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# The accuracy of local MP2 methods for conformational energies

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## Abstract

The relative energies of 95 conformers of four peptide models are studied using MP2 and LMP2 methods and correlation consistent basis sets ranging from double-zeta to augmented quintuple-zeta quality. It is found that both methods yield quite similar results, and the differences between MP2 and LMP2 decrease systematically with increasing basis set. Due to reduced intramolecular basis set superposition effects (BSSE) the LMP2 results converge more slowly to basis set limit for most of these rather small systems. However, for larger peptides, the BSSE has a very large effect on the energy difference between extended and helical structures, leading to a very strong basis set dependence of the canonical MP2 results. It is demonstrated for alanine octapeptides that the basis set error exceeds 30 and 20 kJ/mol, respectively, if augmented double-zeta and triple-zeta basis sets are used. On the other hand, the LMP2 results are only slightly affected by the basis set size, and even with augmented double-zeta basis sets reasonably accurate results are obtained. Furthermore, for the larger systems the computation times for the LMP2 calculations are shown to be up to one order or magnitude shorter than for canonical MP2 calculations with the same basis set.

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## I. INTRODUCTION

Sampling the low-energy region of the phase-space is an essential element for simulating the behavior of macromolecules at finite temperature conditions. The only realistic energy functions for large-scale simulations are of the force field type, but it is desirable to establish the inherent accuracy of these methods. Two of us have recently shown that most force fields in common use have problems reproducing geometries and relative energies of conformations of small peptide models, typically accounting for only half of the conformations.<sup>1</sup> These conclusions were obtained by generating a reference set of structures and energies by a hierarchy of electronic structure methods, with geometry optimizations at the MP2/aug-cc-pVDZ level and relative energies obtained by extrapolating MP2 energies to the basis set limit and adding corrections for higher order electron correlation effects calculated at the CCSD(T) level. For molecules with localized bonding it is anticipated that relative energies of conformations will be insensitive to electron correlation beyond MP2, and it was found that the MP2/aug-cc-pVTZ level represented a suitable compromise between accuracy and computational cost, producing a typical accuracy of 1 kJ/mol for relative energies. We note that Hartree-Fock and density functional methods will be of limited use for systems with several degrees of conformational freedom, as the inadequacy of describing intramolecular dispersion will lead to artifacts in the resulting energy surface.

Having settled on the MP2 method as a suitable level of theory for generating reliable reference data for parameterizing force fields, there remains a question of the computationally most efficient formulation of MP2 theory. The conventional approach is based on canonical molecular orbitals, which leads to a formal  $\mathcal{O}(\mathcal{N}^5)$  scaling of computer time with system size. The local MP2 (LMP2) method<sup>2-9</sup> employs a localization scheme of the molecular orbitals prior to the MP2 step, and by utilizing the locality in the selection of correlating orbitals, the LMP2 method will approach linear scaling for large systems. An additional strategy to reduce the computational requirements is to expand products of functions in an auxiliary basis set,<sup>10-12</sup> a procedure usually called resolution of identity (RI) or density fitting (DF). Both of these procedures involve additional approximations beyond the regular MP2. In the current work we present extensive benchmark data to investigate the accuracy of these approximations relative to conventional MP2. An earlier study on the use of LMP2 for the calculation of conformational energies can be found in Ref. 13.

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3 In section II we summarize the computational details of our calculations. In section III A  
4 we report a comparison of MP2, DF-MP2, and DF-LMP2 methods for 95 conformations of  
5 small glycine, alanine, serine and cysteine model peptide systems. Finally, in section III B  
6 the accuracy and computational savings of the local approximations are investigated for  
7 extended and folded structures of larger alanine peptide chains.  
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## 12 13 14 II. METHOD

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17 All geometries used in Section III A have been taken as the MP2/aug-cc-pVDZ optimized  
18 reported previously,<sup>1</sup> and the performance for energies relative to the lowest energy confor-  
19 mations was evaluated as the mean and maximum absolute deviations (MAD and MAX) relative  
20 to the canonical MP2 results using the cc-pVnZ<sup>14</sup> and aug-cc-pVnZ<sup>15</sup> ( $n = 2 - 5$ ) basis set  
21 families. As will be shown below, the additional diffuse functions in the augmented basis  
22 sets are essential for achieving rapid basis set convergence at both the Hartree-Fock (HF)  
23 and the MP2 levels. These functions are particularly important for the description of the  
24 nitrogen and oxygen lone pairs. However, the diffuse functions on the hydrogen atoms have  
25 only a rather small effect on the relative energies. Therefore, as a cost effective compromise  
26 we recommend mixed basis sets, where the cc-pVnZ sets are used for the hydrogen atoms,  
27 and the aug-cc-pVnZ sets for all other atoms. These basis sets will be denoted aug'-cc-pVnZ.  
28 For each of the 95 conformers, the MP2 complete basis set limit (CBS) has been estimated  
29 using an exponential extrapolation of the HF/aug'-cc-pVnZ energies ( $n = 3 - 5$ ), and a  
30 two-point  $n^{-3}$  extrapolation of the MP2/aug'-cc-pVnZ ( $n = 4 - 5$ ) correlation energies.<sup>16</sup>  
31 These estimates will be denoted MP2/CBS[45].  
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44 In Section III B, the initial extended and helical structures of alanine tetra-, hexa- and  
45 octapeptide were created in Maestro, the graphic interface program of the MacroModel  
46 package.<sup>17</sup> Three, five and seven aminoacid units, respectively, were used for the construction  
47 of our peptides. In addition, acetyl and N-methyl functional groups were added to the C-  
48 terminus and N-terminus to mimic the environment in a longer peptide chain. Geometries  
49 were first pre-optimized at the MM level with the MMFFs<sup>18</sup> force field. The structures  
50 were then refined using the B-P86 density functional<sup>19,20</sup> in combination with the TZVP  
51 basis set.<sup>21</sup> Since no extensive search of the PES was made, there is no guarantee that  
52 the optimized structures are the global minima. However, for the purpose of the present  
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3 benchmarks this is of no relevance.

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5 Density fitting approximations<sup>11,12</sup> have been employed in the HF as well as the  
6 MP2/LMP2 steps, using, respectively, the cc-pVnZ/JKFIT and cc-pVnZ/MP2FIT or aug-  
7 cc-pVnZ/MP2FIT auxiliary basis sets of Weigend et al.<sup>22,23</sup> In each case  $n$  corresponds to the  
8 orbital basis. Local density fitting approximations<sup>11,12</sup> were disabled, except when otherwise  
9 noted. All calculations have been carried out using the MOLPRO<sup>24</sup> program package.  
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### 15 16 III. RESULTS AND DISCUSSION

