

Baseline levels of low-density lipoprotein cholesterol and lipoprotein (a) and the *AvaII* polymorphism of the low-density lipoprotein receptor gene influence the response of low-density lipoprotein cholesterol to pravastatin treatment[☆]

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Abstract

To investigate some individual and genetic factors that may influence the response of low-density lipoprotein cholesterol (LDL-C) to pravastatin treatment, we recruited 440 subjects with hypercholesterolemia (mean age, 57 years; 43% men) from 21 primary health care centers-outpatient clinics into a prospective, multicentered intervention trial. Pravastatin (20 mg/d) was prescribed for 16 weeks. The main outcome was the percentage variation in LDL-C concentration relative to baseline. Blood analyses and genotyping were performed centrally. The results indicated that LDL-C decreased by 20.5% (range, +21% to –66%) after pravastatin treatment. Baseline concentration of LDL-C (the higher the concentration, the greater the decrease), lipoprotein (a) levels (the lower the concentration, the greater the response), and *AvaII* polymorphism of the LDL-receptor gene significantly influenced the hypolipemic effect ($P < .001$, $P = .014$, and $P = .004$, respectively). These 3 factors combined explained 10.6% of the variation in LDL-C response. Age, sex, smoking habit, alcohol consumption, body mass index, and apolipoprotein E genotype had no significant effect on response. We conclude that baseline levels of LDL-C and lipoprotein (a) together with the *AvaII* polymorphism of the LDL-receptor gene have a significant influence on the LDL-C response to pravastatin treatment in patients monitored in a standard primary health care outpatient clinic setting.

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1. Introduction

The prescription of HMG-CoA reductase inhibitors (*statins*) has resulted in a consistent reduction in cardiovascular morbidity and mortality in primary as well as in secondary prevention trials [1–5]. Since their advent in the decade of the 1990s, the use of the statins has become generalized because of their high efficacy and low secondary effects. The average annual increase in their prescription has been

greater than 30% over the past few years in European countries [6]. Their principal action is the reduction of the plasma lipids by inducing a considerable decrease in the concentration of plasma LDL cholesterol while causing a moderate decrease in triglycerides and a modest increase in the concentration of high-density lipoprotein cholesterol (HDL-C) [1–5]. Other possible beneficial effects of the statins not directly related to the decrease in low-density lipoprotein cholesterol (LDL-C) have been described, including anti-inflammatory and antioxidant activities and plaque stabilization; the real importance of these effects remains to be clarified [7].

The statins reduce LDL-C levels between 20% and 60% [8] depending on the dose and type of the drug used. Nevertheless, there appears a wide interindividual variability

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in response to the same level of dose administered [9,10]. For example, in the WOS study, the percentage response of LDL-C to a fixed dose of 40 mg of pravastatin varied between –60% and +20%. This considerable variability in the hypolipidemic response has been attributable to individual environmental or genetic factors. Among these are sex [11–13], age [14,15], tobacco consumption [14], body mass index (BMI) [14,16], alcohol consumption [15], baseline levels of LDL-C [11,14–16], and the concentration of triglycerides [11,15]. The genetic factors studied to date include several polymorphisms of genes related to lipoprotein metabolism. However, their influence on response appears to be moderate and not universally observed in all of the studies [17]. Furthermore, the data generated from controlled clinical trials, with strict inclusion-exclusion criteria and follow-up, cannot be easily extrapolated to a free-living general population.

A better understanding of the factors that influence hypolipemic response could help identify patients who would best respond to the treatment. More importantly, perhaps, would be to identify patients who are likely to have a poor hypolipidemic response and to select a more appropriate treatment so as to avoid unnecessary costs and side effects.

The objective of the present study was to evaluate individual environmental and genetic factors that may influence the response of LDL-C to treatment with pravastatin in a population of subjects with hypercholesterolemia followed up in outpatient clinics.

