

# On the use of sequence homologies to predict protein structure: Identical pentapeptides can have completely different conformations

(cooperativity/protein folding/amino acid sequence homology)

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Communicated by Sir John Kendrew, November 9, 1983

**ABSTRACT** The search for amino acid sequence homologies can be a powerful tool for predicting protein structure. Discovered sequence homologies are currently used in predicting the function of oncogene proteins. To sharpen this tool, we investigated the structural significance of short sequence homologies by searching proteins of known three-dimensional structure for subsequence identities. In 62 proteins with 10,000 residues, we found that the longest isolated homologies between unrelated proteins are five residues long. In 6 (out of 25) cases we saw surprising structural adaptability: the same five residues are part of an  $\alpha$ -helix in one protein and part of a  $\beta$ -strand in another protein. These examples show quantitatively that pentapeptide structure within a protein is strongly dependent on sequence context, a fact essentially ignored in most protein structure prediction methods: just considering the local sequence of five residues is not sufficient to predict correctly the local conformation (secondary structure). Cooperativity of length six or longer must be taken into account. Also, we are warned that in the growing practice of comparing a new protein sequence with a data base of known sequences, finding an identical pentapeptide sequence between two proteins is not a significant indication of structural similarity or of evolutionary kinship.

The folding process of a globular protein is highly selective: a long amino acid chain ends up in one or a few out of a huge number of possible three-dimensional conformations. In contrast, conformational preference of single amino acid residues is weak. So the high selectivity of protein folding is only possible through the interaction of many residues. What is the minimum number of residues for folding into a unique structure? Five residues can form more than one turn of an  $\alpha$ -helix or an entire  $\beta$ -strand. Cooperativity of length five could therefore be deemed sufficient for stabilization of secondary structure. We were thus surprised by the discovery of amino acid sequences of length five that in one protein are in  $\alpha$ -helical and in another, quite different protein, in  $\beta$ -sheet conformation.

## Search for Identical Oligopeptides

Detailed knowledge of protein structure comes mainly from the more than 100 three-dimensional structures solved by x-ray crystallography (1). Of these, at least 62 are known to sufficient resolution to allow assignment of details of hydrogen-bonded (secondary) structure (2). A systematic search among these 62 proteins revealed 25 subsequence identities of length five, not counting identities flanked by more extensive sequence homology. For example, the sequence Lys-Val-Leu-Asp-Ala occurs both in prealbumin and in carbonic anhydrase, two proteins otherwise unrelated in sequence, function, or structural type.

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**Probability of Occurrence.** A systematic search for identical pentapeptides seems not to have been undertaken previously, perhaps because one intuitively, but wrongly, does not expect to find any. An old party joke is analogous: one intuitively does not expect to find two identical birthdays in a group of 30 randomly chosen people, yet one can, statistically, be 70% certain of finding them by chance (3). What matters is not that the number of people is small compared with the number of days in a year but that the number of all possible pair comparisons among 30 people, 435, is larger than 365.

By analogy, the occurrence of identical pentapeptide sequences in unrelated proteins in the data base is actually highly probable: although the number of residues in the data base of known protein structures ( $10^4$ ) is very small compared with the number of possible pentapeptide sequences ( $20^5 = 3.2 \times 10^6$ ), the number of pair comparisons ( $5 \times 10^7$ ) is larger. More precisely, assume we have  $n$  amino acid residues arranged in random order with, for simplicity, frequency of occurrence of  $p = 1/20$  each. The probability that all possible pairs of peptides of length  $l$  are different is

$$P = (1 - p^l)^N, \quad [1]$$

where  $(1 - p^l)$  is the probability for two peptides of length  $l$  to be different and  $N = n(n - 1)/2$  is the number of pair comparisons. The formula holds for  $n \ll 1/p^l$  and neglects the complication of overlap of successive pentapeptides. For pentapeptides ( $l = 5$ ) in the data base of known protein structures ( $n = 10,000$ ), we calculate  $P = 2 \times 10^{-7}$ . The probability to find at least one pair is  $1 - P = 0.9999998$ . Thus the odds are more than 1,000,000:1 for finding one or more such pairs, and indeed we find 25 pairs.