#### 17 18 A. Small peptide model systems

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20 By comparison of the MP2 and DF-MP2 results it was found that typical errors due to the  
21 density fitting approximation are  $\sim 0.01$  kJ/mol. The maximum deviations never exceeded  
22 0.1 kJ/mol and are therefore well within the 1 kJ/mol target accuracy. Thus, **in agreement**  
23 **with earlier investigations on conformational energies<sup>25</sup> and other properties**, the  
24 errors introduced by density fitting are negligible. Therefore, density fitting was used in all  
25 further calculations. For simplicity, the prefix DF will be omitted in the following.  
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33 The LMP2 method involves two distinct approximations: first, the excitations are re-  
34 stricted to pair-specific domains of projected atomic orbitals (PAOs). Secondly, distant pairs  
35 can be treated by multipole approximations<sup>7,8,26</sup> or neglected. Both approximations together  
36 lead to linear scaling of the computational cost with molecular size.<sup>7,8,11</sup> In this benchmark  
37 set, however, the systems were rather small and all pairs have always been included, i.e.,  
38 distant pair approximations were not applied. The impact of pair approximations will be  
39 discussed for larger systems in Section III B.  
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45 When computing small energy differences using local methods it is essential to make sure  
46 that consistent domains are employed for all conformers. In most previous local correlation  
47 calculations a method proposed by Boughton and Pulay<sup>27</sup> (BP) has been used to determine  
48 the domains automatically. Unfortunately, the domains generated by this procedure are  
49 sensitive to the basis set and may also change as a function of the geometry. The former  
50 problem may lead to an erratic basis set convergence, the latter to small steps on poten-  
51 tial energy surfaces<sup>28-30</sup> and to unbalanced results.<sup>30</sup> This also happens when considering  
52 different conformers, and we found that in the present benchmark the BP method leads  
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3 to quite unsatisfactory results, with maximum errors of up to about 10 kJ/mol relative to  
4 canonical MP2. Since the geometry changes between different conformers are substantial,  
5 the problem cannot be avoided by simply freezing the domains. We also tested the LMP2  
6 implementation of the JAGUAR program<sup>31</sup> for the cc-pVDZ and cc-pVTZ basis sets, and in  
7 these cases the average and maximum errors were even somewhat larger than with the BP  
8 procedure in MOLPRO.  
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12 Recently, two of us have developed an alternative method<sup>32</sup> to determine the domains.  
13 This procedure is based on the natural population analysis (NPA) and natural localized  
14 molecular orbitals (NLMOs) proposed originally by Reed and Weinhold.<sup>33,34</sup> It yields do-  
15 mains that are much more stable with respect to the basis set and geometry than the BP  
16 method. In the present work we have applied this NLMO/NPA method in LMP2 calculations  
17 for all 95 conformers using 10 different basis sets ranging from cc-pVDZ to aug'-cc-pV5Z.  
18 The NPA domain selection criterion<sup>32</sup> was chosen to be 0.03. For each of the four model  
19 peptides the domains were consistent (i.e. the same atoms were selected for each orbital  
20 domain) for all conformers and 10 different basis sets. This confirms the superior stability  
21 of the new NLMO/NPA method.  
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25 The results are summarized in Table I, which shows the mean and maximum absolute  
26 deviations of the LMP2 and MP2 results for each basis set relative to the MP2/CBS[45]  
27 results. In addition, in the last two columns the mean and maximum absolute deviations  
28 between the LMP2 and MP2 results for each basis set are presented. The geometries and  
29 individual energies can be found in the supplementary material. The canonical MP2 method  
30 with an aug-cc-pVTZ basis is capable of reproducing the basis set limiting values within  $\approx 1$   
31 kJ/mol. For the aug'-cc-pVnZ basis sets, in which the diffuse functions on the hydrogen  
32 atoms are omitted, the errors for MP2 are larger, while for LMP2 they perform almost  
33 as well as the full sets. On the other hand, the errors of both MP2 and LMP2 increase  
34 significantly if the diffuse functions are entirely omitted, at least for the smaller basis sets.  
35 These findings can be rationalized by the different contribution of basis set superposition  
36 effects (BSSE), as discussed below. It should be noted that the results for the double-zeta  
37 basis sets are rather strongly affected by errors of the HF contribution, and these basis sets  
38 are clearly too small for obtaining reliable energy differences.  
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42 The LMP2 results display convergence towards nearly the same limiting values as the  
43 canonical MP2 method. For the aug'-cc-pVnZ basis sets, the absolute deviations of the  
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3 LMP2 results from the MP2/CBS[45] reference values are typically twice as large as those  
4 of the canonical MP2. Without diffuse functions, the differences between MP2 and LMP2  
5 results are even larger. The different convergence of the two methods with increasing basis  
6 set is attributed to the BSSE, which will be discussed below.  
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10 A closer inspection of the results for the two glycine conformers (Fig. 1) is presented in  
11 Fig. 2. The upper panel shows the convergence of the Hartree-Fock energy differences for  
12 the cc-pVnZ and aug'-cc-pVnZ basis sets. It is obvious that the inclusion of diffuse functions  
13 is essential to achieve rapid convergence. With the aug'-cc-pVDZ basis sets the error still  
14 amounts to 1.4 kJ/mol, but for all larger aug'-cc-pVnZ sets the HF values are very close to  
15 the estimated basis set limit. Note that in the present case the HF energy differences are  
16 negative, i.e., the energetic order of the two conformers is opposite than for MP2.  
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23 The lower panel of Fig. 2 shows the MP2 and LMP2 correlation energy contributions to  
24 the energy difference of the two conformers. The energetically lower conformer has a folded  
25 structure which is stabilized by hydrogen bonding, while the higher one has a stretched  
26 structure. At the more compact folded structure the dynamical correlation energy is larger,  
27 and therefore the correlation contribution to the energy difference is positive. This effect  
28 should increase with increasing basis set. However, as can be seen in the figure, the MP2  
29 correlation contribution decreases with increasing cardinal number  $n$ . This can be attributed  
30 to the BSSE, which should decrease with  $n$ . Apparently, in the present case the decrease of  
31 the BSSE overcompensates the increase of the correlation contribution, leading overall to a  
32 decrease of the energy difference.  
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41 The behavior is entirely different for the LMP2 method, in which the BSSE is strongly  
42 reduced.<sup>6,35,36</sup> When standard NPA domains are used, the correlation contribution converges  
43 from below to the basis set limit, as one would anticipate in the absence of BSSE. The  
44 convergence is slower than for MP2, because there is no compensation of the incomplete  
45 basis set error by the BSSE. If the domains are extended by including the PAOs at the  
46 first shell of neighboring atoms (LMP2(ext)), part of the BSSE is re-introduced, and in this  
47 case the basis set convergence dependence is remarkably weak. The total (HF + LMP2)  
48 triple-zeta value differs only by 0.01 kJ/mol from the quintuple-zeta one. However, the  
49 quintuple-zeta result is still 0.2 kJ/mol below the MP2/CBS[45] limit. This may be due  
50 to the two missing classes of ionic excitations, which are excluded in the LMP2 ansatz by  
51 construction.<sup>36</sup> Interestingly, the extrapolated LMP2(ext) result differs by less than 0.05  
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3 kJ/mol from the MP2 one. However, the extrapolation of local correlation energies should  
4 be considered with care, since the domains become more complete with increasing cardinal  
5 number, and this may lead to a different asymptotic basis set convergence than in the  
6 canonical case. Furthermore, it is of course essential that the domains are consistent for all  
7 basis sets. In the present applications, this is the case with the NLMO/NPA method, but  
8 not with the BP procedure.  
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14 The glycine case discussed above demonstrates well the different basis set convergence of  
15 MP2 and LMP2, but it is somewhat special in the sense that the MP2 correlation contribu-  
16 tion converges from above to the basis set limit. In most other cases of the present benchmark  
17 set the MP2 correlation contributions converge from below to the basis set limit (still being  
18 positive if the energetically lowest conformer is taken as the reference), indicating that the  
19 BSSE is less dominant than in the glycine case. But the BSSE still improves the MP2 results,  
20 in particular for the small basis sets, and therefore the convergence of the LMP2 results is  
21 slower. This effect is reduced when extended domains are used: For LMP2(ext)/aug'-cc-  
22 pVTZ the average and maximum absolute deviations from the MP2/CBS[45] limits are  
23 1.41 and 2.77 kJ/mol, respectively. These values are only 0.4-0.5 kJ/mol larger than the  
24 corresponding canonical MP2 values.  
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### 34 35 36 **B. Alanine peptides** 37

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39 In order to demonstrate the accuracy and computational savings of the LMP2 method for  
40 larger peptides, alanine tetra-, hexa- and octapeptides were chosen as model systems. For  
41 each of these peptides, an extended and an  $\alpha$ -helix conformer were optimized using density  
42 functional theory, as described in section III A. The optimized alpha-helix structures are  
43 shown in Fig. 3. At these structures, the HF, MP2 and LMP2 conformational energies were  
44 computed using aug'-cc-pVnZ basis sets ( $n = 2 - 4$ ). The MP2/CBS[34] basis set limits  
45 were estimated by extrapolation of the triple-zeta and quadruple-zeta correlation energies.  
46 In these calculations the HF energies were not extrapolated, and the aug'-cc-pVQZ values  
47 were taken as the reference. The results are summarized in Table II.  
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55 As for the smaller model systems, the MP2 and LMP2 results converge to approximately  
56 the same basis set limits. However, the basis set convergence of the two methods is very  
57 different. The most striking result in Table II is the slow basis set convergence of the MP2  
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3 results for the octapeptide folding energy. The MP2/aug'-cc-pVTZ result has a deviation of  
4 20 kJ/mol relative to the CBS[34] reference. This amounts to 31% of the total folding energy.  
5 On the other hand, the LMP2 results show a remarkably low basis set dependence. For the  
6 aug'-cc-pVDZ basis set this is partly due to error compensation of the HF and correlation  
7 contributions, but nevertheless for all three peptides the LMP2/aug'-cc-pVDZ results are  
8 already very close to the aug'-cc-pVQZ ones. Very likely, the strong basis set dependence  
9 of the canonical MP2 results is mainly due to BSSE effects, which over-stabilize the folded  
10 structure. The BSSE is largely eliminated in the LMP2, and this leads to the much better  
11 basis set stability, very similar to the case shown in Fig. 1 for the glycine conformers. **The**  
12 **same effect was observed by Head-Gordon and coworkers, while investigating**  
13 **the stability of 27 alanine tetrapeptides.**<sup>25</sup>

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15 The effect is most pronounced for the octapeptide, since the smaller structures, after  
16 optimization, tend to distort significantly from the ideal helix conformation, as shown in  
17 Fig. 3. In the hexamer, only half of the chain is folded, the other section is extended.  
18 In the case of the tetrapeptide, the **polypeptide** chain is too small and the backbone is  
19 approximately planar. However, even in this case, the LMP2 results are almost independent  
20 of the basis set, while the MP2 ones change by more than 40% from aug'-cc-pVDZ to  
21 the CBS[34] limit. Although these examples are simplified models, **the present results**  
22 **confirm earlier findings made for the alanine tetrapeptide.**<sup>25</sup> **Large basis sets are**  
23 **needed when computing folding energies with canonical correlation methods,**  
24 **since BSSE starts to play a crucial role in larger peptides.** As the chain size increases,  
25 the errors accumulate, and at least quadruple-zeta quality basis set are necessary in order to  
26 obtain reasonably accurate results with MP2.<sup>37</sup> On the other hand, local correlation methods  
27 allow to use much smaller basis sets; moreover, for a given basis set the computational effort  
28 is drastically reduced, as will be demonstrated in the following.

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30 The computation times of MP2 and LMP2 calculations for the octapeptides are shown in  
31 Table III. The savings made by the local approximations are quite dramatic. As compared to  
32 the canonical calculation, the total computational time for the extended structure is reduced  
33 by one order of magnitude. As expected, the LMP2 calculations for the  $\alpha$ -helix conformer  
34 with a more more three-dimensional structure are slower than for the extended peptide,  
35 especially for the iterations, but the savings are still significant. The longer computation  
36 times for the helix structure are mainly caused by the larger number of pairs included in  
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the calculation (see below).

Further savings are possible through the use of local density fitting approximations, which asymptotically lead to linear scaling of the computational cost with system size.<sup>11</sup> In the local density fitting method, the 4-index exchange integrals  $K_{rs}^{ij} = (ri|sj)$  are decomposed into sums of products of 2- and 3-index integrals

$$K_{rs}^{ij} \approx \sum_{A \in [i]_{\text{fit}}} D_{ri}^A (sj|A) + \sum_{B \in [j]_{\text{fit}}} (ri|B) D_{sj}^B - \sum_{A \in [i]_{\text{fit}}} \sum_{B \in [j]_{\text{fit}}} D_{ri}^A J_{AB} D_{sj}^B, \quad (1)$$

where the indices  $\{A, B\}$  refer to the auxiliary basis set and  $D_{ri}^A$  are the fitting coefficients obtained by solving systems of linear equations

$$(ri|A) = \sum_{B \in [i]_{\text{fit}}} J_{AB} D_{ri}^B \quad (2)$$

(for further details see Ref. 11). Note that this *robust* fitting approximation is slightly different than the less symmetric approximation described in Ref. 11.

In a conventional implementation, the summations in eqs. (1) and (2) would run over the full fitting basis, leading to  $\mathcal{O}(\mathcal{N}^5)$  scaling. The last two terms in eq. (1) then cancel. In a local calculation, it is possible to use for each orbital pair  $ij$  a truncated fitting basis, in which only the auxiliary function in the vicinity of the localized orbitals  $i$  and  $j$  are included. The default in MOLPRO is to include in the domain  $[i]_{\text{fit}}$  the fitting functions at all atoms that are separated from the atoms in the orbital domain  $[i]$  by at most 3 bonds ( $l_f = 3$ ). Using this value the effect of the local density fitting approximation on the relative energies is negligible. In fact, in the current case even smaller fitting domains with only the atoms that are separated by at most one bond ( $l_f = 1$ ) from the atoms in the domain  $[i]$  are sufficient to obtain accurate results (cf. Table III).

