

## Reply to the Referee 2 comments.

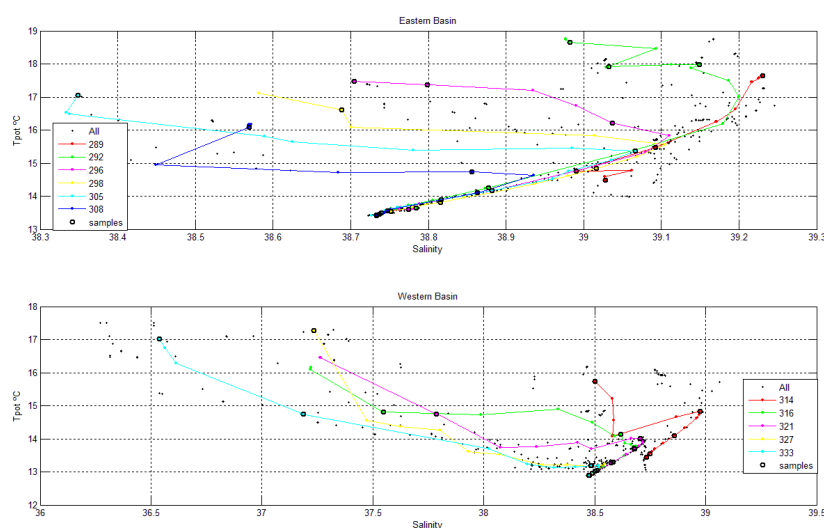
Firstly, we want to thank the reviewer for his/her careful revision and for providing suggestions to improve the manuscript. Our replies are reported in italics below each of the referee comments.

The ms. “Biogeography of planktonic microbial communities across the whole Mediterranean Sea” by Mapelli and co-authors is about the biodiversity of bacterioplankton communities in the Mediterranean Sea. This is an interesting topic, and the manuscript provides a potentially important contribution to this field of investigation. There are however many problems which need to be addressed by the authors before it may become acceptable for Ocean Science.

### Major comments

i) The authors aim at discussing the distribution of bacterial communities according to different water masses. However, there is no discussion about which water masses were sampled. At P304 the authors discuss that the water masses distribution at the large scale investigated is too complex to be described. I do not agree with this statement. A deeper description of the main oceanographic characteristics is needed, and can allow the authors to group samples according to specific water masses, and to learn more about bacterial distribution. My suggestion is including this description in the first para (3.1) of the Results section, and to re-write the corresponding Discussion section.

*In our manuscript we were not aimed to discuss the patterns in bacterial assemblages according to water masses, since they were not precisely defined for each station/samples. The main topic of the paper was a microbiological study that did not aspire to provide an exhaustive oceanographic survey. However, we agree with the referee about the importance to provide more data on the characterization of the different water masses in the sampled area. To clarify the differences between the different seawater samples we revised the section 3.1, as suggested by the referee, improving the discussion of those physico-chemical parameters that are used for water masses identification. Moreover, to provide a framework of the characteristics of the sampled water we added the Supplementary Figure 1 showing a section of salinity in the Mediterranean Sea recorded during the Meteor cruise M84/3, where the samples collected and analyzed for bacterial community structure and/or abundance are indicated. Finally, the Figure A included in this file shows the T/S diagrams illustrating that different water masses were indeed sampled across the water column of the eight stations selected for the finer vertical scale investigation.*



**Figure A:** T-S diagrams of the stations sampled at finer vertical scale for the depiction of prokaryotic abundance and/or bacterial community structure across the water column.

ii) The ms. may benefit without doubt of a check of the English language. Possibly by a native speaker. There are many typos (a few examples: P292 L4 “marine microbiology investigation were”; P304 L24 “pattern were related”; Legend to Figure 2 “station name label are reported”, etc.) *The typos were removed. English language has been revised throughout the manuscript by a native English speaker.*

iii) Many terms are often used improperly. Some examples are reported (the list is not exhaustive): P292 L8 “vertical transects” P292 L13 “the boundary of the water column” P293 L5 “marine ecosystem hot-spot” P294 L16 “Mediterranean marine biomes” P296 L28 “the interaction among the environmental variables explaining biotic similarity” P298 L21-22 “according to the conditions that rule the subsurface and deep realms” P299 L13-14: “deep layer dwelling microbiome” P299 L23: “abyssal” P300 L21: “microbial stratification data” P301 L6: “microbial communities colonizing surface water” P303 L15: “the edge of the water profile” P304 L29: “bacterial zonation” Please check the entire ms for the use of the correct terms, and pay attention to a proper usage of terms for microbial oceanography and ecology.