2. Subjects and methods

The design of the study has been described previously [18]. Briefly, the subjects included in the present analysis participated in the RAP study, whose objective was to evaluate the factors that may influence hypolipidemic response to pravastatin. The RAP study is a prospective, multicentered intervention trial in which subjects with hypercholesterolemia who, despite a diet low in saturated fat and cholesterol, required hypolipemic drug therapy based on the National Cholesterol Education Program criteria [19]. Subjects received 20 mg/d of pravastatin over 16 weeks. Participants were recruited from 21 primary health care centers distributed throughout Spain and followed up by their respective physicians at the primary health care center where they provided blood samples before and after the 16 weeks of treatment. Among the exclusion criteria were the following: plasma triglycerides of greater than 4.5 mmol/L, diabetes mellitus, treatment with other hypolipemic agents, acute illness in the previous 3 months, serious or uncontrolled renal, hepatic, digestive, or endocrine disorders, secondary hypercholesterolemias, and those known to be hypersensitive to statins. Over a period of 8 months, there were 656 subjects recruited who, after the dietary phase, fulfilled the criteria for medication. In 442 subjects (76.4%), a complete clinical history was

obtained, lipid levels had been measured before and after the treatment, and compliance (assessed by pill counting), was greater than 80%. These patients represent the basis of the present analysis. To all patients with a BMI higher than 25 kg/m², a weight-reducing hypocaloric diet was prescribed. Included in the statistical analyses were age, sex, BMI, blood pressure, smoking habit, weight change, and consumption of alcohol. Alcohol intake was self-reported in units per week. The study was approved by the Committee on Ethics and Clinical Investigation of the Hospital Carlos III in Madrid.

3. Laboratory measurements

Venous blood was taken after a 12-hour fast. Cholesterol and triglycerides were measured using enzymatic methods (Boehringer Mannheim, Mannheim, Germany). High-density lipoprotein cholesterol was measured after the precipitation of the apolipoprotein B (apoB)-containing particles with phosphotungstic acid. Low-density lipoprotein cholesterol was calculated using the Friedewald formula. Lipoprotein (a) [Lp(a)] was determined using radioimmunoassay kits (Trinity Biotech, Bray, Ireland). All blood analyses were performed in a centralized laboratory.

The *PvuII* polymorphism of the LDL-receptor gene was determined after amplification of a 800-base pair (bp) fragment using the polymerase chain reaction (PCR) in a thermocycler (PTC-100 MJ Research, Mass). The primers used were 5'-TCC CCT TCA AAA TGC CCT CTT-3' and 5'-AGC CAC CGA GCC CAG CCT AAG AA-3'. The final volume for the PCR mixture was 25 μ L and contained 2 mmol/L of MgCl₂, 0.2 mmol/L of dNTP, and 1 U of Taq DNA polymerase. The amplification was for 30 cycles: 95°C for 1 minute, 63°C for 1 minute, and 72°C for 2 minutes 30 seconds. After the digestion of the PCR product with the restriction enzyme *PvuII*, the fragments were separated by electrophoresis in 1.5% agarose gel and visualized under UV light.

The *AvaII* polymorphism was determined after the PCR amplification of a 228-bp zone in exon 13 of the LDL-receptor gene. The primers were 5'-GTC ATC TTC CTT GCT GCC TGT TTA G-3' and 5'-GTT TCC ACA AGG AGG TTT CAA GGT T-3'. The 25- μ L PCR mixture contained 1.5 mmol/L of MgCl₂, 0.2 mmol/L of dNTP, 0.3 μ mol/L of each primer, and 1.5 U of Taq DNA polymerase. Amplification of the polymorphic region was performed with 28 cycles: 94°C for 1 minute, 68°C for 2 minutes, and 72°C for 1 minute. The digestion of the amplified product was performed with the restriction enzyme *AvaII*. The fragments were separated by electrophoresis in 2% agarose gels and visualized under UV light.

The apolipoprotein E (apoE) genotype was performed using PCR amplification of a 303-bp fragment. The primers were 5'-CGG GCA CGG CTG TCC AAG GAG-3' and 5'-CAC GCG GCC CTG TTC CAC GAG-3'. The 25- μ L PCR reaction mixture contained 1.6 mmol/L of MgCl₂,

0.2 mmol/L of dNTP, 10% of DMSO, and 1 U of Taq DNA polymerase. The amplification was for 30 cycles: 94°C for 30 seconds, 65°C for 30 seconds, and 72°C for 30 seconds. After the digestion of the PCR product with the restriction enzyme *Cfo*-1, the fragments were separated by electrophoresis in 8% polyacrylamide gels. Subsequently, the gel was treated with ethidium bromide and the fragments were visualized under UV light.