The number of pairs included in the LMP2 and therefore onset of linear scaling and the CPU-time depends on the the distance criterium  $R_{vd}$  for neglecting very distant pairs.<sup>6,7</sup> Orbital pairs  $ij$  are neglected if the closest distance  $R_{ij}$  between an atom in the orbital domain  $[i]$  and an atom in the orbital domain  $[j]$  is larger than  $R_{vd}$ . Reducing this distance criterion below its default value of 15 bohr leads to significant savings, but increases the error in the energy difference (cf. Table III). If the distance criterion is set to 12 bohr the errors already exceed 1 kJ/mol. The sensitivity of the energy difference is due to the

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3 different three-dimensional arrangement of the conformers. In the helix structure, more pairs  
4 are removed when  $R_{vd}$  is decreased: if  $R_{vd}$  is reduced from 15 to 12 bohr, about 800 pairs  
5 are removed in the helix case, while in the extended conformer only 500 pairs are removed.  
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7 Therefore, the helix energy is more affected than the energy of the extended conformer, and  
8 the energy difference decreases.  
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12 Optionally, the integrals for distant pairs ( $R_d < R_{ij} \leq R_{vd}$ ) can be approximated by  
13 multipole approximations, which also reduce the overall cost.<sup>8,26</sup> However, as shown in Table  
14 III for various choices of  $R_d$ , this approximation leads to rather large errors. As already  
15 pointed out in Ref. 26, this is due to the neglect of certain exchange contributions, and such  
16 approximations are therefore not recommended in the study of intermolecular forces or for  
17 cases in which long-range interactions play a crucial role.  
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22 Finally, it should be noted that the CPU-time for the Hartree-Fock calculation (about  
23 8.3 hours, using density fitting and the aug'-cc-pVTZ basis) exceeds that of the LMP2 step.  
24 The differences are even greater when the aug'-cc-pVQZ basis (3860 contracted functions)  
25 is used. The HF and MP2 calculations took about 85 and 110 hours, respectively, while  
26 the LMP2 calculation took only 28 hours (helix structure, without local density fitting  
27 approximations).  
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#### IV. CONCLUSIONS

We have investigated the effect of local approximations on the relative energies of different conformers. In order to obtain reliable LMP2 energy differences it is important that the orbital domains of the different conformers are defined consistently. This can be achieved using a recently proposed method that is based on natural population analysis.<sup>32</sup> With this method consistent domains were obtained for all conformers and all basis sets studied in this work, and a smooth convergence with increasing basis set size to the basis set limit was always achieved.

For all model systems studied, the MP2 and LMP2 methods yield very similar results at the basis set limit. However, due to the reduced BSSE in the LMP2, the convergence of MP2 and LMP2 with increasing basis sets is different. For most of the small systems in the benchmark set the convergence of the LMP2 results is found to be somewhat slower than for MP2, since in these systems the BSSE partly compensates for other basis set deficiencies.

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3 However, the BSSE increases with system size, and our calculations for larger peptide chains  
4 demonstrate that canonical MP2 may strongly over-stabilize helical structures. For the  
5 alanine-octapeptide the basis set error was found to be more than 30 and 20 kJ/mol, with  
6 augmented double-zeta and triple-zeta basis sets, respectively. In contrast, the LMP2 results  
7 are only weakly basis set dependent, and already with augmented double-zeta sets results  
8 close to the basis set limit are obtained. Moreover, the local approximations reduce the  
9 computation times by up to one order of magnitude.

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15 (IAA400550702), and the German Fonds der Chemischen Industrie.

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Tables

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TABLE I: Mean (MAD) and maximum (MAX) absolute deviations of relative energies (in kJ/mol) for 91 conformations of four model peptide systems.

Basis set	MP2 <sup>a</sup>		LMP2 <sup>a</sup>		LMP2 <sup>b</sup>	
	MAD	MAX	MAD	MAX	MAD	MAX
cc-pVDZ	3.02	10.55	2.34	7.21	2.39	6.02
cc-pVTZ	0.91	3.48	1.94	4.43	2.20	5.36
cc-pVQZ	0.34	0.86	1.23	2.78	1.16	3.02
cc-pV5Z	0.20	0.47	0.82	2.00	0.67	1.71
aug-cc-pVDZ	1.68	4.30	3.03	5.58	1.99	5.14
aug-cc-pVTZ	0.64	1.64	1.77	3.48	1.38	3.36
aug'-cc-pVDZ <sup>c</sup>	2.13	5.48	3.00	5.51	1.50	4.02
aug'-cc-pVTZ <sup>c</sup>	0.92	2.38	1.85	3.61	1.10	2.79
aug'-cc-pVQZ <sup>c</sup>	0.38	0.89	0.85	1.80	0.54	1.30
aug'-cc-pV5Z <sup>c</sup>	0.19	0.45	0.49	1.06	0.33	0.79
CBS[45] <sup>d</sup>	(0.0)	(0.0)	0.12	0.33	0.12	0.33

a) Relative to the MP2/CBS[45] values.

b) Relative to MP2 values for each basis set.

c) aug' indicates that diffuse functions are included only on non-hydrogen atoms.

d) Basis set limits estimated from extrapolations of the aug'-cc-pVnZ energies, see text.



TABLE II: Energy difference  $E_{\alpha\text{-helix}} - E_{\text{extended}}$  (in kJ/mol) between the helical and extended conformers of the alanine peptides. The HF contribution is included in the MP2 and LMP2 values.

Peptide	Basis	HF	MP2	LMP2
(ala) <sub>4</sub>	aug'-cc-pVDZ	27.69	12.58	18.21
	aug'-cc-pVTZ	29.71	15.74	18.61
	aug'-cc-pVQZ	30.71	17.26	19.06
	CBS[34] <sup>a</sup>	—	18.03	19.06
(ala) <sub>6</sub>	aug'-cc-pVDZ	42.84	47.29	46.15
	aug'-cc-pVTZ	41.47	45.55	44.27
	aug'-cc-pVQZ	41.61	45.62	45.18
	CBS[34] <sup>a</sup>	—	45.57	45.75
(ala) <sub>8</sub>	aug'-cc-pVDZ	-15.32	-94.49	-60.08
	aug'-cc-pVTZ	-2.38	-84.03	-63.19
	aug'-cc-pVQZ	-0.87	-71.78	-60.84
	CBS[34] <sup>a</sup>	—	-63.95	-60.22

a) Calculated from the aug'-cc-pVTZ and aug'-cc-pVQZ correlation energies and the aug'-cc-pVQZ HF value.

TABLE III: CPU-times (in minutes, using 2.8 GHz opteron processors) for conventional and local correlation calculations<sup>a</sup> with the aug'-cc-pVTZ basis set on the extended/helix conformers of the alanine octapeptide. The conformational energies (in kJ/mol)  $\Delta E = E(\alpha\text{-helix}) - E(\text{extended})$  are also shown.

Method	$l_f$	$R_{vd}$	$R_d$	Integrals <sup>b</sup>	Iterations <sup>c</sup>	Total	$\Delta E$
MP2	-	-	-	—	—	1509/1514	-84.03
LMP2	-	-	-	162/176	413/413	590/604	-63.01
LMP2	-	15	-	106/149	95/283	214/448	-63.19
LMP2	1	15	-	45/84	95/283	152/380	-63.13
LMP2	1	12	-	44/78	68/219	124/310	-61.91
LMP2	1	10	-	39/65	43/135	94/212	-58.19
LMP2	1	15	12	44/75	94/256	152/347	-62.30
LMP2	1	15	10	37/70	78/242	128/328	-60.40
LMP2	1	15	8	32/52	70/198	114/264	-52.48

- a)  $R_{vd}$  and  $R_d$  (in bohr) are the distance criteria for neglecting very distant pairs and for using multipole approximations, respectively;  
 $l_f$  determines the size of the local fitting domains, see text.
- b) CPU-time for integral evaluation and transformation.
- c) CPU-time to solve the first-order LMP2 equations.

### Figure Captions

Figure 1: **Ball-and-stick** representation of the two glycine tripeptide conformers discussed in the text and Fig. 2. The upper structure corresponds to the minimum energy conformation.

Figure 2: Hartree-Fock (upper panel) and correlation contributions (lower panel) to the relative energy of the glycine conformers as a function of cardinal number  $n$  of the basis set.

Figure 3: **Ball-and-stick** representation of the alanine tetra-, hexa- and octapeptide optimized helical conformers.

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FIG. 1: Jakub et al., Molecular Physics