*The following terms have been revised: P292 L8 “vertical transects” / P292 L13 “the boundary of the water column” / P293 L5 “marine ecosystem hot-spot” / P294 L16 “Mediterranean marine biomes” / P296 L28 “the interaction among the environmental variables explaining biotic similarity” / P298 L21-22 “according to the conditions that rule the subsurface and deep realms” / P299 L23: “abyssal” / P300 L21: “microbial stratification data” / P301 L6: “microbial communities colonizing surface water” / P298 L21-22 “according to the conditions that rule the subsurface and deep realms” / P303 L15: “the edge of the water profile”.*

*We did not coin the phrase at P299 L13-14 “deep layer dwelling microbiome”, which was previously used in microbial oceanography and ecology (Fuhrman et al., 2008; Yilmaz et al., 2012). Similarly, we did not change the terms “bacterial zonation”, that was previously used in many others microbial oceanography and ecology papers like, for example, those authored by DeLong et al. (2006), Fenchel et al. (2008), Galand et al. (2009), Moeseneder et al. (2001).*

*Concerning the two terms that we did not change, we are nonetheless open to specific suggestions by the referee.*

iv) The title may be misleading. “Microbial” must be replaced with “bacterial”. I have also concerns on the use of the term “biogeography”. The authors used a low-resolution, fingerprinting technique (ARISA), which is better suited to infer diversity drivers and patterns than biogeographical features. NGS of the 16S rRNA gene would have been more useful in this sense.

*As suggested by the referee, the word “microbial” has been replaced by “bacterial” in the title and throughout the manuscript. Surely the referee is right saying that nowadays more powerful methods are available, yet the cost of NGS technology made this approach unsuitable for the large number of samples included in the present work. We do not agree about the unsuitability of the term “biogeography” due to the use of ARISA fingerprinting to depict bacterial community composition. ARISA has been exploited by many authors to analyze bacterial distribution over space and time in biogeography studies published in high ranking scientific journals (Hewson et al., 2007; Fuhrman et al., 2008; Lear et al., 2013).*

v) Abstract, first sentence: a cruise itself is not an opportunity to justify a survey, or a scientific paper. Please remove the first sentence, and replace with another one introducing the scientific topic, and explaining why this study is important in this scientific context.

*The sentence has been modified taking in consideration the referee remark.*

vi) why “sub-surface” and not “epipelagic”, as for the deeper layers?

We thank the referee for his/her suggestion. The term "sub-surface" has been replaced by "epipelagic" throughout the manuscript.

vii) Prokaryotic abundance: Figure 2 and Supplementary Table. Please provide standard deviation for each of the values presented.

*The error of the cell counting method has been established on a sub-set of samples analyzed in triplicate. Method error was estimated to be 13.8% as average (varying from 5.1 to 25.6 %). This information has been added to the material and method section*

viii) P295 L19-25: how many replicates were analyzed for ARISA? If the analysis was limited to only one water sample per station or sampling depth, the results may be biased. Small scale variability may be high. Please provide clarifications about the use of replicates. If only one replicate was analyzed, this should be clearly underlined as a potential limitation of this study.

*From all the stations/ sampling depths the water samples were collected, subsequently filtered and analyzed as a single sample for DAPI counts, DNA extraction and ARISA fingerprinting. However, the similarity/dissimilarity within the samples and the distribution of the bacterioplankton communities were never discussed in the manuscript by looking at the differences within each single samples. On the contrary, the samples were considered and discussed as replicate of a certain group: for example we compared the samples as members of two groups corresponding to the Eastern and Western basin epipelagic seawater or, similarly, the bacterial communities diversity across the water column was not discussed for each single station but comparing the differences in the epi-, meso- and bathypelagic layers in the eight analyzed station. Considering that the ARISA samples were discussed throughout the manuscript as replicates of a certain group of samples we do not agree with the referee comment about the limitation of this study. Of course we agree that it would have been preferable to collect replicate samples for all the analyzed stations/depths but we faced constraints of water availability and processing time that could not be overcome during the sampling cruise.*

ix) P296 L6-10: the authors say that ARISA fingerprints were obtained in two research institutes, and the two datasets were analyzed separately. This is good (there may be inter-laboratory variability), but there is no further mention about these two datasets in the Results, nor in the Discussion section.