4. Statistical analyses

All the statistical analyses were performed with the SPSS statistical package (SPSS Inc, Chicago, Ill). Quantitative variables are presented as the mean and the SD and the qualitative variables as percentages. To check for normality of distribution, the Kolmogorov-Smirnov test was applied. The triglycerides and Lp(a) values were not normally distributed and needed to be log transformed before applying the statistical analyses. For a clearer presentation, the original nontransformed values are presented in the tables.

To evaluate the trends of the effects of pretreatment variables on LDL response, basal values of LDL-C and Lp(a) were segregated in quartiles. Comparisons between quantitative variables were performed by analysis of variance and between qualitative variables by the χ^2 test. Comparisons between lipid levels before and after the treatment were performed with the Student *t* test for paired samples. Relationships between LDL-C response and other measured variables were evaluated using linear regression analysis with the dependent variable being the percentage variation of the LDL-C relative to baseline. A multiple linear regression model was used to assess the simultaneous contributions of different variables. Only those variables that had *P* values less than .10 in the univariate analyses were included in the multivariate analyses. The *P* values for all tests were 2 tailed, and differences were considered to be statistically significant at the .05 level.

5. Results

Of the 440 participants, 43% were men and the overall mean age was 57.4 years. Table 1 summarizes the characteristics of the study population, including the baseline lipoprotein concentrations. There were no significant differences with respect to baseline characteristics between the subjects who were included and those who were excluded

Table 1
Patients' characteristics at baseline

Characteristic	N = 440
Age [y; mean (SD)]	57.4 (11.6)
Sex (% men)	43.0
BMI [kg/m ² ; mean (SD)]	27.2 (3.5)
Hypertensive (%)	38.3
Current smokers (%)	22.3
Alcohol intake [g/wk; mean (SD)]	59.9 (108)
Cardiovascular disease (%)	10.9

Table 2

Percentage variation, relative to baseline, of lipid and lipoprotein concentrations in the overall study population after treatment with pravastatin

	Baseline	Final	% Change	<i>P</i>
Cholesterol (mmol/L)	7.28 (1.10)	6.11 (1.02)	−15.5 (12.2)	<.001
LDL-C (mmol/L)	5.19 (1.06)	4.08 (0.96)	−20.5 (15.8)	<.001
HDL-C (mmol/L)	1.34 (0.96)	1.36 (0.34)	3.7 (19.6)	.097
Triglycerides (mmol/L)	1.60 (0.76)	1.45 (0.70)	−3.7 (35.4)	<.001
Lp(a) (mg/dL)	18.3 (16.0)	19.1 (16.4)	11.8 (67.4)	.015

All values are expressed as the mean (SD).

from the study (data not shown). The treatment with 20 mg/d of pravastatin significantly reduced total cholesterol, LDL-C, and triglyceride levels while increasing HDL-C (albeit without reaching statistical significance) and significantly increasing Lp(a) concentration (Table 2). Low-density lipoprotein cholesterol response varied between +21% and −66% (Fig. 1). Also, there was a mean weight loss of 0.360 kg (95%CI, 0.07–0.66; *P* = .015) during the study.

The *Pvu*II polymorphism of the LDL-receptor gene was determined in 331 subjects. The allelic frequency was 0.765 for the (−) allele and 0.235 for the (+) allele. The *Ava*II polymorphism of the LDL-receptor gene was determined in 335 subjects. The allelic frequency was 0.513 for the (−) allele and of 0.487 for the (+) allele. The apoE polymorphism was determined in 398 subjects. The allelic frequency was 0.016 for the ϵ 2 allele, 0.855 for the ϵ 3 allele, and 0.125 for the ϵ 4 allele. The 3 polymorphisms were distributed according to Hardy-Weinberg equilibrium (χ^2 = 0.432, *P* = .511; χ^2 = 0.374, *P* = .543; and χ^2 = 0.97, *P* = .808, respectively).