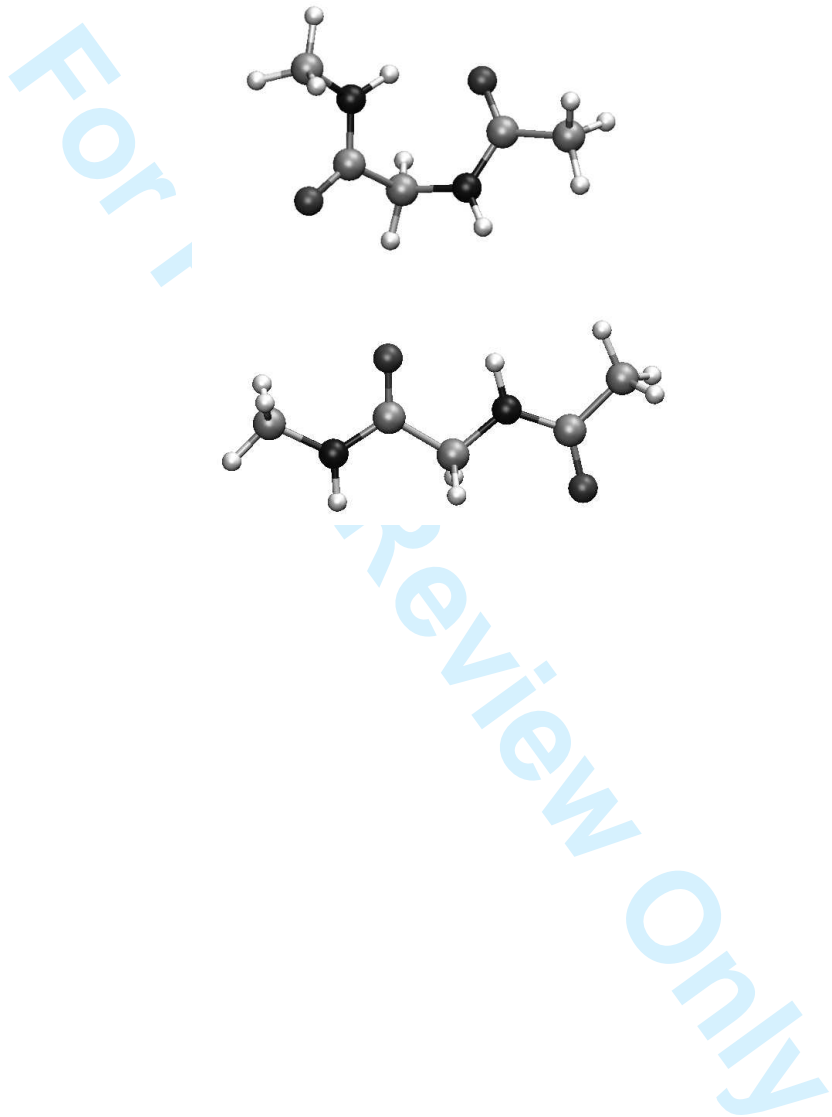


FIG. 2: Jakub et al., Molecular Physics

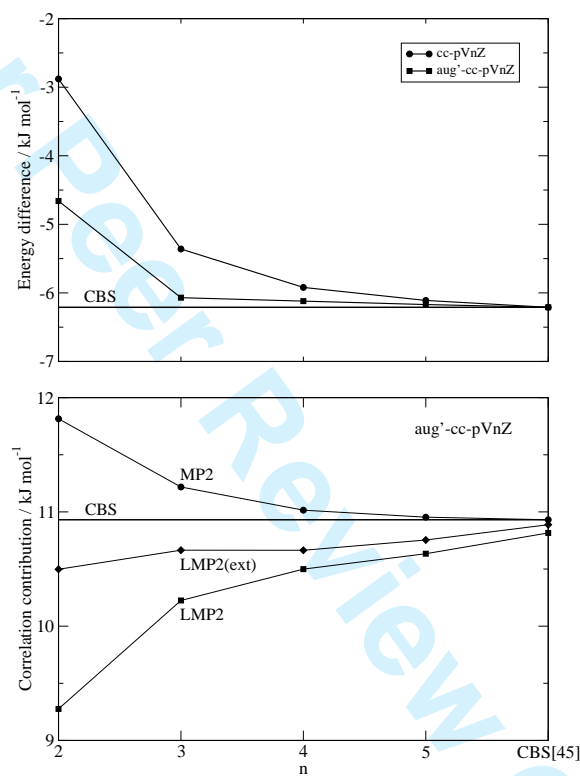
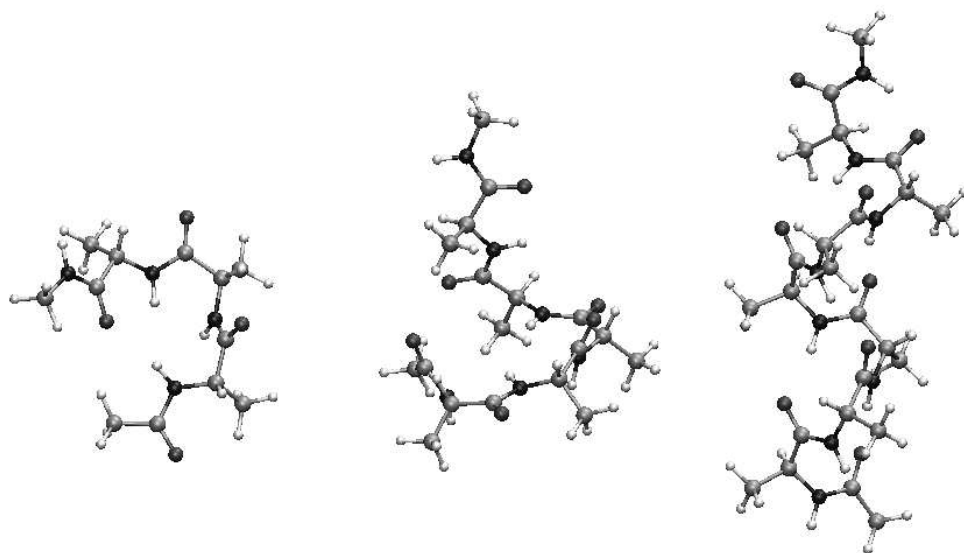
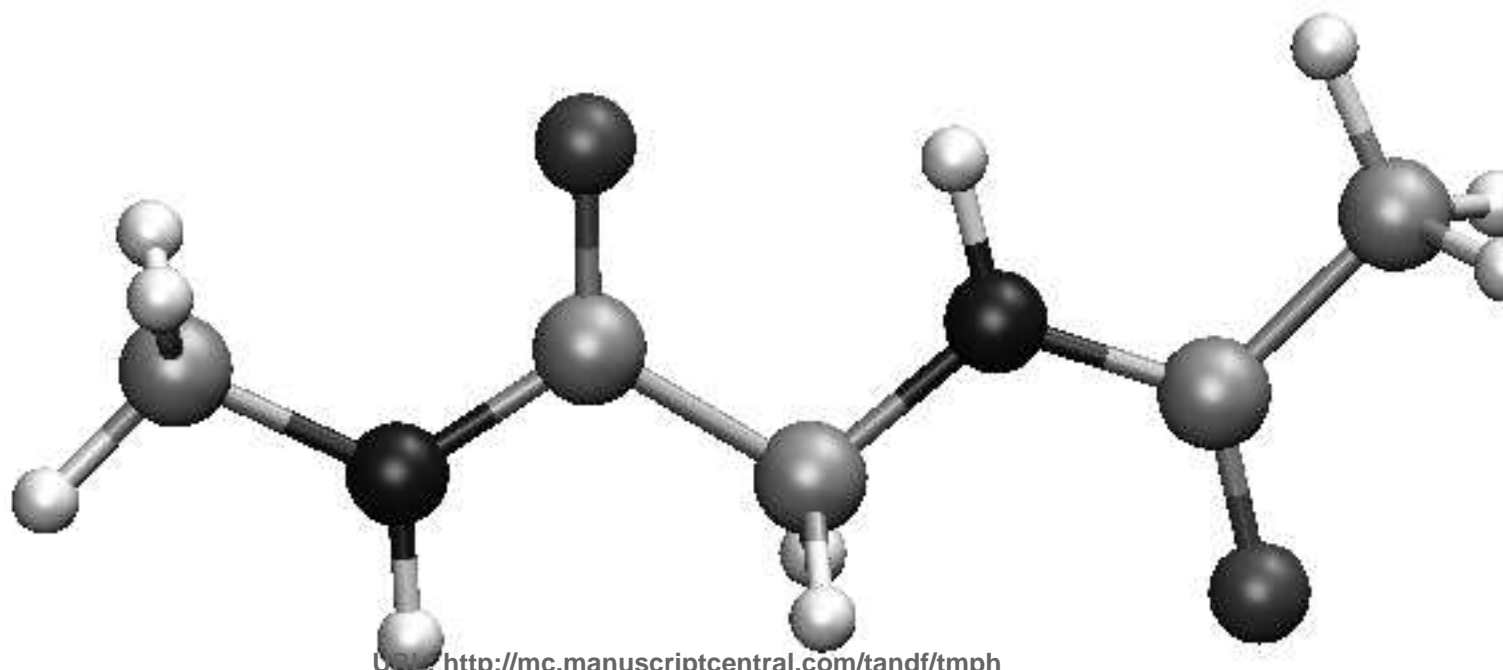
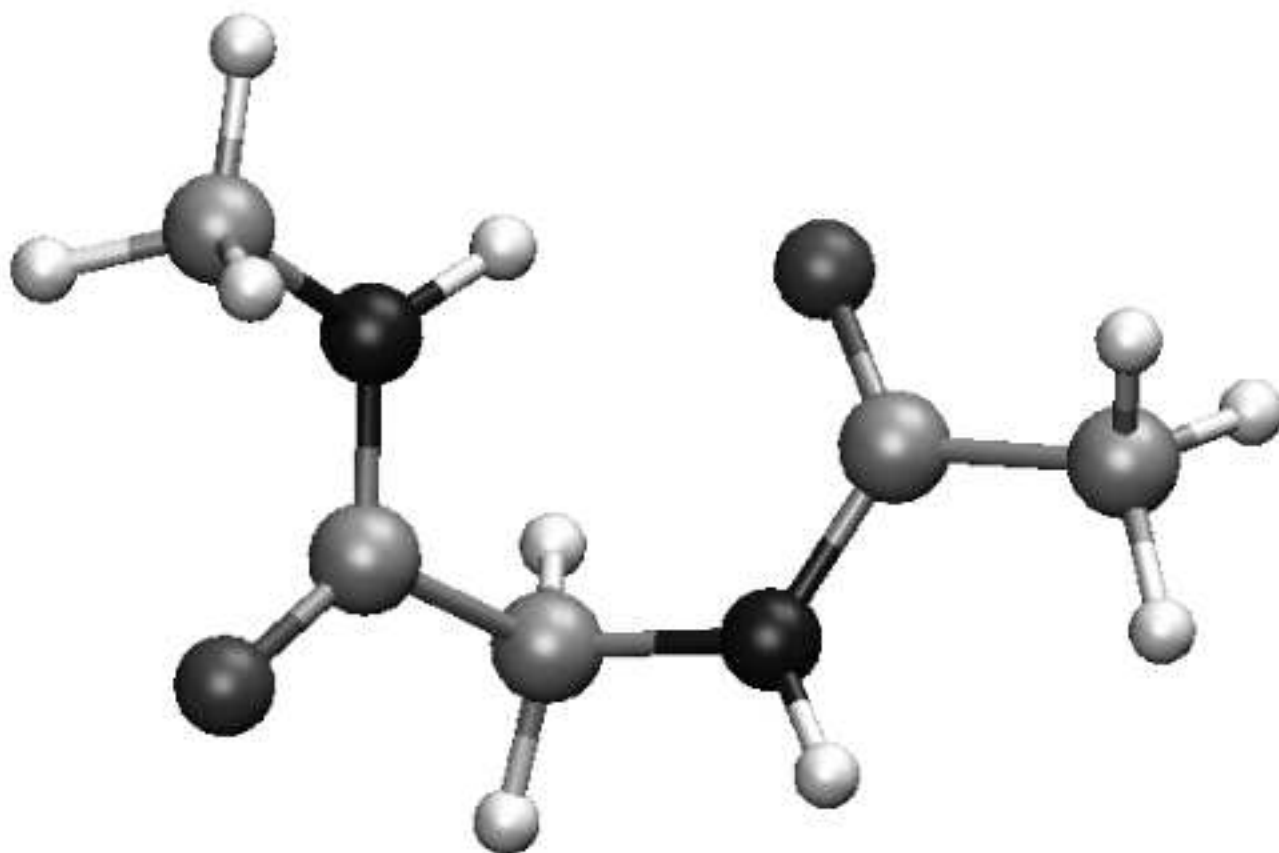


