proteins that have to bind to positively charged molecules have surfaces rich in negatively charged amino acids such as glutamate and aspartate, while proteins binding to negatively charged molecules have surfaces rich in positively charged amino acids like lysine and arginine. For example, lysine and arginine are present in large amounts in the low-complexity regions of nucleic-acid binding proteins.[40] There are various hydrophobicity scales of amino acid residues.[41] Some amino acids have special properties. Cysteine can form covalent disulfide bonds to other cysteine residues. Proline forms a cycle to the polypeptide backbone, and glycine is more flexible than other amino acids. Glycine and proline are strongly present within low complexity regions of both eukaryotic and prokaryotic proteins, whereas the opposite is the case with cysteine, phenylalanine, tryptophan, methionine, valine, leucine, isoleucine, which are highly reactive, or complex, or hydrophobic.[40][42][43] Many proteins undergo a range of posttranslational modifications, whereby additional chemical groups are attached to the amino acid residue side chains sometimes producing lipoproteins (that are hydrophobic),[44] or glycoproteins (that are hydrophilic)[45] allowing the protein to attach temporarily to a membrane. For example, a signaling protein can attach and then detach from a cell membrane, because it contains cysteine residues that can have the fatty acid palmitic acid added to them and subsequently removed.[46] "Amino acid code" redirects here. For base-pair encoding of amino acids, see Genetic code § Codons. Main article: Proteinogenic amino acid Although one-letter symbols are included in the table, IUPAC–IUBMB recommend[7] that "Use of the one-letter symbols should be restricted to the comparison of long sequences". The one-letter notation was chosen by IUPAC-IUB based on the following rules:[47] Initial letters are used where there is no ambiguity: C cysteine, H histidine, I isoleucine, M methionine, S serine, V valine,[47] Where arbitrary assignment is needed, the structurally simpler amino acids are given precedence: A Alanine, G glycine, L leucine, P proline, T threonine,[47] F PHenylalanine and R aRginine are assigned by being phonetically suggestive,[47] W tryptophan is assigned based on the double ring being visually suggestive to the bulky letter W,[47] K lysine and Y tyrosine are assigned as alphabetically nearest to their initials L and T (note that U was avoided for its similarity with V, while X was reserved for undetermined or atypical amino acids); for tyrosine the mnemonic tYrosine was also proposed,[48] D aspartate was assigned arbitrarily, with the proposed mnemonic asparDic acid;[49] E glutamate was assigned in alphabetical sequence being larger by merely one methylene –CH2– group,[48] N asparagine was assigned arbitrarily, with the proposed mnemonic asparagiNe;[49] Q glutamine was assigned in alphabetical sequence of those still available (note again that O was avoided due to similarity with D), with the proposed mnemonic Qlutamine.[49] Amino acid 3- and 1-letter symbols Side chain Hydropathy index[50] Molar absorptivity[51] Molecular mass Abundance in proteins (%)[52] Standard genetic coding,IUPAC notation 3 1 Class Chemical polarity[53] Net chargeat pH 7.4[53] Wavelength,λmax (nm) Coefficient ε(mM−1·cm−1) Alanine Ala A Aliphatic Nonpolar Neutral 1.8 89.094 8.76 GCN Arginine Arg R Fixed cation Basic polar Positive −4.5 174.203 5.78 MGR, CGY[d] Asparagine Asn N Amide Polar Neutral −3.5 132.119 3.93 AAY Aspartate Asp D Anion Brønsted base Negative −3.5 133.104 5.49 GAY Cysteine Cys C Thiol Brønsted acid Neutral 2.5 250 0.3 121.154 1.38 UGY Glutamine Gln Q Amide Polar Neutral −3.5 146.146 3.9 CAR Glutamate Glu E Anion Brønsted base Negative −3.5 147.131 6.32 GAR Glycine Gly G Aliphatic Nonpolar Neutral −0.4 75.067 7.03 GGN Histidine His H Cationic Brønsted acid and base Positive, 10%Neutral, 90% −3.2 211 5.9 155.156 2.26 CAY Isoleucine Ile I Aliphatic