## Instructions for using the Excel file to compute the J-DP4 probabilities

- In order to simplify the calculation of the J-DP4 probabilities, an Excel file is provided from the authors at:
sarotti-NMR.weebly.com
iquir-conicet.gov.ar/Sarotti-NMR
Digital CSIC (http://dx.doi.org/10.20350/digitalCSIC/8634)
- The file contains 4 sheets: "Main", "Unscaled", "Scaled" and "Errors" (Figure S1).
- The "Main" sheet contains the enabled cells to introduce the experimental and calculated NMR data, and provides the results of the J-DP4 calculations. It is divided in 5 different regions: A, B, C, D and E.

Region A Region B Region E


Figure $S 1$

## Region A: user selection (drop down lists):

- Settings: indicates the settings to be employed to compute the J-DP4 probability (Default or Custom). The choice will be reflected in Region B.
- Type of Data: indicates the type of calculated NMR data entered in Region C (Shielding Tensors, Unscaled Shifts or Scaled Shifts).


## Region B: settings to compute the J-DP4 probability

The J-DP4 probability is built with the standard deviation and degrees of freedom [ $\sigma, \nu$ ] of the shifts and $J$ errors series, and the scaling parameters of $J$ as well. These values depend upon the level of theory employed during the calculations.

If the user selects "Settings>Default" in Region $A$, the Default settings will be highlighted in Region B. These are the settings used in this work and were obtained at the B3LYP/6-31G**//MMFF level, and are fixed.

If the user selects "Settings>Custom" in Region A, the Custom settings will be highlighted in Region B. These settings can be changed freely depending on the user preferences (for example, those obtained by using other levels of theory). Warning: to obtain meaningful results, the modified parameters must be estimated at the desired level of theory using a large set of known compounds.

## Region C: enabled cells to enter the data:

- Type: enter the letter " C " (without quotes) for ${ }^{13} \mathrm{C}$ data, the letter " H " (without quotes) for ${ }^{1} \mathrm{H}$ data, and the letter " "" (without quotes) for J data.
- Experimental: enter the experimental ${ }^{13} \mathrm{C}$ and/or ${ }^{1} \mathrm{H}$ chemical shifts and/or $J$ couplings.
- Isomer 1, Isomer 2, etc: enter the computed data for the candidate structures.

Region D: displays the J-DP4 probabilities once the data is entered in Region C. Region E: displays the four most likely candidates (in descending order) depending on the values given in Region D.

## Workflow of dJ-DP4, iJ-DP4 and iJ/dJ-DP4 methods



## J-DP4 calculations tutorial

Step 1: perform a conformational search at the MMFF level using a suitable package (Spartan, MacroModel, etc). It is recommended to keep all conformations within $5 \mathrm{kcal} / \mathrm{mol}(\sim 21 \mathrm{~kJ} / \mathrm{mol})$ from the global minimum.

- For dJ-DP4: free conformational search.
- For iJ-DP4 and $\mathrm{iJ} / \mathrm{dJ}$-DP4: use experimental $J$ information to constrain the conformational sampling. This can be done in two different ways:
- Running full conformational searches and keeping only the suitable conformations (that is, those conformations showing dihedral angles in agreement with the experimental ${ }^{3} J_{\mathrm{HH}}$ values).
- Running constrained searches by freezing (within a safe range) the dihedral angle/s in agreement with the experimental ${ }^{3} J_{\mathrm{HH}}$ values.

The agreement between a given dihedral angle and the experimental ${ }^{3} J_{\mathrm{HH}}$ value can be easily estimated using the proper Karplus equation for that system. To avoid missing relevant conformations, the constrained sampling should be done within a safe range ( $\pm 2.5 \mathrm{~Hz}$ from the experimental value). As a rough guide, if the experimental ${ }^{3} J_{\mathrm{Ha}-\mathrm{Hb}}$ value is low ( $<4 \mathrm{~Hz}$ ) it should be recommended to keep the conformations showing $\mathrm{Ha} / \mathrm{Hb}$ dihedral angles in the range $50-120^{\circ}$ (absolute value). On the other hand, if the experimental ${ }^{3} J_{\mathrm{Ha}-\mathrm{Hb}}$ value is high ( $>8 \mathrm{~Hz}$ ) the conformations showing $\mathrm{Ha} / \mathrm{Hb}$ dihedral angles in the ranges $0-30^{\circ}$ and/or $140-180^{\circ}$ (absolute value) should be kept.