FIG. 3: Jakub et al., Molecular Physics

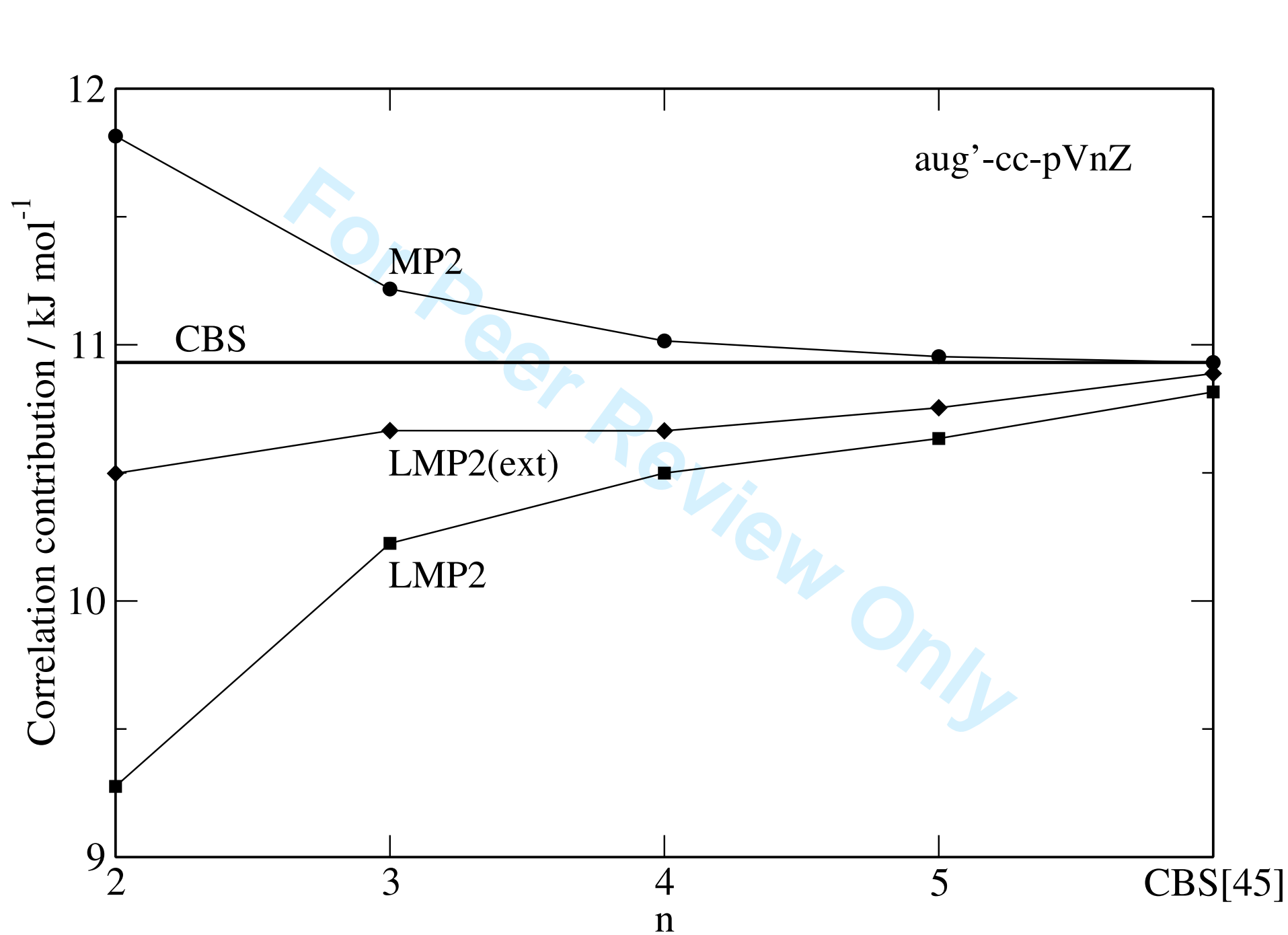


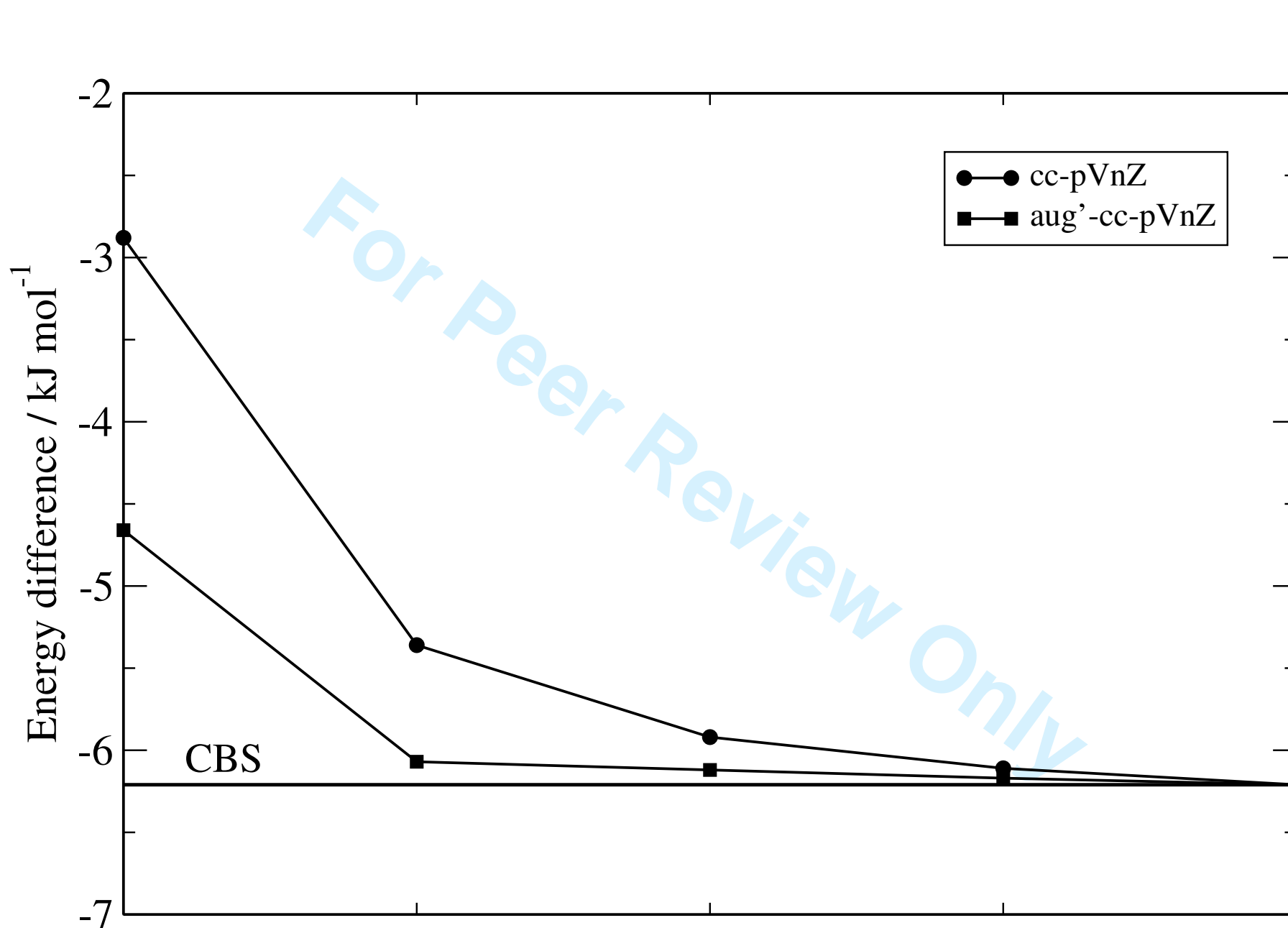
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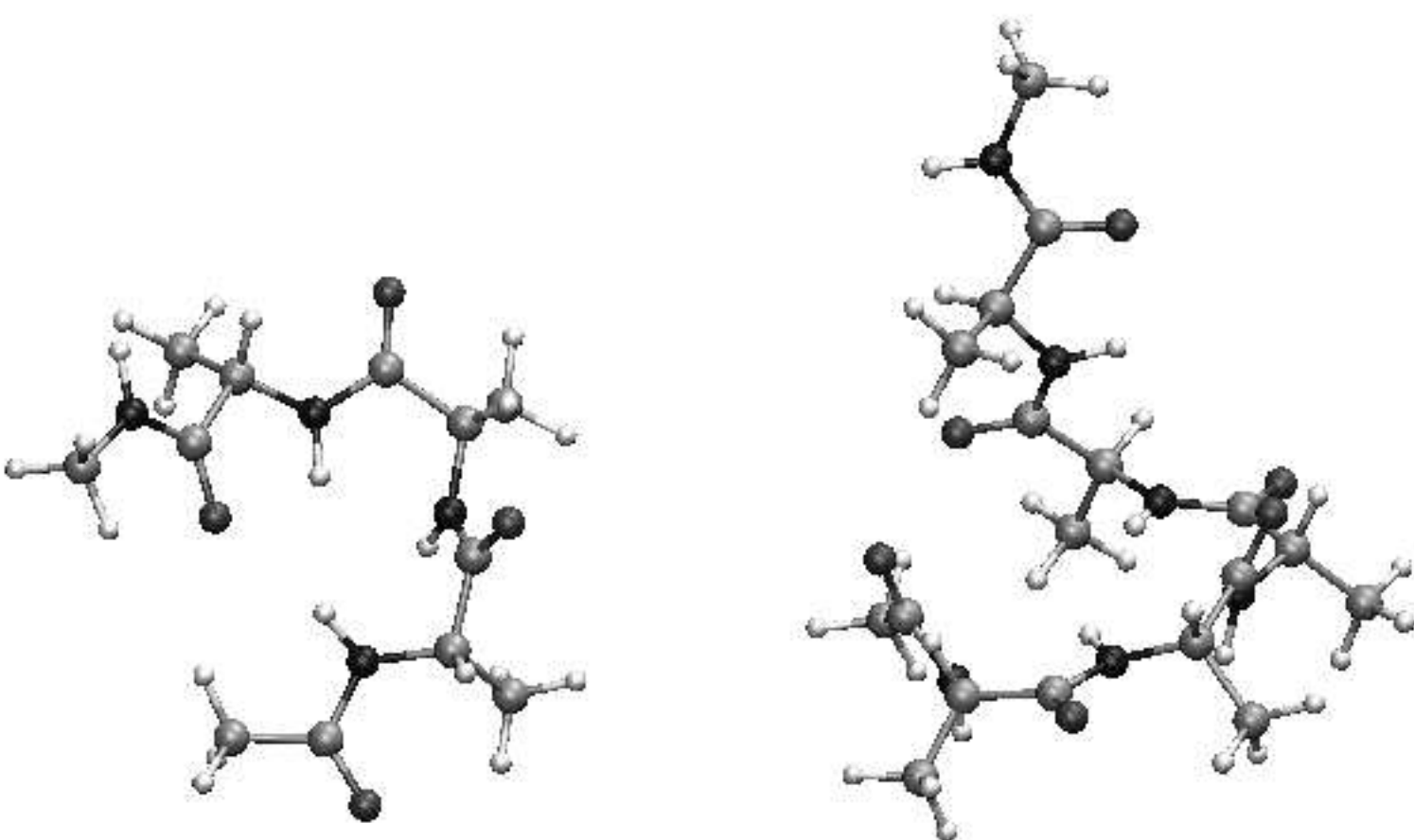