*This information was previously mentioned in the Material and Methods section 2.3 (L 6-10 P296), and, thanks to the referee remark, the paragraph has been modified to improve the clarity of this information.*

x) Figure 2 is hardly readable. I would suggest using a simpler and more common format.

*Figure 2 was prepared using the Surfer software, commonly used in oceanography. Our figure has been created with a "classed post map" that identifies different ranges of data by automatically assigning a different color to each data range. Unfortunately, it was not possible to use a contour plot because of the poor vertical resolution at some stations that we wanted to include in the plot, where one or few prokaryotic abundance data were available. We preferred to include in the figure all the available data, even stations with poor vertical resolution, and hence were forced to use this type of graphical output.*

xi) P296 L14. please provide more information about the analysis of ARISA outputs. For instance, how peaks were binned?

*Additional information concerning ARISA data binning has been included in the manuscript.*

xii) P298 L 1-5: the authors are missing recent papers investigating the abundance and metabolism in deep water layers at the whole basin-scale (Luna et al. 2012 GlobBiogeochem Cycles; Zaccone et al. 2012 MicrobEcol), which are useful to compare the abundance data. In some cases (e.g. St. 297,

303, 319), data from the present study are around  $10^6$  cell L<sup>-1</sup>, which is one order of magnitude lower than reported (see the two papers above and also Yokokawa et al. 2010). How can the authors explain these differences?

*In the present study, the prokaryotic abundance measured in the bathypelagic waters ranged between  $2.88 \times 10^6 - 1 \times 10^8$  cell L<sup>-1</sup> ( $4.55 \times 10^7 \pm 2.50 \times 10^7$ , mean  $\pm$  SE). The paper authored by Yokokawa et al. (2010) analyzed the prokaryotic abundance only in the Eastern Mediterranean Sea and did not report an average value for prokaryotic abundance, however it indicated at 3000 meters a value of  $0.2 \times 10^5$  cells ml<sup>-1</sup> that is included in range reported in our study and comparable to the average value. Moreover, it is important to consider that all the papers cited by the referee (Luna et al., 2012; Yokokawa et al., 2010; Zaccone et al., 2012) investigated a much lower number of stations compared with the present study (63 samples of which 32 bathypelagic samples), a factor that possibly influenced the results, concurring in the explanation of the different reported observations in specific stations. Luna et al (2012) investigated the prokaryotic abundance, by using a different staining molecule from that applied in the present study, in 9 out of the 19 sampled stations, and all the samples analyzed for prokaryotic abundance were located in the Western Mediterranean Sea, preventing any comparison at whole basin-scale. Nonetheless, the values reported by Luna et al. (2012) for the bathypelagic waters are included in the range indicated in the present manuscript. Similarly, in the paper authored by Zaccone et al (2012), the 10 stations mean value of prokaryotic abundance was evaluated in the bathypelagic waters showed values comprised in the range reported in our manuscript. The references suggested by the referee have been added into the manuscript.*

xiii) P298 L6 and L8: please be consistent with the term abundance. “Concentrations” and “cell numbers” are not appropriate terms.

*Revised.*

xiv) P298 L12-15: this sentence is unclear. Which statistics are the authors referring to?

*The sentence refers to the previous lanes (L 6-11 P298) where the results of the PERMANOVA analysis are reported, showing that the variation in the prokaryotic abundance is related to depth but not to the different sampling regions.*

xv) P298 L18-20: this sentence is not needed. I suggest removing it.

*Revised, the sentence has been removed.*

xvi) P299 L1: where are the ARISA data? A table displaying the number of OTUs per sample and Shannon Index should be provided. Please provide also another table showing the size and % of each OTUs found in the different samples. Both tables can be provided as Supplementary tables, if preferred.