Step 2: perform the NMR GIAO calculations at the B3LYP/6-31G** level of theory.

- For dJ-DP4 and iJ/dJ-DP4: compute both the shielding tensors and coupling constants (FC only).
- For iJ-DP4: compute only the chemical shifts.

Step 3: compute the Boltzmann-averaged values for each compound.

- For dJ-DP4 and $\mathrm{i} /$ /dJ-DP4: both the shielding tensors and coupling constants (FC only).
- For iJ-DP4: only the shielding tensors.

Step 4: open the Excel file.
Step 5: select the Settings and Type of data (Region A).
Recommended: Settings>Default Type of data>Shielding tensors.

- If selected Settings>Custom: introduce the desired parameters in the enabled cells of Region B
- If selected Type of data>Unscaled shifts: compute the unscaled chemical shifts (in a different file) from the Boltzmann-averaged shielding tensors calculated for all isomers and the corresponding value of a suitable standard of reference (TMS, MSTD, etc) according to:

$$
\delta_{\text {unscaled }}=\sigma_{\text {ref }}-\sigma_{x}+\delta_{\text {ref }}
$$

- If selected Type of data>Scaled shifts: compute the scaled chemical shifts (in a different file) from the unscaled chemical shifts according to:

$$
\delta_{\text {scaled }}=\left(\delta_{\text {unscaled }}-\mathrm{b}\right) / \mathrm{m}
$$

where $b$ and $m$ are the intercept and slope, respectively, obtained from a large dataset or from the plot of $\delta_{\text {unscaled }}$ Vs $\delta_{\text {exp }}$.

Step 6: Introduce the experimental data in Region C.

- Column A (Type of data): Identify the type of data (C for carbon shifts, H for proton shifts, J for coupling constants).
- Column B (Exp): Introduce the experimental values.
- For dJ-DP4 and $\mathrm{i} / \mathrm{dJ}$-DP4: both the chemical shifts and coupling constants
- For iJ-DP4: only the chemical shifts

Step 7: Introduce the calculated data in Region C. All the DP4 values (proton data, carbon data, J data, all data) are automatically calculated and displayed in Region D for each isomer above the number of isomer. The most likely candidates are also shown in Region E. Important: the NMR data must be assigned (know which shift corresponds to which nuclei). Using unassigned or misassigned NMR data can lead to erroneous results.

Step-by-step example: assignment of compound 38 by J-DP4 (4 possible diastereoisomers).





Following the recommended procedure (see tutorial steps 1-3), and using a full conformational search (with no constrains) the Boltzmann averaged isotropic shielding values and coupling constants (FC only) of isomers 1-4 computed at the B3LYP/6-31G**//MMFF level are:

Table S1

| Atom | Exp | Calculated shielding tensors |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | Isomer 1 | Isomer 2 | Isomer 3 | Isomer 4 |
| C1 | 14.3 | 175.532 | 175.673 | 175.683 | 175.517 |
| C2 | 19.7 | 168.959 | 168.608 | 168.763 | 168.326 |
| C3 | 31.3 | 156.000 | 151.710 | 151.031 | 157.009 |
| C4 | 83.1 | 109.040 | 105.543 | 105.599 | 109.155 |
| C5 | 73.8 | 117.994 | 115.138 | 115.721 | 117.408 |
| C6 | 44.7 | 148.007 | 148.477 | 147.884 | 147.635 |
| C7 | 78.2 | 113.363 | 113.404 | 112.236 | 112.214 |
| C8 | 143.8 | 48.873 | 50.084 | 51.154 | 51.130 |
| C9-C13 | 125.3 | 72.345 | 72.438 | 72.100 | 72.647 |
| C10-C12 | 128.3 | 68.274 | 68.482 | 69.081 | 68.955 |
| C11 | 127.1 | 70.868 | 70.994 | 71.346 | 71.446 |
| H1 | 0.94 | 30.749 | 30.775 | 30.774 | 30.737 |
| H2a | 1.40 | 30.191 | 30.305 | 30.036 | 30.275 |
| H2b | 1.48 | 30.191 | 30.040 | 30.275 | 30.008 |
| H3a | 1.58 | 30.128 | 30.335 | 30.407 | 29.983 |
| H3b | 1.66 | 29.993 | 30.416 | 30.287 | 30.432 |
| H4 | 3.99 | 27.652 | 27.632 | 27.795 | 27.600 |
| H5 | 4.30 | 27.831 | 27.763 | 27.660 | 27.713 |
| H6a | 2.39 | 29.296 | 29.253 | 29.557 | 29.341 |
| H6b | 2.02 | 29.508 | 29.696 | 29.928 | 30.091 |
| H7 | 5.19 | 26.490 | 26.415 | 26.174 | 26.101 |
| H9 | 7.26 | 24.230 | 24.252 | 24.295 | 24.314 |
| H10 | 7.25 | 24.328 | 24.340 | 24.391 | 24.390 |
| H11 | 7.18 | 24.518 | 24.525 | 24.557 | 24.556 |
| $J_{4,5}$ | 2.9 | 2.664 | 2.777 | 2.340 | 2.092 |
| $J_{5-6 a}$ | 1.0 | 4.444 | 5.278 | 3.528 | 0.809 |
| $\mathrm{J}_{5-6 \mathrm{~b}}$ | 4.5 | 0.721 | 3.760 | 4.707 | 3.823 |
| $\mathrm{J}_{6 \mathrm{a}-7}$ | 6.5 | 10.254 | 8.545 | 6.430 | 6.172 |
| $\mathrm{J}_{6 \mathrm{~b}, 7}$ | 9.7 | 1.112 | 4.532 | 8.126 | 10.834 |

This information should be copy-pasted into the Excel file as shown in Figure S2. Warning: do not cut-paste information in this Excel file since it modifies the cell references for the hidden equations).


Figure $S 2$

The DP4 probabilities computed are shown in Region D (Figure S3). Since the shifts and coupling constants were calculated after a full conformational search, the last row indicates the dJ-DP4 results.

| Isomer № |  | $\mathbf{1}$ | $\mathbf{2}$ | $\mathbf{3}$ | $\mathbf{4}$ |
| :---: | :---: | :---: | :---: | :---: | :---: |
|  | H | 95.76 | 3.41 | 0.80 | 0.03 |
|  | $\rightarrow$ DP4 results using H data only |  |  |  |  |
| DP4 (\%) | C | 35.58 | 0.03 | 0.02 | 64.37 |$\rightarrow$ DP4 results using C data only

Figure 53

In the sheet "Unscaled" (Figure S4) are shown the unscaled chemical shifts computed according to $\delta_{\text {unscaled }}=$ $\sigma_{T M S}-\sigma_{x}$ with the $\sigma_{T M S}$ values indicated in the Region $B$ of the main sheet.