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3 This file contains:  
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5 1.) DF-HF results  
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7 2.) DF-MP2 results  
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9 3.) DF-LMP2 results  
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11 4.) Geometries (xyz format)  
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14  
15 Basis sets:  
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17 DZ: cc-pVDZ  
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19 TZ: cc-pVTZ  
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21 QZ: cc-pVQZ  
22

23 5Z: cc-pV5Z  
24

25 ADZ: aug-cc-pVDZ  
26

27 ATZ: aug-cc-pVTZ  
28

29 (A)DZ: (aug)-cc-pVTZ  
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31 (A)TZ: (aug)-cc-pVTZ  
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33 (A)QZ: (aug)-cc-pVTZ  
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35 (A)5Z: (aug)-cc-pVTZ  
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39 The (aug)-cc-pVnZ basis sets do not include diffuse function on H-atoms.  
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42 All results obtained with density fitting, using the cc-pVnZ/JKFIT sets for DF-HF  
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44 the cc-pVnZ/MP2FIT for MP2/cc-pVnZ, and aug-cc-pVnZ/MP2FIT for both MP2/aug-cc-pVnZ and  
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49 All relative energies in kJ/mol  
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55 DF-HF results  
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	DZ	TZ	QZ	5Z	ADZ	ATZ	(A)DZ	(A)TZ	(A)QZ	(A)5Z	XPOL	REF
Glycine												
1	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
2	-2.839	-5.361	-5.925	-6.112	-4.822	-5.984	-4.656	-6.071	-6.119	-6.170	-6.208	-6.208
Alanine												
1	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
2	1.447	-1.511	-1.840	-1.935	-0.646	-1.767	-0.554	-1.804	-1.916	-1.944	-1.957	-1.957
3	13.250	12.498	12.605	12.609	12.507	12.483	12.606	12.547	12.588	12.610	12.624	12.624
4	13.187	10.404	10.202	10.252	10.718	10.320	10.597	10.290	10.258	10.264	10.272	10.272
5	18.994	20.741	21.444	21.691	20.905	21.692	20.718	21.653	21.712	21.730	21.739	21.739
6	19.124	18.738	19.200	19.311	18.436	19.196	18.248	19.114	19.307	19.330	19.330	19.330
7	23.513	23.057	23.325	23.496	23.671	23.574	23.886	23.563	23.569	23.539	23.513	23.513
Serine												
1	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
2	13.844	10.698	9.746	9.448	10.145	9.502	10.348	9.537	9.444	9.428	9.424	9.424
3	12.472	9.426	8.723	8.424	8.994	8.519	9.020	8.494	8.430	8.395	8.371	8.371
4	17.834	13.502	12.334	11.921	13.667	12.030	14.015	12.091	11.922	11.873	11.848	11.848
5	20.647	22.421	23.008	23.141	21.749	22.941	21.653	22.931	23.131	23.173	23.187	23.187
6	15.426	12.122	11.262	10.867	11.820	10.977	11.857	10.974	10.868	10.826	10.802	10.802
7	23.339	19.539	18.701	18.308	18.518	18.281	18.642	18.364	18.304	18.268	18.244	18.244
8	23.679	20.370	19.553	19.204	19.529	19.194	19.677	19.225	19.194	19.167	19.147	19.147
9	29.021	28.362	28.327	28.249	28.126	28.140	28.188	28.135	28.235	28.258	28.267	28.267
10	22.293	17.524	16.577	16.260	17.495	16.411	17.598	16.382	16.282	16.241	16.215	16.215

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5	11	27.520	23.690	22.624	22.275	22.546	22.325	22.803	22.354	22.285	22.241	22.210
6		22.210										
7												
8	12	23.642	18.392	17.537	17.219	18.566	17.366	18.665	17.363	17.230	17.186	17.162
9		17.162										
10												
11	13	25.152	19.858	18.632	18.239	19.599	18.397	19.359	18.354	18.250	18.211	18.188
12		18.188										
13												
14	14	27.222	27.371	27.328	27.276	26.983	27.333	26.994	27.316	27.283	27.283	27.286
15		27.286										
16												
17	15	38.663	32.597	31.414	30.935	31.446	30.807	31.690	30.867	30.890	30.879	30.866
18		30.866										
19												
20	16	30.655	25.646	25.066	24.864	25.280	24.915	25.198	24.875	24.886	24.861	24.838
21		24.838										
22												
23	17	36.766	30.626	29.399	28.889	29.370	28.739	29.523	28.811	28.846	28.842	28.835
24		28.835										
25												
26	18	30.755	23.365	21.634	21.011	23.179	21.175	23.246	21.144	20.991	20.947	20.925
27		20.925										
28												
29	19	34.717	31.625	31.148	30.920	31.248	30.792	31.669	30.853	30.909	30.901	30.888
30		30.888										
31												
32	20	39.578	33.338	32.094	31.570	32.100	31.451	32.364	31.490	31.522	31.520	31.516
33		31.516										
34												
35	21	32.233	26.920	26.226	25.941	26.242	25.980	26.179	25.978	25.957	25.928	25.905
36		25.905										
37												
38	22	27.087	25.817	25.797	25.743	25.532	25.824	25.560	25.756	25.790	25.766	25.742
39		25.742										
40												
41	23	33.156	28.584	27.570	27.159	27.746	27.224	27.976	27.144	27.153	27.110	27.071
42		27.071										
43												
44	24	37.647	35.761	35.374	35.160	34.759	35.076	34.809	35.104	35.162	35.161	35.154
45		35.154										
46												
47	25	30.682	30.470	30.622	30.493	29.559	30.393	29.511	30.360	30.480	30.481	30.469
48		30.469										
49												
50	26	33.773	31.498	31.098	30.845	29.987	30.730	29.709	30.704	30.827	30.820	30.800
51		30.800										
52												
53	27	33.596	33.537	33.620	33.505	32.648	33.427	32.621	33.375	33.488	33.495	33.489
54		33.489										
55												
56	28	33.054	35.697	36.546	36.734	36.020	36.639	35.749	36.538	36.732	36.770	36.782
57		36.782										
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6 30 40.237 38.007 37.389 37.236 38.169 37.370 38.650 37.410 37.289 37.245 37.220  
7 37.220

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9 31 37.942 34.582 33.696 33.370 34.231 33.460 34.239 33.464 33.381 33.358 33.347  
10 33.347

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12 32 39.473 36.612 36.154 35.896 35.278 35.806 35.040 35.734 35.879 35.872 35.852  
13 35.852

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15 33 42.574 38.401 37.711 37.420 37.265 37.393 37.069 37.364 37.386 37.371 37.357  
16 37.357

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18 34 42.537 38.410 37.812 37.540 36.939 37.501 36.874 37.436 37.537 37.528 37.509  
19 37.509

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21 35 48.278 45.415 45.006 44.905 45.541 44.969 46.022 44.999 44.971 44.910 44.861  
22 44.861

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24 36 58.549 53.979 53.472 53.094 54.125 52.971 54.265 53.031 53.049 53.060 53.068  
25 53.068

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27 37 54.922 53.327 53.121 52.909 52.726 52.870 52.556 52.837 52.870 52.901 52.924  
28 52.924

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30 38 61.061 55.832 54.797 54.415 55.292 54.556 55.371 54.544 54.418 54.383 54.366  
31 54.366

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33 39 68.255 60.615 58.704 58.068 60.266 58.412 60.424 58.425 58.107 58.026 57.991  
34 57.991

35  
36 Cysteine

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38 1 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000

39  
40 2 6.037 1.573 0.607 0.260 1.298 0.505 1.028 0.388 0.261 0.225 0.209 0.209

41  
42 3 4.561 2.863 2.382 2.244 3.007 2.440 2.904 2.274 2.234 2.210 2.194 2.194

43  
44 4 12.161 9.829 9.338 9.181 9.751 9.361 9.180 9.152 9.092 9.075 9.066 9.066

45  
46 5 6.315 4.609 4.200 4.134 4.500 4.307 4.387 4.217 4.144 4.124 4.114 4.114

47  
48 6 7.893 6.097 5.630 5.466 6.107 5.687 5.750 5.570 5.443 5.426 5.424 5.424

49  
50 7 7.516 2.751 2.033 1.774 3.217 2.167 2.821 1.947 1.780 1.726 1.698 1.698

51  
52 8 9.627 7.264 6.689 6.567 7.328 6.695 7.223 6.679 6.542 6.521 6.516 6.516