*As suggested by the referee, the information about the number of OTUs and Shannon index diversity are provided in Table S2. The addition of a table reporting the size of each OTU in the different samples would not add any useful information to the manuscript. To our knowledge, ARISA raw data are normally never provided in microbiological papers, but are rather reported only synthetic data obtained from their statistical elaboration (see for example Fuhrman et al., 2006; Fuhrman et al., 2008; Hewson et al., 2006; Hewson et al., 2007; Lear et al., 2013; Yokokawa et al., 2010). Nonetheless, the qualitative matrix obtained from ARISA fingerprinting is reported at the end of this file as requested by the referee.*

xvii) P299 L1-19 and below: please specify to which ARISA dataset the results are referring to (the one from University of Milan or that from the IEO?) I guess the results may have been slightly different, leading to different statistical outputs.

*The differentiation between the two dataset has been better clarified now in the manuscript (section 2.3). Sections 3.2 and 3.3 discussed the University of Milan dataset while the IEO dataset, concerning the eight stations where the finer vertical sampling was realized, is discussed in the section 3.5.*

xviii) P299 L17-19: this sentence is unclear. Similarity in community composition should be tested using SIMPER.

*The sentence has been revised.*

xix) P301 L26 to P302 L15: the hypothesis of a longitudinal gradient in epipelagic bacterial communities, and its dependence upon the Suez influence, is fascinating to me, but sounds highly speculative. Microbes may behave differently to marine macroorganisms.

*The text at P301 L26 to P302 L10 reports the results obtained by previous published papers authored by different scientists, hence it does not consist in a mere speculation. Similarly, we reported that Coll et al. (2010) were able to identify a distribution pattern of exogenous species entering the Mediterranean Sea from the Suez channel. In the sentence P302 L13-15 we hypothesized, due to the observation of distinct bacterial assemblages in the epipelagic water of the Eastern and Western Mediterranean, that the same pattern could be followed by microorganisms. It can be argued, as the referee did, that microorganisms do not follow the same diversity pattern showed by macroorganisms, however any clear conclusion has been achieved in this direction and the theories summarized by Martiny et al. (2006) are still debated. Scientists studying the distribution of soil bacterial community in two elevation gradients (Fierer et al, 2011; Wang et al., 2011) showed that their partitioning patterns differed from that of macroorganisms. On the opposite, other studies (Lear et al., 2013; Sul et al., 2013) reported that aquatic microorganisms could behave differently, following similar biogeography pattern of macroscopic organisms. For these reasons we trust that our sentence P302 L13-15 can be included in the text, providing also an input to this long-standing debate.*

xx) Analogously, the influence of latitude should be taken with caution. The Fuhrman et al. cited study covered a very large latitudinal gradient (from tropics to poles), while latitude in the Mediterranean Sea varies as little as a few degrees. Which hypothesis is behind the existence of a latitudinal gradient in the Mediterranean Sea?

*As the referee correctly highlighted, the study of Fuhrman et al (2008) demonstrated the significant relationship between community richness and latitude investigating a much larger latitudinal gradient than that hosted by the Mediterranean Sea. Nonetheless a previous work realized on samples collected in the Eastern Mediterranean pointed out the influence of the geographic origin of the samples on the bacterial community investigated by 16S rRNA libraries (Moeseneder et al., 2001). The geographic area encompassed in the study authored by Moeseneder and coauthors corresponded to the Aegean Sea and the samples were distributed in a latitudinal gradient comprised between the 40°N and 36°N, demonstrating that the influence of latitude on the bacterial community inhabiting the Mediterranean Sea cannot be a priori excluded. Moreover, in our manuscript we refer to the influence of latitude in the clustering of bacterial communities in the surface waters since it was proved by the applied statistical analysis (DistLM).*

xxi) P303 L9: why distinguishing between upper and lower mesopelagic?