| 1 | ${ }_{\text {a }}^{\text {Ape }}$ | ${ }_{\text {exp }}^{\text {Exp }}$ | ${ }_{1}$ | $\stackrel{0}{2}$ | $\stackrel{\text { \% }}{\substack{3 \\ \hline}}$ | ${ }_{+}^{5}$ | - ${ }_{5}$ | ${ }_{6}^{\mathrm{H}}$ | $1 \quad 1$ | $\stackrel{1}{1}$ | $\stackrel{\mathrm{k}}{\square}$ | L <br> 10 | $\|$$n$ <br> $n$ <br> 1 | ${ }_{12}{ }_{12}$ | ${ }_{13}{ }^{\circ}$ |  | $\left\lvert\, \begin{aligned} & \text { a } \\ & \text { is }\end{aligned}\right.$ | \| $\begin{gathered}\text { R } \\ 16\end{gathered}$ | s 17 | \| ${ }_{18}^{\text {18 }}$ | $\mathrm{H}_{19}^{\text {U }}$ | $\stackrel{1}{20}_{20}$ | ${ }_{21}^{W}$ |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 2 | c | ${ }^{14.3}$ | 16.76 | 16.62 | 16.61 | 16.78 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 3 | c | ${ }_{313}^{19,}$ | ${ }^{23,38}$ | ${ }^{23,69}$ | ${ }_{4}^{23,53}$ | ${ }_{23,98}^{23,9}$ |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| $\stackrel{4}{5}$ | ${ }_{c}^{\text {c }}$ | ${ }_{83,1}^{31.3}$ | ${ }_{3}^{36,29} 8$ | ${ }_{\substack{40.58 \\ 88,75}}^{\substack{\text { a }}}$ | ${ }_{\substack{4126 \\ 889}}$ |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 6 | ${ }^{\text {c }}$ | ${ }_{73.8}$ | 73.30 | 7.16 | 76.57 | 7.489 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 7 | $\stackrel{1}{c}$ | 4.7 | ${ }_{4}^{429}$ | ${ }_{4}^{4382}$ | ${ }_{\text {and }}$ |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| $\stackrel{8}{9}$ | c | ${ }_{123.8}^{18.2}$ |  | ${ }_{\substack{1828 \\ 1224}}$ | ${ }_{\text {cole }}$ | ${ }^{201216}$ | : |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 10 | ${ }^{\text {c }}$ | 125.3 | 11995 | 119.86 | 120.19 | 119.65 | - |  |  |  | . |  |  |  | . |  |  |  | . |  |  |  |  |
| ${ }_{12}^{11}$ | ${ }_{c}^{\text {c }}$ | ${ }_{\substack{128.3 \\ 127.1}}$ | ${ }_{\substack{124.02 \\ 12148}}$ | ${ }_{\substack{123.31 \\ 12130}}$ | $\substack{123.21 \\ 12095}_{\substack{\text { a }}}$ | ${ }_{\substack{123.34 \\ 12085}}^{\substack{\text { ces }}}$ | : |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ${ }_{14}^{13}$ |  |  |  |  |  |  | . |  | . |  | : |  |  |  | . |  |  |  |  |  |  |  |  |
| ${ }_{15}$ | ${ }_{\text {H }}$ | 14 | ${ }_{1}^{1.84}$ | ${ }_{1.153}$ | ${ }_{1}^{1.79}$ | ${ }_{1}^{1.56}$ |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ${ }_{17}^{17}$ | ${ }_{\text {H }}^{\text {H }}$ | $\underset{\substack{1.48 \\ 1.58}}{ }$ |  | ${ }_{1}^{1.50}$ | 1.56 1.42 | 1.82 <br> 1.85 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ${ }^{18}$ | ${ }^{\text {H }}$ | 1.156 <br> 1.96 | ${ }_{1}^{1.98}$ | ${ }_{1}^{1.45}$ | ${ }^{1.54}$ | 1.400 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ${ }_{20}^{19}$ | H | 3.98 <br> 4.3 | ${ }_{4.00}^{4.18}$ | ${ }_{4}^{4.07}$ | ${ }_{4}^{4.48}$ | ${ }_{4.12}^{4.23}$ |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ${ }_{22}^{22}$ | H | 2.29 <br> 202 | (2, | 2, | 2.27 1.90 1 | - |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ${ }^{23}$ | H | 5.19 <br> 126 |  | 5,28 <br> 58 |  |  | - |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ${ }_{25}^{24}$ | ${ }_{\text {H }}^{\text {H }}$ | 7.25 7.25 | ${ }_{\substack{7,60 \\ 7,50}}$ | - | ${ }_{7}^{7} 74$ | ${ }_{7}^{7} 7$ |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ${ }_{27}^{26}$ | H | 7.8 | ${ }_{7} 71$ | ${ }_{7} 7.3$ | 7.27 | 7.27 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ${ }^{28}$ | ; | 29 | 2.66 | 2,78 | 234 | 209 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ${ }_{30}^{28}$ | ; | ${ }_{4}^{1.5}$ | ${ }_{0}^{4.48}$ | 5,28 <br> 3,6 | ${ }_{4.71}^{3.38}$ | ${ }_{\substack{0.81 \\ 3.82}}$ |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| $\begin{aligned} & 30 \\ & \begin{array}{l} 31 \\ 32 \end{array} \end{aligned}$ | , | ¢ <br> 9.5 <br> 9 | (10.28 | (ess | ${ }_{\substack{4.13 \\ 8.3 \\ \hline \\ \hline}}$ | 3.38 <br> .1 .17 <br> 108 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ${ }_{3}^{32}$ | ! | 9.7 | 1.11 | 4.33 |  |  |  |  | ! |  | : |  | : |  | : |  |  |  |  |  |  |  |  |
| ${ }_{35}^{23}$ |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ${ }^{\frac{36}{37}}$ |  | : | : | : | : |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ${ }^{38} 8$ |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| - |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ${ }_{4}^{41}$ |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| ${ }_{4}^{43}$ |  |  |  | : |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| 45 |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