For hexapeptides, the odds for finding one or more pairs in unrelated proteins are 1:1 ( $P = 0.5$ ,  $1 - P = 0.5$ ). Consistent with that, within the data base the systematic search yields none. Outside the data base, without a systematic search, we have so far found two: (i) Cys-Arg-Asp-Lys-Ala-Ser are residues 63–68 in rhodanese (data set 1RHD) and residues 151–156 in a gonococcal pilus protein (Thomas Meyer, personal communication) and (ii) Gly-Tyr-Ile-Thr-Asp-Gly are residues 92–97 in actinidin (data set 2ACT) and residues 68–73 in phage T4 DNA ligase (John Armstrong, personal communication).

## Conformation of Identical Pentapeptides

How similar in conformation are the discovered identical pentapeptides? A good objective measure of similarity of three-dimensional structure is the minimum rms distance [ $d(\text{rms})$ ] between the  $C(\alpha)$  atom positions of equivalent residues obtainable by rotation and translation (4). Table 1 gives the pentapeptide pairs in their sequence context ordered in terms of decreasing  $d(\text{rms})$ —i.e., increasing structural similarity. Considering that five residues can be more than one turn of an  $\alpha$ -helix and that many  $\beta$ -strands are not longer

Table 1. Conformation of identical pentapeptides occurring in two different proteins