*The subdivision of the mesopelagic layer of the water column in upper and lower zones allowed a better description of the partitioning of bacterial communities in the eight stations sampled at finer vertical profile. The improvement in the resolution of bacterial patterns was putatively linked to the sampling of different water masses across the water column, as shown for different stations in Figure A (in this file) and Figure S1 (in the revised manuscript).*

xxii) P303 L17: sharply?  
*The sentence has been changed.*

xxiii) P303 L27: beta-diversity comes out from the blue. How was it calculated, and why only here?  
*The term beta-diversity was used to indicate the bacterial community diversity between the samples. Since beta-diversity was not quantified in this work, we recognize the improper use of the term and, thanks to the referee comment, we removed it from the manuscript.*

xxiv) The study by De Corte et al. 2009 was carried in the Med, not in another oceanic region.  
*The sentence has been revised.*

xxv) P305 L16: longitude is not a physico-chemical parameter  
*The sentence has been revised.*

xxvi) The Conclusions section is too long.  
*The Conclusion section has been revised according to the referee comment.*

xxvii) Table 2, 3 and 4: unclear what each number stands for (RDA1, RDA2, ecc.). Are numbers referring to specific environmental variables?  
*The numbers reported in the Tables 2,3 and 4 do not refer to specific environmental parameters. These tables come from the dbRDA routine showing more information about dbRDA Axes. The first two columns relate to the percentage explained out of the fitted model (individuated with the DistLM analysis). The second two columns relate to the percentage explained out of the total variation in the resemblance matrix used to built up the DistLM model. This explanation has been added in tables captions*

xxviii) Legend to Fig. 3, 4 and 5: Diversity of waters? And, I cannot see any biotic data in the PCA analysis. Please check carefully these legends.  
*We thank the referee for his/her remark. The terms “diversity of water” have been replaced in the legend of figures 3,4 and 5 by “Distribution of the bacterial communities”. The referee correctly noticed that no biotic data were included in the PCA analysis (panel B of Fig. 3-4-5): as reported in the legend, the PCA was performed on the environmental data characterizing the analyzed samples.*

Other comments:

i) P292 L15-17: “different physico-chemical factors were significantly related to microbial zonation both according to geographic position and across the water column in the whole Mediterranean Sea”. I think the opposite may be true, i.e. that microbial diversity was related with the different water masses.

*The consideration of the referee is in agreement with our statement on the physico-chemical in correlation to the bacterial communities’ structure, which significance was statistically tested by DistLM in the present study. Due to the significant role of salinity, temperature and oxygen, parameters used by physical oceanographers for discriminating different water masses, we also suggested at P292, L17-20, that bacterial communities are possibly related to water masses. Nonetheless, even if in the revised version we provided a deeper discussion on water masses in the sampled area (section 3.1 and Figure S1), we cannot claim an absolute correlation between bacterial community structure and water masses composition since the latter was not identified in each of the sample analyzed by ARISA.*

ii) P293 L14-16: the Mediterranean Sea has indeed peculiar characteristics, but deep waters layers of all the oceans are hospitable for active microbial communities. Please reformulate this sentence.  
*The sentence has been reformulated.*

iii) Legend to Figure 1: replace “bacterial abundance” with “prokaryotic abundance”. Stations are not “occupied”, but “sampled”. Why showing also stations where no microbiological investigations were carried out? No clear reasons to show them.

*Figure 1 and its legend have been revised according to the referee suggestions.*

iv) Fig.1: if the map was drawn using the ODV Software, it should be specified by citing the relative bibliographic source (Schlitzer R., Ocean Data View, <http://odv.awi.de>, 2013).

*The software used to generate Figures 1 and 2 is SURFER 11- Golden Software and this information is now specified in the corresponding legends.*

v) Supplementary table: pressure is not needed.

*Pressure is one of the physical parameters tested by DistLM analysis while investigating the role of environmental parameters in shaping the bacterial communities of the epi-, meso- and bathypelagic seawater. For this reason we decided to include the pressure values in the supplementary table 1.*