Figure S4

In the sheet "Scaled" (Figure S5) are shown the scaled chemical shifts and coupling constants. The chemical shifts are scaled according to $\delta_{\text {scaled }}=\left(\delta_{\text {unscaled }}-\mathrm{b}\right) / \mathrm{m}$, where m and b are the slope and intercept, respectively, obtained from the plot of $\delta_{\text {unscaled }}$ vs $\delta_{\text {exp }}$, whereas the $J$ values are scaled according to $J_{\text {scaled }}=\left(J_{\text {unscaled }}-\mathrm{b}\right) / \mathrm{m}$, where m and b are the slope and intercept scaling $J$ values introduced in the Region $B$ of the main sheet.


Figure S5

In the sheet "Errors" (Figure S6) are shown the differences between experimental and scaled values, which in turn are used to compute the different DP4 probabilities.


Figure S6

In order to reduce the overall computational cost, an $\mathrm{i} / \mathrm{dJ}$-DP4 approach can be carried out. For example, using the experimental $J_{5-6 \mathrm{a}}$ value of 1.0 Hz the number of suitable conformations for NMR calculations can be narrowed down. According to Karplus equation, the two protons ( $\mathrm{H}-5$ and $\mathrm{H}-6 \mathrm{a}$ should be almost perpendicular). Hence, the conformational sampling can be restricted by keeping all conformations showing dihedral angles within a safe range (between 600 and $120 \%$ ). The resulting conformations ( $21 \%$ of the total obtained with a full conformational search) are submitted to NMR calculations (both shifts and coupling), and the Boltzmann averaged values are placed in the Excel file as indicated above.

According to the experimental NMR data of compound 22, both the $J_{1,2}$ and $J_{2,3}$ are small ( 2.7 and 1.9 Hz , respectively). Hence, according to Karplus equations, the $\mathrm{H}-1 / \mathrm{H}-2$ and $\mathrm{H}-2 / \mathrm{H}-3$ pairs should display a near perpendicular arrangement, or should be in equilibrium between two gauche conformers.


To compute iJ-DP4 or iJ/dJ-DP4 calculations, the conformational search of compound $\mathbf{2 2}$ can be constrained as follows:

Step 1: Run a full conformational search using MMFF, exploring all rotatable bonds. Using Spartan (6-fold sampling, systematic search) we found 39 unique conformations within the $5 \mathrm{kcal} / \mathrm{mol}$ window (similar results were obtained in Macromodel), but the number of conformers found might depend on the software and search options.

Step 2: Measure the $\mathrm{H}-1 / \mathrm{H}-2$ and/or $\mathrm{H}-2 / \mathrm{H}-3$ dihedral angles (Table S2).
Step 3: Remove the conformations showing dihedral angles in disagreement with the experimental J values. In this case, those with syn (dihedral angles in range $0-30^{\circ}$ ) or anti (dihedral angles in range 150-180 ${ }^{\circ}$ ) relationships should be removed.