Among the pretreatment lipid levels, only the baseline concentrations of LDL-C (*P* < .001) and the Lp(a) (*P* = .011) significantly influenced the LDL-C response to treatment in the univariate analysis. To better assess this effect, the baseline concentrations of LDL-C and Lp(a) were divided into quartiles (Tables 3 and 4). The change in

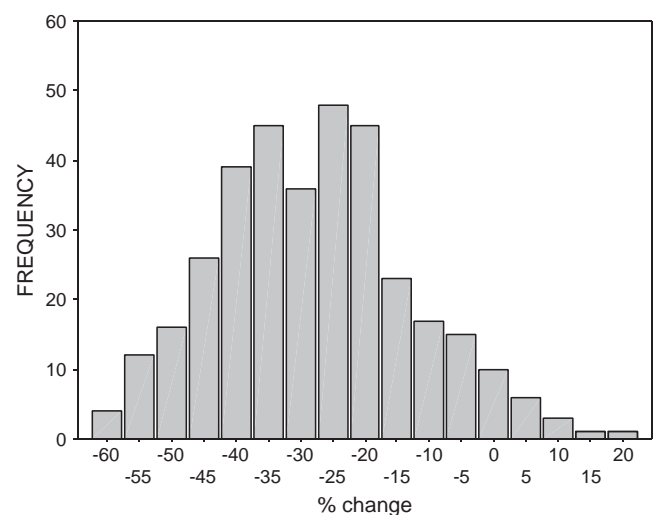


Fig. 1. Percentage change, relative to baseline, in LDL-C after treatment.

Table 3

Percentage and absolute decrease in LDL-C in the overall study population and when subjects were segregated into quartiles of baseline LDL-C concentrations

N = 440	All	Q1	Q2	Q3	Q4	P
Mean baseline (mmol/L)	5.19 (1.06)	4.04 (0.36)	4.80 (0.17)	5.40 (0.18)	6.59 (0.95)	–
Absolute decrease (mmol/L)	–1.11 (0.94)	–0.59 (0.69)	–0.93 (0.75)	–1.13 (0.77)	–1.81 (1.06)	.001
Percentage decrease	–20.5 (15.7)	–14.7 (16.8)	–19.4 (15.8)	–21.0 (14.3)	–27.1 (13.5)	.001

Values are expressed as the mean (SD) of each quartile.

LDL-concentration in response to treatment was significant in absolute values ($P < .001$) as well in percentages ($P < .001$) (Table 3). With respect to Lp(a), an elevation in baseline levels was related to a decrease in LDL-C response not only in absolute terms ($P = .022$) but also in percentages ($P = .018$) (Table 4). The mean percentage decrease of LDL-C in the subjects with Lp(a) of greater than 40 mg/dL was 13% and in those with Lp(a) of greater than 50 mg/dL was 9.7%.

To identify factors influencing the LDL-C response, we introduced several individual environmental and genetic factors into a univariate analysis. The results indicated that age, sex, BMI, alcohol consumption, weight change, smoking habit, and the presence of hypertension did not significantly influence the response of the LDL-C to pravastatin treatment.

In the univariate analysis, none of the 3 genotypes studied had a statistically significant effect on LDL-C response to treatment, although there was a significant trend in the *AvaII* polymorphism in that those homozygous for the (–) allele responded less than those heterozygous and these, in turn, responded less than those homozygous for the (+) allele (P of tendency = .032) (Table 5).

In the multivariate analysis, the only 3 factors significantly influencing the LDL-C response were the baseline LDL-C concentration, the baseline Lp(a) concentration, and the *AvaII* polymorphism (Table 6). These 3 variables together accounted for 10.6% of the variance in LDL-C response. In the multivariate analysis, none of the other variables including age, sex, and apoE polymorphism had any statistically significant effect on the LDL-C response to treatment.

6. Discussion

The results of the present study confirm the considerable variability of LDL-C response to a fixed dose of statin, the response varying between –66% and +21%. A daily dose of 20 mg of pravastatin produced a significant decrease in total cholesterol, LDL-C, and triglycerides, together with an increase in the HDL-C. These findings are similar to those

described in other studies using the same dose [20–22]. Similarly, the treatment produced a significant increase in the concentration of Lp(a) of slightly less than 1 mg/dL and which is of uncertain clinical relevance. It is not clear what the effects of the statins are in general, or pravastatin in particular, on the concentration of Lp(a). Generally, the concentration of Lp(a) is not modified with statin treatment [23–25] although increments [16,26] as well as decreases [27] have been described, but always in very modest amounts. Also, these increments have been described in studies of short duration [28], whereas in studies of longer duration, the concentrations remain constant [23,24]. The consensus appears to be that there is a transitory increase in Lp(a) concentrations in the first weeks of statin treatment that, subsequently, returns to baseline values.