#### *Cited literature:*

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	290-B	290-E	291-B	291-E	292-E	293-B	293-E	294-B	294-E	298-E	299-B	299-E	301-B	302-B
240	0	x	0	0	0	0	0	0	0	0	0	0	0	0
241	0	0	0	x	x	0	x	0	x	0	0	0	0	0
245	0	0	0	0	0	0	0	0	0	0	0	0	0	0
248	0	x	0	0	0	0	0	0	0	0	0	x	0	0
254	0	0	0	0	0	0	0	0	0	0	0	0	0	0
255	0	0	0	0	0	0	0	0	0	0	0	0	0	0
256	x	0	x	0	0	0	0	x	0	0	x	0	0	0
257	0	0	0	x	x	0	0	0	0	0	0	0	0	0
259	0	0	0	0	0	0	0	0	0	0	0	0	0	0
263	0	0	0	0	x	0	0	0	0	0	0	0	0	0
264	0	0	0	0	0	0	0	0	0	0	0	0	0	0
265	x	0	0	0	0	0	0	0	0	0	x	0	0	0
267	x	0	0	0	0	0	0	0	0	0	0	0	0	0
269	0	0	0	0	0	0	0	0	0	0	0	0	0	0
270	0	0	0	0	0	0	0	0	0	0	0	0	0	0
271	0	0	0	0	0	0	0	0	0	0	0	0	0	0
275	0	0	0	0	0	0	0	0	0	0	0	0	0	0
277	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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279	0	0	x	0	0	0	0	0	0	0	0	0	0	0
280	0	0	0	0	0	0	0	0	0	0	0	0	0	0
281	0	0	0	0	0	0	0	0	0	0	0	0	0	0
283	0	0	0	0	0	0	0	0	0	x	0	0	0	0
284	x	0	x	0	0	0	0	x	0	0	x	0	0	0
286	0	0	0	0	0	0	0	0	0	0	0	0	x	0
288	0	0	0	0	0	0	0	0	0	x	0	0	0	0
293	0	0	0	0	0	0	0	0	0	x	0	x	0	0
297	0	0	0	0	0	0	0	0	0	0	0	0	0	0
298	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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300	0	0	x	0	0	0	0	x	0	0	0	0	0	0
301	0	0	0	0	0	0	0	0	0	0	0	0	0	0
303	x	0	x	0	0	x	0	0	x	0	x	0	0	0
306	0	0	x	0	0	0	0	0	0	0	0	0	0	0
309	0	0	0	0	x	0	0	0	x	0	0	0	0	0
312	0	0	0	0	0	0	0	0	0	0	0	0	0	0
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342	0	0	0	0	0	0	0	0	0	x	0	0	0	0
345	x	0	x	0	0	x	0	x	0	0	x	0	x	0
348	0	0	0	0	0	0	0	0	0	0	0	0	0	0
354	0	0	0	0	0	0	0	0	0	0	0	0	0	0
357	0	0	0	0	0	0	0	0	0	x	0	x	0	0
360	0	0	x	0	0	x	0	x	0	x	x	x	0	0







309-B 309-E 310-B 313-B 316-B 316-E 317-B 317-E 319-B 320-B 320-E 326-B 326-E

240	0	0	0	0	0	0	0	0	0	0	0	0	0
241	0	0	0	0	0	x	0	x	0	0	x	0	x
245	0	0	0	0	0	x	0	0	0	0	0	0	0
248	0	0	0	0	0	0	0	0	0	0	0	0	0
254	0	0	0	0	0	0	0	0	0	0	x	0	0
255	0	0	0	0	0	x	0	x	0	0	0	0	x
256	0	0	0	0	x	0	x	0	0	x	0	0	0
257	0	0	0	0	0	0	0	0	0	0	0	0	0
259	0	0	0	0	0	0	0	0	0	0	0	0	0
263	0	0	x	x	0	0	0	0	0	0	0	0	0
264	0	0	0	0	0	0	0	x	0	0	0	0	0
265	0	0	0	0	0	0	0	0	0	0	0	0	0
267	0	0	0	0	0	0	0	0	0	0	0	0	0
269	0	0	0	0	0	0	0	0	0	0	0	0	0
270	0	0	0	0	0	x	0	x	0	0	0	0	0
271	0	0	0	x	0	0	0	0	0	0	0	0	0
275	0	0	0	x	0	0	0	0	0	0	0	0	0
277	0	0	0	0	0	0	x	0	0	0	0	0	0
278	0	0	0	0	0	0	0	0	0	0	0	0	0
279	x	0	x	0	0	0	0	0	0	0	0	0	0
280	0	x	0	0	0	0	0	0	0	0	0	0	0
281	0	0	0	0	0	0	0	0	x	0	0	0	0
283	0	0	0	0	0	0	0	0	0	0	0	0	0
284	x	0	0	0	x	0	x	0	x	0	0	0	0
286	0	0	0	0	0	0	0	0	0	0	0	0	0
288	0	0	0	0	0	x	0	x	0	0	x	0	x
293	0	0	0	0	0	0	0	0	0	0	0	0	0
297	0	0	x	x	0	0	0	0	0	0	0	0	0
298	0	0	0	0	0	0	0	0	0	0	0	0	x
299	0	0	0	x	0	0	0	0	0	0	0	0	0
300	0	0	x	x	0	0	0	0	0	0	0	0	0
301	0	0	0	0	0	0	0	x	0	0	0	0	0
303	x	0	x	x	x	0	x	0	0	0	x	x	0
306	0	0	0	0	0	0	0	0	0	0	0	0	0
309	0	0	0	0	0	0	0	0	0	0	0	0	0
312	0	0	0	0	0	x	0	0	0	0	0	0	0
315	x	0	0	0	x	0	0	0	0	0	0	0	0
318	x	0	0	0	x	0	0	0	x	0	0	0	0
324	0	0	0	0	0	0	0	0	0	0	0	0	0
333	0	0	0	0	0	0	0	0	0	0	0	0	0
336	0	0	0	0	0	0	0	0	0	0	0	0	0
339	0	0	0	0	0	0	0	x	0	0	x	0	0
342	0	0	0	x	0	0	0	x	0	x	x	0	x
345	x	0	x	x	x	0	x	0	x	x	0	x	0
348	0	0	0	x	0	0	0	0	0	0	0	0	0
354	0	0	0	0	0	0	0	x	0	0	0	0	0
357	0	0	0	0	0	0	0	0	0	0	0	0	0
360	0	0	0	0	0	0	x	0	x	x	0	0	0