Different conformation in different proteins ( $d > 2.5 \text{ \AA}$ )					Similar conformation in different proteins ( $d < 2.1 \text{ \AA}$ )				
$d, \text{ \AA}$	Protein subsequence (conformation)	Protein (secondary structure of pentapeptide)	Data set	Residues	$d, \text{ \AA}$	Protein subsequence (conformation)	Protein (secondary structure of pentapeptide)	Data set	Residues
4.5	NIEAD VNTFV ASHKP hhh hhhh hhhgg DRCKP VNTFV HESLA ss s eeeee s hh	erythrocrucorin (hemogl.) alpha-helix ribonuclease-s beta-strand	1ECD	80-84	2.0	CCQEA YGVSV IVGVP tb tt t eee e QGQTH YGVSV VGIGR t ees ss ee s	alcohol dehydrogenase thermolysin (protease)	4ADH	286-290 2TLN 251-255
4.3	CPLMV KVLDA VRGSP eee eeee tttee NPKLQ KVLDA LQAIA gggh hhhht gggt	prealbumin beta-strand carbonic anhydrase B alpha-helix	2PAB	6-10	2.0	AHTDF AGAEA AWGAT hhs g ggghh hhhh KFAGQ AGAEA ELAQR hhht tt tss ehhh	erythrocrucorin (hemogl.) cytochrome C551	1ECD	115-119 251C 38-42
4.1	DNGIR LAPVA ttee bb CTTNC LAPVA KVLHE hhhhh hhhh hhhh	acid protease beta-strand GP dehydrogenase alpha-helix	1APR	320-324	1.7	AKKIV SDGDG MNAWV hhhhh hsssg gggh LKAGD SDGDG KIGVD hhht tt ss ehhh	lysozyme (hen) Ca binding parvalbumin	7LYZ	100-104 1CPV 91-95
4.1	LIGQK VAHAL AEGLG hhhhh hhhh hht VSVNG VAHAL TAGHC eeett eeeee e hhh	triose phosph. isomerase alpha-helix strep. proteinase A beta-strand	1TIM	112-116	1.6	LMVKV LDAVR GSPAI eeee eett t tee PVYDS LDAVR RCALI hhhhh t t t hhhh	prealbumin lysozyme (phage)	2PAB	8-12 1LZM 91-95
4.1	LSGEE KAAVL ALWDK hhh hhhh hhhht KVIKC KAAVL WEEKK s eee eeeb stts	hemoglobin (horse) alpha-helix alcohol dehydrogenase beta-strand	2MHB	150-154	1.4	LLILP DEAAV GNLVG see ssttt gggt QQKRW DEAAV NLAKS hht tt tss sstts	acid protease lysozyme (phage)	1APR	229-233 1LZM 127-131
3.9	GFFSK IIGEL PNIEA hhhhh hhhht t hh LSKTF IIGEL HPDDR hgghg eeeee gggh	erythrocrucorin (hemogl.) alpha-helix cytochrome B5 beta-strand	1ECD	69-73	1.3	SLKPL SVSYD QATSL ts e eee t t NADAT SVSYD VDLND ts e eeeee tt	carbonic anhydrase C concanavalin A beta-strand	1CAC	45-49 3CNA 74-78
3.3	KITVL GVRQV GMACG eeee tthh hhhh AAKTD GVRQV QPNYQ sb s eeee ss h	lactate dehydrogenase alpha-helix start papain (protease) beta-strand	1LDX	27-31	1.2	TLFPP SSEEL QANKA e tttt ttt AIHPT SSEEL VTLLR sss sgggh ss	immunoglobulin glutathione reductase 3-10-helix	1FAB	117-121 2GRS 453-457
3.3	GNEGS TGSSS TVGYT s stts bt VTISC TGSSS NIGAG eeee e tt tttss	subtilisin BPN' immunoglobulin	1SBT	159-163	1.1	ELPGR SVIVG AGYIA s ss eeee shhh EAYGV SVIVG VPPDS ttt e eee tt	glutathione reductase beta-strand alcohol dehydrogenase beta-strand	2GRS	173-177 4ADH 289-293
3.1	FIPLS GGDIV VAHEL b gg g hhh hhhh DTQVQ GGDIV TGGPQ b sss b s tt	thermolysin acid protease	2TLN	135-139	0.6	GNWVC AAKFE SNFNT hhhhh hhhh tssbt KETA AAKFE RQHMD h hhhh hhhb	lysozyme (hen) alpha-helix ribonuclease-s alpha-helix	7LYZ	31-35 1RNS 5-9
3.1	KAGIQ LSKTF VKVVS stt e eette eeee TDARE LSKTF IIGEL hhhhh hgghg eeee	GP dehydrogenase cytochrome B5	1GPD	299-303	0.5	LTESQ AALVK SSWE t hhh hhhh hhhh ZKAND AALVK MRAAA ttth hhhh hhhh	leghemoglobin alpha-helix cytochrome B562 alpha-helix	1HBL	8-12 156B 28-32
3.0	LVKKM TDDKG AKTKM ttttt s s s KLGIQ TDDKG HIIVD ttt b tts b	cytochrome C550 glutathione reductase	155C	90-94	0.3	VFSTE LPASQ QSGHS e bss s hhh htts RYGFL LPASQ IIPTA sstt ggg hhhh	acid proteinase alpha-helix start carboxypeptidase 3-10-helix	1APP	46-50 1CPA 280-284
2.9	GRPIY VLKFS TGGSN s eee eeee s ss NAGVE VLKFS QVKEV tss eette eeee	carboxypeptidase glutathione reductase	1CPA	48-52					
2.8	DFPIA KGERQ SPVDI s ggg g ss ss ee AGIKK KGERQ DLVAY hhhhh hhhh	carbonic anhydrase C cytochrome C	1CAC	21-25					
2.6	LDNLK GTFAA LSELH ggghh hshh hhhh GGAUV GTFAA RVFPF ttee eeeee ee s	hemoglobin (horse) alpha lytic protease	2MHB	225-229					

Each pair of pentapeptide conformations is preceded by the structural dissimilarity  $d$ , the minimum possible rms distance between equivalent C( $\alpha$ ) positions. Pairs with the strongest structural discrepancy are listed first; those with the best structural agreement are listed last. Each occurrence of the pentapeptide is given with its (first line) local sequence context ( $\pm$  five residues), protein name, Protein Data Bank identifier, residue number range, and (second line) conformation/secondary structure (h,  $\alpha$ -helix; g, 3- to 10-helix; e,  $\beta$ -strand; b,  $\beta$ -bridge; t, three-, four-, or five-turn; s, bend; space, straight piece not in  $\beta$ -structure). Residue numbers and structure notation are from the Dictionary of Protein Secondary Structure (2) and may differ from those given elsewhere. The amino acid one-letter code is A, Ala; C, Cys; D, Asp; E, Glu; F, Phe; G, Gly; H, His; I, Ile; K, Lys; L, Leu; M, Met; N, Asn; P, Pro; Q, Gln; R, Arg; S, Ser; T, Thr; V, Val; W, Trp; Y, Tyr. Structural dissimilarity per atom,