Nonpolar Neutral 4.5 131.175 5.49 AUH Leucine Leu L Aliphatic Nonpolar Neutral 3.8 131.175 9.68 YUR, CUY[e] Lysine Lys K Cation Brønsted acid Positive −3.9 146.189 5.19 AAR Methionine Met M Thioether Nonpolar Neutral 1.9 149.208 2.32 AUG Phenylalanine Phe F Aromatic Nonpolar Neutral 2.8 257, 206, 188 0.2, 9.3, 60.0 165.192 3.87 UUY Proline Pro P Cyclic Nonpolar Neutral −1.6 115.132 5.02 CCN Serine Ser S Hydroxylic Polar Neutral −0.8 105.093 7.14 UCN, AGY Threonine Thr T Hydroxylic Polar Neutral −0.7 119.119 5.53 ACN Tryptophan Trp W Aromatic Nonpolar Neutral −0.9 280, 219 5.6, 47.0 204.228 1.25 UGG Tyrosine Tyr Y Aromatic Brønsted acid Neutral −1.3 274, 222, 193 1.4, 8.0, 48.0 181.191 2.91 UAY Valine Val V Aliphatic Nonpolar Neutral 4.2 117.148 6.73 GUN Two additional amino acids are in some species coded for by codons that are usually interpreted as stop codons: 21st and 22nd amino acids 3-letter 1-letter Molecular mass Selenocysteine Sec U 168.064 Pyrrolysine Pyl O 255.313 In addition to the specific amino acid codes, placeholders are used in cases where chemical or crystallographic analysis of a peptide or protein cannot conclusively determine the identity of a residue. They are also used to summarize conserved protein sequence motifs. The use of single letters to indicate sets of similar residues is similar to the use of abbreviation codes for degenerate bases.[54][55] Ambiguous amino acids 3-letter 1-letter Amino acids included Codons included Any / unknown Xaa X All NNN Asparagine or aspartate Asx B D, N RAY Glutamine or glutamate Glx Z E, Q SAR Leucine or isoleucine Xle J I, L YTR, ATH, CTY[f] Hydrophobic Φ V, I, L, F, W, Y, M NTN, TAY, TGG Aromatic Ω F, W, Y, H YWY, TTY, TGG[g] Aliphatic (non-aromatic) Ψ V, I, L, M VTN, TTR[h] Small π P, G, A, S BCN, RGY, GGR Hydrophilic ζ S, T, H, N, Q, E, D, K, R VAN, WCN, CGN, AGY[i] Positively-charged + K, R, H ARR, CRY, CGR Negatively-charged − D, E GAN Unk is sometimes used instead of Xaa, but is less standard. Ter or * (from termination) is used

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Media related to Amino acids at Wikimedia Commons Retrieved from " 2 2-Aminoisobutyric acid Names Preferred IUPAC name 2-Amino-2-methylpropanoic acid Other names α-Aminoisobutyric acid2-Methylalanine Identifiers CAS Number 62-57-7 Y 3D model (JSmol) Interactive image ChEBI CHEBI:27971 Y ChemSpider 5891 Y DrugBank DB02952 Y ECHA InfoCard 100.000.495 EC Number 200-544-0 KEGG C03665 Y PubChem CID 6119 UNII 1E7ZW41IQU Y CompTox Dashboard (EPA) DTXSID0058772 InChI InChI=1S/C4H9NO2/c1-4(2,5)3(6)7/h5H2,1-2H3,(H,6,7) YKey: FUOOLUPWFVMBKG-UHFFFAOYSA-N YInChI=1/C4H9NO2/c1-4(2,5)3(6)7/h5H2,1-2H3,(H,6,7)Key: FUOOLUPWFVMBKG-UHFFFAOYAD SMILES O=C(O)C(N)(C)C Properties Chemical formula C4H9NO2 Molar mass 103.12 g/mol Appearance white crystalline powder Density 1.09 g/mL Boiling point 204.4 °C (399.9 °F; 477.5 K) Solubility in water soluble Acidity (pKa) 2.36 (carboxyl; H2O)10.21 (amino; H2O)[1] Except where otherwise noted, data are given for materials in their standard state (at 25 °C [77 °F], 100 kPa). Y verify (what is YN ?) Infobox references Chemical compound 2-Aminoisobutyric acid (also known as α-aminoisobutyric acid, AIB, α-methylalanine, or 2-methylalanine) is the non-proteinogenic amino acid with the structural formula H2N-C(CH3)2-COOH. It is rare in nature, having been only found in meteorites,[2] and some antibiotics of fungal origin, such as alamethicin and some lantibiotics. In the laboratory, 2-aminoisobutyric acid may be prepared from acetone cyanohydrin, by reaction with ammonia followed by hydrolysis.[3] Industrial scale synthesis can be achieved by the selective hydroamination of methacrylic acid. 2-Aminoisobutyric acid is not one of the proteinogenic amino acids and is rather rare in nature (cf. non-proteinogenic amino acids). It is a strong helix inducer in peptides due to Thorpe–Ingold effect of its gem-dimethyl group.[4] Oligomers of AIB form 310 helices. 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