53  
54 9 10.283 7.886 7.342 7.221 8.226 7.494 7.902 7.374 7.198 7.164 7.154 7.154

55  
56 10 10.677 7.418 6.686 6.437 7.569 6.762 7.094 6.453 6.383 6.352 6.333 6.333

57  
58 11 11.006 8.186 7.769 7.654 9.238 7.996 8.968 7.856 7.675 7.634 7.618 7.618  
59  
60

12	19.615	15.998	15.397	15.202	15.995	15.303	15.750	15.202	15.137	15.140	15.148
13	11.807	8.434	8.031	7.912	9.609	8.280	9.436	8.040	7.923	7.877	7.851
14	17.211	14.253	13.795	13.622	14.379	13.721	14.021	13.599	13.560	13.569	13.580
15	14.672	11.860	11.371	11.294	11.945	11.553	11.633	11.360	11.272	11.244	11.230
16	16.248	12.213	11.544	11.381	13.403	11.670	13.391	11.553	11.379	11.341	11.327
17	17.014	13.658	13.304	13.235	13.596	13.450	13.029	13.300	13.245	13.231	13.224
18	22.606	19.782	19.367	19.277	19.564	19.247	19.808	19.287	19.232	19.239	19.250
19	23.240	22.114	21.813	21.694	21.978	21.820	21.751	21.724	21.662	21.671	21.684
20	18.705	14.050	13.240	13.036	15.010	13.261	14.946	13.128	13.005	12.961	12.936
21	25.047	22.563	21.875	21.607	22.505	21.830	22.084	21.663	21.559	21.555	21.562
22	18.202	18.118	18.293	18.339	17.794	18.466	17.102	18.268	18.306	18.313	18.315
23	21.532	19.960	19.884	19.867	19.783	20.079	19.212	19.887	19.831	19.823	19.822
24	22.109	17.811	17.297	17.264	17.827	17.387	17.645	17.344	17.251	17.239	17.238
25	21.793	15.770	14.566	14.212	16.669	14.636	16.249	14.387	14.159	14.094	14.064
26	29.758	27.651	27.441	27.366	27.791	27.519	27.664	27.398	27.399	27.372	27.350
27	22.834	22.484	22.672	22.795	22.113	22.815	22.063	22.797	22.796	22.797	22.798
28	23.435	24.919	25.254	25.382	25.147	25.523	24.853	25.392	25.361	25.364	25.370
29	31.672	28.385	27.649	27.445	28.200	27.457	28.202	27.411	27.358	27.365	27.375
30	27.913	27.231	27.222	27.104	26.477	27.163	25.955	27.001	27.089	27.093	27.087



1												
2												
3	31	29.731	27.816	27.743	27.758	28.067	27.939	27.863	27.778	27.793	27.769	27.748
4	27.748											
5												
6	32	37.791	36.611	36.412	36.254	36.170	36.342	36.044	36.181	36.210	36.231	36.247
7	36.247											
8												
9	33	30.291	28.257	27.869	27.909	28.627	28.102	28.472	28.051	27.899	27.890	27.899
10	27.899											
11												
12	34	29.825	28.981	29.045	29.033	27.980	28.916	27.876	28.890	29.019	29.034	29.032
13	29.032											
14												
15	35	43.592	44.209	44.525	44.642	42.943	44.341	43.171	44.468	44.632	44.687	44.715
16	44.715											
17												
18	36	32.642	36.044	36.830	37.002	36.345	37.058	35.916	36.829	36.986	37.020	37.033
19	37.033											
20												
21	37	44.943	43.157	43.349	43.310	44.162	43.365	44.080	43.254	43.313	43.313	43.306
22	43.306											
23												
24	38	34.631	30.509	29.519	29.199	30.511	29.563	30.102	29.401	29.219	29.181	29.167
25	29.167											
26												
27	39	35.958	35.367	35.257	35.189	35.517	35.506	34.666	35.187	35.083	35.061	35.053
28	35.053											
29												
30	40	37.001	34.033	33.453	33.363	34.663	33.710	34.631	33.554	33.387	33.337	33.313
31	33.313											
32												
33	41	46.626	45.445	45.085	44.829	44.072	44.877	43.335	44.588	44.762	44.766	44.752
34	44.752											
35												
36	42	42.164	38.284	37.451	37.255	38.631	37.644	37.984	37.332	37.178	37.132	37.111
37	37.111											
38												
39	43	42.729	38.386	37.465	37.232	38.498	37.463	38.369	37.347	37.218	37.176	37.154
40	37.154											
41												
42	44	43.975	41.187	40.341	40.192	41.761	40.455	42.000	40.415	40.216	40.176	40.163
43	40.163											
44												
45	45	50.252	50.674	50.588	50.505	49.967	50.570	49.451	50.284	50.401	50.405	50.398
46	50.398											
47												
48	46	44.696	42.275	41.789	41.650	42.540	41.947	42.534	41.800	41.663	41.619	41.597
49	41.597											
50												
51	47	51.553	46.740	45.349	44.985	47.109	45.431	46.807	45.196	44.942	44.875	44.845
52	44.845											

MAD

1 3.735 0.837 0.254 0.047 0.865 0.188 0.886 0.128 0.041 0.016 0.000

MaxAD

1  
2  
3 1 10.264 2.625 0.713 0.149 2.605 0.586 2.433 0.434 0.116 0.049 0.000  
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10 DF-MP2 results (using DF-HF reference functions)  
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	DZ	TZ	QZ	5Z	ADZ	ATZ	(A)DZ	(A)TZ	(A)QZ	(A)5Z	XPOL	REF
Glycine												
1	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
2	7.957	6.321	5.194	4.900	7.348	5.729	7.155	5.418	4.895	4.783	4.680	4.680
Alanine												
1	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
2	8.645	6.555	5.806	5.699	7.115	6.268	7.005	6.025	5.695	5.631	5.582	5.582
3	11.780	9.992	9.945	10.014	9.522	9.526	9.877	9.752	9.928	10.014	10.095	10.095
4	15.921	13.388	12.865	13.005	12.947	12.789	12.652	12.679	12.929	13.022	13.121	13.121
5	17.219	18.962	19.774	20.242	18.582	19.785	18.301	19.705	20.168	20.321	20.471	20.471
6	20.622	20.111	20.314	20.457	18.110	19.754	17.577	19.444	20.222	20.385	20.531	20.531
7	24.756	25.839	26.546	27.002	26.881	26.651	27.017	26.629	27.042	27.117	27.201	27.201
Serine												
1	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
2	18.352	14.933	13.810	13.471	13.939	13.491	14.045	13.469	13.436	13.483	13.546	13.546
3	19.039	16.685	15.493	15.076	16.195	15.244	15.755	15.110	15.039	15.006	14.985	14.985
4	23.293	19.992	18.288	17.776	19.809	18.195	19.960	18.217	17.849	17.769	17.712	17.712
5	15.919	17.941	18.623	19.024	17.218	18.291	17.000	18.295	19.046	19.158	19.246	19.246
6	24.248	20.709	19.182	18.618	20.179	19.064	19.707	18.930	18.604	18.557	18.526	18.526

1												
2												
3		18.526										
4												
5	7	30.796	26.215	24.645	24.089	23.463	23.958	23.641	23.867	23.951	24.013	24.091
6		24.091										
7												
8	8	29.240	26.175	24.899	24.427	23.795	24.197	23.842	24.021	24.275	24.351	24.439
9		24.439										
10												
11	9	28.942	27.567	27.393	27.563	25.725	26.581	26.037	26.648	27.457	27.674	27.887
12		27.887										
13												
14	10	30.767	27.039	25.699	25.354	26.142	25.553	25.880	25.286	25.327	25.348	25.389
15		25.389										
16												
17	11	33.022	30.003	28.897	28.540	27.410	28.327	27.549	28.242	28.471	28.528	28.603
18		28.603										
19												
20	12	32.966	28.572	27.180	26.849	27.485	27.130	27.318	26.833	26.738	26.771	26.828
21		26.828										
22												
23	13	35.386	29.632	27.642	27.147	27.296	27.277	26.608	26.889	26.970	27.038	27.127
24		27.127										
25												
26	14	28.518	29.384	29.536	29.653	28.001	29.316	27.768	29.141	29.557	29.733	29.921
27		29.921										
28												
29	15	41.581	34.244	32.498	31.967	30.185	31.032	30.746	31.107	31.671	31.878	32.095
30		32.095										
31												
32	16	36.451	32.610	31.906	31.775	30.427	31.236	29.693	30.840	31.570	31.792	32.030
33		32.030										
34												
35	17	42.603	34.648	32.647	32.063	30.530	31.367	30.689	31.333	31.837	32.027	32.223
36		32.223										
37												
38	18	43.046	35.972	33.358	32.516	33.430	32.832	32.905	32.419	32.302	32.385	32.497
39		32.497										
40												
41	19	36.722	32.738	31.928	31.764	31.080	31.195	31.842	31.350	31.704	31.812	31.921
42		31.921										
43												
44	20	43.729	36.482	34.606	34.043	32.479	33.370	32.726	33.293	33.834	34.018	34.209
45		34.209										
46												
47	21	39.861	34.791	33.760	33.503	31.982	32.995	31.426	32.683	33.286	33.518	33.769
48		33.769										
49												
50	22	33.788	34.035	34.164	34.284	33.219	34.156	32.744	33.793	34.214	34.316	34.425
51		34.425										
52												
53	23	39.815	36.868	35.783	35.430	34.144	35.216	33.835	34.720	35.262	35.388	35.526
54		35.526										
55												
56	24	38.437	36.847	36.468	36.360	34.504	35.560	34.545	35.664	36.254	36.426	36.601
57		36.601										
58												
59												
60												

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2  
3 25 37.089 36.755 36.802 36.670 33.839 35.864 33.237 35.500 36.304 36.557 36.809  
4 36.809

5  
6 26 41.671 38.574 37.609 37.305 34.145 36.557 33.661 36.175 36.975 37.223 37.471  
7 37.471

8  
9 27 37.472 38.249 38.409 38.329 35.462 37.457 34.880 37.052 37.978 38.232 38.484  
10 38.484

11  
12 28 32.449 36.773 37.914 38.316 34.995 37.287 33.995 36.836 38.000 38.316 38.619  
13 38.619