Step 4: The conformations kept (in this case, those with dihedral angles in the range $50-120^{\circ}$ ) must be employed for further GIAO NMR calculations at DFT level. Note that the filter can be done with $J_{1,2}, J_{2,3}$ or both. The number of remaining conformations will depend on the $J$ employed to constrain the search ( 29 when filtering with $J_{1,2}, 22$ when filtering with $J_{2,3}$, and 15 when filtering with both $J_{1,2}$ and $J_{2,3}$ ).

Table S2

| Conformation | MMFF Rel. Energy (kcal/mol) | Dihedral angles calculated at the MMFF level |  | Filter using exp. $\mathrm{J}_{1,2}$ information | Filter using exp. $J_{2,3}$ information | Filter using exp. $J_{1,2}$ and $J_{2,3}$ information |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  | H-1/H-2 | H-2/H-3 |  |  |  |
| c01 | 0.00 | -71.26 | 60.50 | keep | keep | keep |
| c02 | 0.12 | 174.99 | 61.78 | remove | keep | remove |
| c03 | 0.44 | -64.50 | 68.73 | keep | keep | keep |
| c04 | 0.75 | -69.15 | 63.19 | keep | keep | keep |
| c05 | 0.87 | 179.11 | 63.62 | remove | keep | remove |
| c06 | 1.50 | 178.44 | 63.06 | remove | keep | remove |
| c07 | 1.82 | -61.70 | -170.78 | keep | remove | remove |
| c08 | 2.05 | -78.81 | -62.81 | keep | keep | keep |
| c09 | 2.09 | -63.46 | -173.66 | keep | remove | remove |
| c10 | 2.22 | -68.33 | 67.12 | keep | keep | keep |
| c11 | 2.70 | -63.27 | -172.68 | keep | remove | remove |
| c12 | 2.74 | 60.73 | 178.74 | keep | remove | remove |
| c13 | 2.75 | 59.87 | 179.72 | keep | remove | remove |
| c14 | 2.86 | 176.15 | -70.49 | remove | keep | remove |
| c15 | 2.90 | 62.40 | 81.74 | keep | keep | keep |
| c16 | 2.98 | -172.43 | -58.61 | remove | keep | remove |
| c17 | 3.03 | -178.38 | 65.33 | remove | keep | remove |
| c18 | 3.12 | -81.88 | -65.50 | keep | keep | keep |
| c19 | 3.20 | -64.89 | -173.02 | keep | remove | remove |
| c20 | 3.26 | 65.01 | 179.88 | keep | remove | remove |
| c21 | 3.60 | 60.43 | 177.19 | keep | remove | remove |
| c22 | 3.71 | -172.97 | -177.49 | remove | remove | remove |
| c23 | 3.72 | -73.70 | -58.58 | keep | keep | keep |
| c24 | 3.85 | 60.29 | -45.65 | keep | keep | keep |
| c25 | 3.94 | 64.75 | 80.63 | keep | keep | keep |
| c26 | 3.95 | -171.12 | -174.67 | remove | remove | remove |
| c27 | 3.98 | -67.47 | -176.39 | keep | remove | remove |
| c28 | 4.12 | 58.02 | -40.63 | keep | keep | keep |
| c29 | 4.20 | 63.38 | 177.97 | keep | remove | remove |
| c30 | 4.25 | 48.85 | -58.29 | keep | keep | keep |
| c31 | 4.31 | -64.98 | -173.47 | keep | remove | remove |
| c32 | 4.34 | 177.71 | -67.25 | remove | keep | remove |
| c33 | 4.39 | 55.97 | 77.12 | keep | keep | keep |
| c34 | 4.45 | -62.82 | -171.30 | keep | remove | remove |
| c35 | 4.45 | 65.12 | 179.73 | keep | remove | remove |
| c36 | 4.53 | -169.85 | -176.47 | remove | remove | remove |
| c37 | 4.68 | -66.93 | -174.92 | keep | remove | remove |
| c38 | 4.73 | -82.50 | -65.12 | keep | keep | keep |
| c39 | 4.75 | 53.43 | 73.94 | keep | keep | keep |
|  |  | total kept total removed |  | 29 | 22 | 15 |
|  |  | 10 | 17 | 24 |  |  |