Several authors have studied the effect of baseline lipid levels on the response to statin treatment [11,14–16,29]. All of them observed a direct association between the baseline concentration of the LDL-C and its decrease with the treatment. In our study, as with the study of Miserez et al [11], we observed that the decrease in LDL-C was greater when the baseline concentration was higher, not only in absolute levels but also in percentages. These findings can be explained on the basis of subjects with the higher concentrations of circulating cholesterol having a higher rate of cholesterol synthesis and a higher activity of HMG-CoA reductase (the rate-limiting enzyme in the intracellular synthesis of cholesterol). Hence, with administration of a statin, the inhibition of the enzyme would be higher and the resultant reduction in LDL-C would be greater.

In contrast to other authors, we did not find that the baseline concentration of triglycerides negatively influenced the response of LDL-C to treatment [11,15,30]. This may be better observed in the presence of hypertriglyceridemia [11] and, probably, would be caused by the LDL particles of these subjects being poorly bound to the LDL receptor because of its lower density and the different distributions of the apoB on the surface of the molecule [31]. In our study population, the mean concentration of the triglycerides was moderate, the selection criterion being subjects with less than 4.5 mmol/L, and only 5% of the subjects having had

Table 4

Percentage and absolute decrease in LDL-C in the overall study population and when subjects were segregated into quartiles of baseline Lp(a) concentrations

n = 434	All	Q1	Q2	Q3	Q4	P
Mean baseline (mg/dL)	18.0 (15.8)	1.6 (1.4)	8.8 (2.8)	21.4 (4.1)	39.5 (11.6)	–
Absolute decrease (mg/dL)	–1.12 (0.94)	–1.27 (1.10)	–1.14 (0.89)	–1.13 (0.89)	–0.95 (0.95)	.022
Percentage decrease	–20.5 (15.8)	–22.6 (16.3)	–21.6 (16.0)	–20.9 (14.2)	–17.4 (16.5)	.018

Values are expressed as the means (SD) for each quartile.

levels of greater than 3 mmol/L. Hence, this masking effect is less likely to be observed.

The baseline concentration of Lp(a) was inversely related to the LDL-C response to treatment with pravastatin: the higher the concentration of Lp(a), the lower the decrease in LDL-C. This effect has not been described previously but can be explained quite logically. Lipoprotein (a) is a particle within the LDL and in which the apoB-100 is bound via a single interchain disulfide bridge to a single glycoprotein, apolipoprotein (a) [32]. Its density is somewhat greater than that of LDL such that it overlaps with the fractions corresponding to LDL and HDL₂ when separating lipoproteins by ultracentrifugation. However, when quantifying the amount of cholesterol transported in the LDL molecule using the Friedewald formula, the cholesterol transported by the Lp(a) is included in this subfraction [33] and, given that the concentration of the Lp(a) is hardly modified by the treatment with statins, the higher the Lp(a) concentration, the lower the response of the LDL-C will be. In extreme cases of concentrations of Lp(a) being greater than 50 mg/dL, the decrease in LDL-C was less than half of that reached in the overall study population. Hence, in individuals classified as hyporesponders to statin treatment, one would need to take into account the presence of hyperapoproteinemia (a) as a possible confounding factor.

Among the genetic polymorphisms that could modulate the response to treatment with statins, without doubt the most studied is that of apoE. We [34] as well as others [35–37] did not observe that this polymorphism had any influence on the response of LDL-C, although there are conflicting results in the literature [10,38]. This lack of consistency in the results could be attributable to the several possible effects of the apoE genotype on hypolipidemic response such as that which occurs with its effect on plasma lipids. Factors such as age, sex, BMI, and diet modulate the effect of apoE on baseline lipids and, as such, could also influence the response to statin treatment [39,40].