	327-B	327-E	329-B	329-E	331-B	331-E	333-B	333-E	334-B	336-B
240	0	0	0	0	0	0	0	0	0	0
241	0	x	0	x	0	x	0	0	0	0
245	0	0	0	0	0	x	0	x	0	0
248	0	0	0	0	0	0	0	0	0	0
254	0	0	0	0	0	0	0	0	0	0
255	0	x	0	0	0	0	0	0	0	0
256	0	0	0	0	0	0	0	0	0	0
257	0	0	0	0	0	0	0	0	0	0
259	0	0	0	0	0	0	0	0	0	x
263	0	0	0	0	0	x	0	0	0	0
264	0	0	0	0	0	0	0	0	0	0
265	0	0	0	0	0	0	0	0	0	0
267	x	0	0	0	0	0	0	0	0	0
269	0	0	0	0	0	x	0	0	0	0
270	0	x	0	0	0	0	0	x	0	0
271	0	0	0	0	0	0	0	0	0	0
275	0	0	0	0	0	0	0	0	0	0
277	0	0	0	0	0	0	0	0	0	0
278	0	0	0	0	0	0	0	0	0	0
279	0	0	0	0	0	0	0	0	0	0
280	0	0	0	0	0	0	0	0	0	0
281	0	0	0	0	0	0	0	0	0	0
283	0	0	0	0	0	0	0	0	x	0
284	0	0	0	0	0	0	0	0	0	x
286	0	0	0	0	0	0	0	0	0	0
288	0	x	0	0	0	x	0	x	0	0
293	0	0	0	0	0	0	0	0	0	0
297	0	0	0	0	0	0	0	0	0	x
298	0	0	0	0	0	0	0	0	0	0
299	0	0	0	0	0	0	0	0	0	0
300	0	0	0	0	0	0	0	0	0	0
301	0	0	0	0	0	0	0	0	0	0
303	x	0	x	0	x	0	0	0	0	0
306	0	0	0	0	x	0	0	0	0	0
309	0	0	0	0	0	0	0	0	0	0
312	0	0	0	0	0	0	0	0	0	0
315	x	0	x	0	x	0	0	x	x	x
318	0	0	0	0	x	0	0	0	0	x
324	0	0	0	0	0	0	0	0	0	x
333	0	0	x	0	x	0	0	0	0	0
336	0	0	0	0	0	0	0	0	0	0
339	0	0	0	0	0	x	x	0	x	x
342	0	0	0	x	0	x	0	0	x	0
345	x	0	x	0	x	0	x	0	x	x
348	0	0	0	0	0	0	x	0	0	0
354	0	0	0	0	0	0	0	0	0	0
357	x	0	0	0	0	0	0	0	0	0
360	x	0	x	0	x	0	x	0	0	0