$$d = \left[ \frac{1}{n-2} \sum_{i=1}^n (r_i - r'_i)^2 \right]^{1/2},$$

is normalized by  $n-2$ , the number of nontrivial degrees of freedom. This is because the superposition of sets of two C( $\alpha$ ) vectors trivially has  $d = 0$  due to the peptide bond geometry.

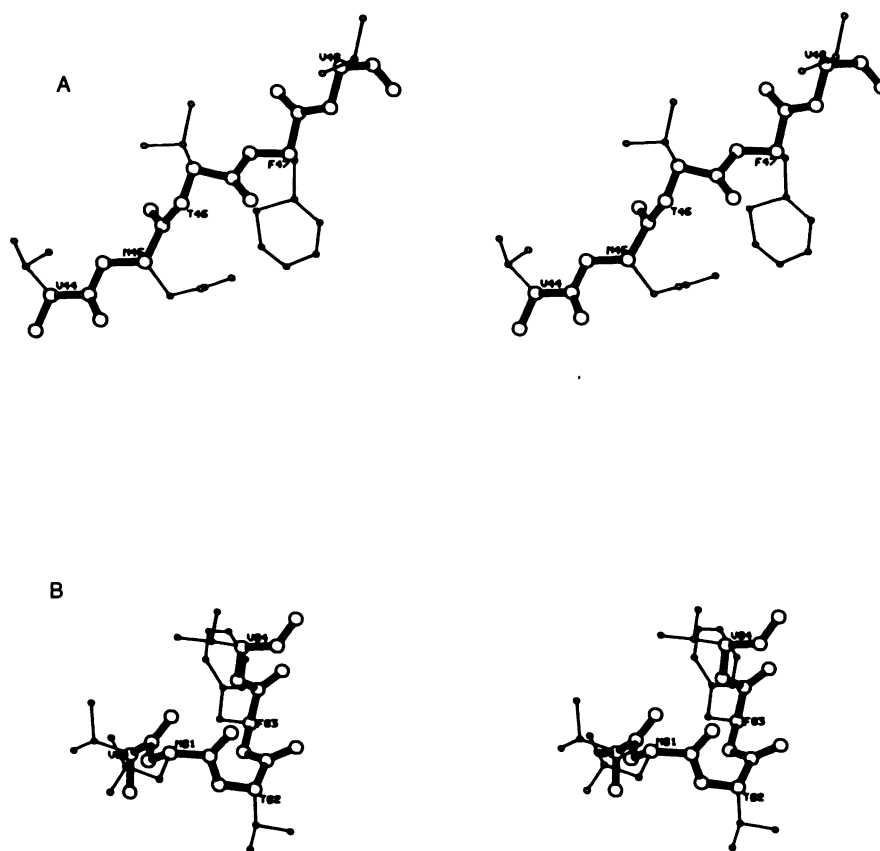


FIG. 1. Stereo view of variability of pentapeptide structure: the sequence Val-Asn-Thr-Phe-Val is part of a  $\beta$ -strand in ribonuclease (5) (A) and part of an  $\alpha$ -helix in the hemoglobin erythrocruorin (6) (B). The figure was drawn by using the program PLUTO (W. D. S. Motherwell, Crystallographic Data Centre, University Chemical Laboratory, Cambridge, England, personal communication).

than five residues (2), the observed differences in structure are surprising.