Given the important role that the LDL receptor plays in the homeostasis of plasma cholesterol, several genetic variations at the LDL-receptor locus have been reported in

Table 6

Multivariate regression analysis: variables that significantly influence the LDL-C response to treatment

Variable	B	95% CI	P
Baseline LDL-C	4.210	2.630 to 5.791	<.001
Baseline Lp(a)	−3.833	−6.884 to −0.781	.014
<i>AvaII</i> polymorphism	3.407	−5.713 to −1.101	.004

relation to baseline levels of LDL-C and to response to treatment with statins [41–44]. For example, *AvaII* and *PvuII* polymorphisms of the LDL-receptor gene have been shown to influence the levels of baseline LDL-C not only in subjects with normocholesterolemia [42] but also in those with hypercholesterolemia [41,45]. As such, these polymorphisms may modulate the response to treatment with statins. Salazar et al [44] investigated 55 subjects with hypercholesterolemia treated with fluvastatin. The results indicated that those who did not carry the restriction site (+/+) of the *AvaII* polymorphism had a lower hypolipemic response than those who did. We, as well, observed that this polymorphism significantly modulates the response to pravastatin, but in the opposite direction to that observed by Salazar et al (ie, the carriers of the (+) allele had a better response in a dose-dependent manner). This disparity in the results can be explained by the treatment schedules used. Salazar et al used 2 different doses of fluvastatin (40 and 80 mg/d) and, when presenting the response with respect to genotypes, they did not discriminate between the 2 doses. Furthermore, the percentage response had not been adjusted for the baseline levels of LDL-C. Their results also indicated that carriers of the allele P2 of the *PvuII* polymorphism had a better response than those subjects homozygous for the P1 allele [44]. We were not able to confirm this finding. It is difficult to explain the mechanism by which these polymorphisms can have an influence on cholesterol response to statin treatment because the *PvuII* restriction site is located in an intron and the polymorphism of the *AvaII* does not produce amino acid substitution [42]. As such, any observed effect would need to be mediated by a functional mutation in the gene in linkage disequilibrium with these restriction sites or in a closely linked gene.

Results from the multivariate analysis indicated that only the baseline levels of the LDL-C and the Lp(a) together with the *AvaII* polymorphism of the LDL-receptor gene significantly influenced the LDL-C response to pravastatin treatment. However, these 3 factors explain only 10.6% of the overall variance in response. As such, their clinical importance is relatively small.

The value of determining genetic polymorphisms to predict the hypolipidemic effects of treatment with statins remains unclear. Their use in routine clinical practice is dubious because no specific polymorphism that has a clinically significant influence on response has been described to date. Furthermore, direct associations between the effect of the polymorphism on the hypolipemic response and clinical outcomes and/or angiographic data are not

Table 5

PvuII, *AvaII*, and apoE genotype distributions and baseline and percentage variations in LDL-C concentrations after treatment with pravastatin and segregation with respect to the different genotypes

Polymorphism	Genotypes	Basal LDL-C	% Fall	P ANOVA	P Trend
<i>PvuII</i>	−/− (n = 192)	5.14 (0.97)	−19.8 (16.6)	.392	.784
	−/+ (n = 123)	5.06 (0.89)	−20.1 (14.4)		
	+/+ (n = 16)	5.49 (0.32)	−14.2 (16.4)		
<i>AvaII</i>	−/− (n = 85)	5.34 (1.02)	−17.3 (14.4)	.091	.032
	−/+ (n = 173)	5.10 (1.06)	−20.7 (16.2)		
	+/+ (n = 77)	5.17 (0.83)	−22.5 (14.9)		
ApoE	2/3 (n = 13)	4.75 (0.85)	−17.1 (15.9)	.090	.135
	3/3 (n = 293)	5.24 (1.03)	−21.5 (15.8)		
	3/4 and 4/4 (n = 92)	5.12 (1.03)	−17.6 (15.5)		

ANOVA indicates analysis of variance.

always demonstrable [46]. Nor has there been any cost-effectiveness analysis demonstrating any benefit in using these genotypes as markers of statin response.

In conclusion, we identified 3 factors, levels of baseline LDL-C and Lp(a) and the *AvaII* polymorphism, that significantly influence the response of LDL-C to pravastatin treatment administered to patients attending a standard primary health care clinic. However, the amount of variance in response explained by these factors combined was modest.

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Appendix A.

The RAP Study Group (*Respuesta Ambulatoria a Pravastatina*)

The RAP study group consists of 195 primary health care clinicians in 17 provinces in Spain and is coordinated by the following principal investigators:

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