The most striking examples of "same sequence-different structure" are the seven pentapeptides Val-Asn-Thr-Phe-Val (Fig. 1), Lys-Val-Leu-Asp-Ala, Leu-Ala-Pro-Val-Ala, Val-Ala-His-Ala-Leu, Lys-Ala-Ala-Val-Leu, Ile-Ile-Gly-Glu-Leu, and Gly-Val-Arg-Gln-Val: each occurs once as part of an  $\alpha$ -helix and once as part of a  $\beta$ -strand, two very different types of hydrogen-bonded secondary structure. This is possible only if their structure is determined by sequence context—that is, by their interaction with other parts of the protein.

At the other extreme, "same sequence-same structure," each of the six protein subsequences Leu-Pro-Ala-Ser-Gln, Ala-Ala-Leu-Val-Lys, Ala-Ala-Lys-Phe-Glu, Ser-Val-Ile-Val-Gly, Ser-Ser-Glu-Glu-Leu, and Ser-Val-Ser-Tyr-Asp have very similar conformations in one protein and in another unrelated protein. As the sequence context for each occurrence is different, either the local conformational preference of these pentapeptides dominates over the interaction with neighboring segments or the influence of the neighboring segments is similar in each protein.

## Conclusions

**Interpretation of Amino Acid Sequence Comparisons.** In attempts to predict protein function, it has become routine to compare the sequence of a new protein with the data base of proteins whose structure or function is known (7). Significant homology is interpreted to imply similarity of structure or function. For example, the (very) probable function of the *sis* oncogene protein was dramatically elucidated by the discovery of a 100-residue homology with platelet-derived

growth factor (8, 9). Often, however, the discovered sequence homologies are marginal and the predictions, speculative. For example, weak homologies have been reported between the p21 protein of the *ras* oncogene family and, separately, an ATPase (10), some dinucleotide-binding enzymes (11), and the guanine nucleotide binding site of elongation factor Tu (R. Leberman and U. Schneider, personal communication). From these, partly conflicting (11) predictions of *ras* oncogene structure were derived. Our survey puts a definite lower bound on the length of an uninterrupted stretch of identical residues deemed statistically significant or structurally meaningful.

**Statistical Significance of Identical Pentapeptides.** The survey shows that an isolated uninterrupted homology of length five between a new protein and the data base is in itself not a safe indication of evolutionary kinship. The statement depends, of course, on the total length of the sequences compared. For example, suppose the new protein sequence has length  $m = 300$  and you find one pentapeptide identity between it and a protein in the data base of  $n = 10,000$  residues. Substituting in Eq. 1  $N = n \times m$ , the number of comparisons, we get  $P = 0.39$  for the probability not to find this identity by chance. Appropriate values for  $n$  and  $m$  must be used when comparing a given length of protein with a data base.

The danger of overinterpretation of temptingly strong but too short sequence homologies is, of course, a particular case of the general danger of overzealous homology searches. A good example of temptingly long but too weak homologies is the 16-residue homology dispersed among 129 residues between ribonuclease and lysozyme postulated by Manwell in 1967 (12) and shown by Haber and Koshland (13) as well as by others to be statistically insignificant. Inciden-

tally, the identical pentapeptide Ala-Ala-Lys-Phe-Glu (Table 1) was not part of Manwell's alignment.

**Structural Meaning of Identical Pentapeptides.** Table 1 shows that it is wrong to deduce similarity of conformation from a single pentapeptide homology between otherwise not homologous sequences. This result is independent of the size of the data base or any statistical estimate. It is, however, likely that particular pentapeptide sequences vary in structural adaptability.

**Message to Protein Folders.** Why is the accuracy of current widely used secondary structure prediction methods not better than 56% [correctly predicted residues in a three-state model (14)]? The structural discrepancies in Table 1 show that even complete statistics on the conformational preferences of pentapeptides (which would require at least 300 times the current data base) in themselves are not sufficient to correctly predict protein structure. The key to improved protein structure prediction is not better statistics but new approaches. Some are appearing (15, 16). We can be sure that the strictly hierarchical approach of first predicting secondary structure segments, then tertiary structure by interaction of those segments, cannot succeed unless cooperativity of sequence range larger than five is taken into account in the first step.

We thank the referees for suggestions and the Deutsche Forschungsgemeinschaft for support to the Protein Structure Theory project.

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