14  
15 29 44.335 41.179 40.494 40.270 37.826 39.959 36.633 39.193 40.070 40.288 40.524  
16 40.524

17  
18 30 40.752 40.301 40.088 40.214 40.242 40.055 40.589 40.028 40.270 40.390 40.537  
19 40.537

20  
21 31 43.815 41.110 40.189 39.859 38.883 39.708 38.529 39.379 39.728 39.851 39.993  
22 39.993

23  
24 32 45.850 42.879 41.942 41.677 38.645 40.837 38.116 40.405 41.343 41.605 41.865  
25 41.865

26  
27 33 48.272 43.064 41.950 41.615 39.155 40.895 38.904 40.621 41.307 41.523 41.751  
28 41.751

29  
30 34 47.703 43.999 43.154 42.942 39.676 42.018 39.112 41.647 42.616 42.884 43.156  
31 43.156

32  
33 35 51.056 49.640 49.749 49.975 49.848 49.529 50.290 49.562 50.018 50.119 50.241  
34 50.241

35  
36 36 59.537 54.486 53.666 53.360 52.099 52.722 51.936 52.582 53.193 53.407 53.627  
37 53.627

38  
39 37 55.494 54.607 54.558 54.461 50.661 53.240 49.659 52.764 53.975 54.388 54.813  
40 54.813

41  
42 38 65.537 61.912 61.306 61.117 59.223 60.394 58.639 59.957 60.863 61.208 61.591  
43 61.591

44  
45 39 77.596 71.888 70.286 69.769 69.614 69.935 69.116 69.451 69.676 69.836 70.053  
46 70.053

47 Cysteine

48  
49 1 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000

50  
51 2 12.862 10.062 8.688 8.239 9.145 8.807 8.748 8.543 8.281 8.247 8.232 8.232

52  
53 3 9.129 9.710 9.657 9.640 9.013 9.816 8.072 9.237 9.537 9.646 9.770 9.770

54  
55 4 14.261 12.434 12.032 11.939 11.592 11.734 10.845 11.273 11.637 11.790 11.960  
56 11.960

1												
2												
3	5	11.784	11.669	11.364	11.346	11.353	11.568	10.729	11.090	11.291	11.339	11.401
4		11.401										
5												
6	6	12.885	13.472	13.360	13.300	12.953	13.521	12.209	13.021	13.231	13.311	13.411
7		13.411										
8												
9	7	16.126	14.092	13.268	13.120	13.154	13.781	12.315	13.083	13.056	13.095	13.164
10		13.164										
11												
12	8	16.735	16.168	15.970	15.965	15.702	16.120	15.089	15.537	15.844	15.950	16.079
13		16.079										
14												
15	9	16.025	16.316	16.516	16.659	15.996	16.807	15.061	16.366	16.573	16.686	16.830
16		16.830										
17												
18	10	17.513	17.349	17.235	17.241	16.303	17.407	14.831	16.439	17.032	17.215	17.421
19		17.421										
20												
21	11	17.417	16.329	16.100	16.100	16.938	16.533	16.028	15.925	16.070	16.129	16.219
22		16.219										
23												
24	12	21.976	18.728	18.305	18.317	16.583	17.717	16.204	17.423	18.033	18.305	18.596
25		18.596										
26												
27	13	19.525	17.918	17.546	17.535	17.498	18.064	16.671	17.265	17.450	17.498	17.571
28		17.571										
29												
30	14	21.413	19.140	19.008	19.093	17.669	18.757	16.848	18.289	18.888	19.128	19.382
31		19.382										
32												
33	15	21.544	20.718	20.564	20.709	20.594	20.831	19.766	20.134	20.590	20.721	20.874
34		20.874										
35												
36	16	24.041	22.804	22.214	22.154	22.482	22.664	21.514	22.058	22.063	22.109	22.183
37		22.183										
38												
39	17	22.111	21.790	22.109	22.331	20.841	22.080	19.416	21.491	22.237	22.482	22.748
40		22.748										
41												
42	18	25.978	23.423	23.330	23.512	21.889	23.007	21.605	22.574	23.285	23.542	23.815
43		23.815										
44												
45	19	22.670	23.667	24.076	24.237	22.284	23.747	21.701	23.465	24.080	24.327	24.590
46		24.590										
47												
48	20	27.296	24.485	23.737	23.649	24.116	23.992	23.180	23.095	23.416	23.544	23.701
49		23.701										
50												
51	21	26.992	26.232	26.086	25.994	24.554	25.723	23.479	25.180	25.766	26.024	26.306
52		26.306										
53												
54	22	23.575	25.409	26.053	26.379	23.607	26.127	22.223	25.327	26.143	26.407	26.678
55		26.678										
56												
57	23	25.902	25.559	25.915	26.194	23.791	25.855	22.768	25.280	25.963	26.213	26.482
58		26.482										
59												
60												

24	29.345	27.632	27.496	27.743	26.493	27.463	25.462	26.877	27.598	27.838	28.101
28.101											
25	33.274	30.431	29.575	29.458	29.825	30.003	27.939	28.821	29.154	29.299	29.489
29.489											
26	29.391	28.486	28.322	28.346	26.707	27.832	26.824	27.634	28.260	28.398	28.548
28.548											
27	28.015	28.777	29.445	29.826	27.193	29.453	26.465	28.810	29.612	29.865	30.131
30.131											
28	24.727	28.825	29.902	30.374	28.205	30.145	26.871	29.566	30.174	30.419	30.678
30.678											
29	33.764	32.050	31.887	31.919	30.311	31.375	29.739	30.894	31.598	31.914	32.250
32.250											
30	31.308	32.721	33.083	33.027	30.047	32.393	29.449	32.029	32.813	33.042	33.272
33.272											
31	31.846	31.686	31.850	32.126	30.728	31.681	30.503	31.295	32.083	32.243	32.414
32.414											
32	36.645	34.830	34.261	34.200	32.108	33.541	31.827	33.253	33.973	34.197	34.425
34.425											
33	31.530	31.977	32.439	32.826	32.003	32.637	31.238	32.265	32.747	32.956	33.192
33.192											
34	34.835	35.497	35.837	35.884	32.346	35.079	31.941	34.705	35.625	35.872	36.116
36.116											
35	36.253	35.647	35.699	35.822	32.143	34.637	32.945	34.934	35.733	35.953	36.156
36.156											
36	29.985	35.045	35.891	36.190	33.010	35.436	31.626	34.595	35.807	36.128	36.441
36.441											
37	40.619	39.187	39.392	39.565	38.931	39.209	38.578	38.900	39.566	39.723	39.882
39.882											
38	41.100	40.950	40.881	40.840	39.402	40.928	38.203	40.100	40.715	40.964	41.253
41.253											
39	38.481	40.856	41.524	41.870	39.328	41.434	37.366	40.442	41.398	41.762	42.159
42.159											
40	39.739	40.359	40.694	41.000	39.954	40.799	39.548	40.395	40.890	41.116	41.382
41.382											
41	44.276	43.635	43.223	43.004	38.971	41.629	37.794	40.891	42.402	42.834	43.270
43.270											
42	45.193	44.781	45.010	45.222	43.867	44.733	42.198	43.731	44.791	45.185	45.623
45.623											

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3 43 47.666 47.318 47.409 47.534 46.099 47.274 45.159 46.449 47.287 47.608 47.968  
4 47.968

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6 44 47.003 47.626 47.551 47.641 46.908 47.586 46.602 47.219 47.570 47.731 47.929  
7 47.929

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9 45 47.884 50.067 50.202 50.368 46.862 49.399 45.207 48.344 49.748 50.189 50.639  
10 50.639

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12 46 48.344 49.642 49.966 50.268 48.650 49.946 47.972 49.554 50.037 50.278 50.554  
13 50.554

14  
15 47 57.296 56.224 55.879 55.901 55.221 55.838 53.951 54.847 55.568 55.853 56.193  
16 56.193

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18 MAD

19  
20 1 3.024 0.908 0.343 0.203 1.681 0.636 2.128 0.920 0.375 0.194 0.000

21  
22 MaxAD

23  
24 1 10.549 3.475 0.861 0.474 4.299 1.640 5.475 2.378 0.891 0.450 0.000

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28 =====  
29 =====  
30  
31 DF-LMP2 results, standard NLMP/NPA domains, npasel=0.03, DF-HF reference functions

32  
33 Last column: LMP2(ext)/(A)TZ

34  
35 -----  
36  
37 DZ TZ QZ 5Z ADZ ATZ (A)DZ (A)TZ (A)QZ (A)5Z XPOL REF  
38 LMP2(ext)

39  
40 Glycine

41  
42 1 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000  
43 0.000

44  
45 2 5.041 3.953 4.048 4.277 4.455 4.286 4.616 4.155 4.379 4.464 4.568 4.680  
46 4.595

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48 Alanine

49  
50 1 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000  
51 0.000

52  
53 2 6.733 4.608 4.822 5.093 5.149 5.068 5.252 5.015 5.203 5.337 5.495 5.582  
54 5.345

55  
56 3 11.850 10.262 10.194 10.154 9.991 10.036 10.071 10.116 10.127 10.146 10.158  
57 10.095 10.071

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3 4 14.753 12.026 12.355 12.758 12.054 12.268 11.910 12.225 12.744 12.923 13.113  
4 13.121 12.338

5  
6 5 17.285 18.875 19.928 20.310 19.100 19.803 18.865 19.762 20.251 20.366 20.477  
7 20.471 19.669

8  
9 6 21.430 20.111 20.451 20.493 19.312 19.792 19.083 19.732 20.316 20.435 20.535  
10 20.531 19.675

11  
12 7 23.553 24.278 25.718 26.517 25.148 25.760 25.427 25.829 26.658 26.898 27.155  
13 27.201 26.020

14  
15 Serine

16  
17 1 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000  
18 0.000

19  
20 2 15.934 13.560 13.181 13.156 12.803 12.868 13.044 12.930 13.217 13.368 13.540  
21 13.546 13.116

22  
23 3 15.501 13.659 14.012 14.326 12.638 13.706 12.807 13.723 14.423 14.675 14.953  
24 14.985 14.257

25  
26 4 19.868 17.657 17.410 17.446 17.555 17.182 18.011 17.297 17.511 17.646 17.816  
27 17.712 17.608

28  
29 5 16.615 18.897 19.652 19.732 18.715 19.197 18.264 19.208 19.559 19.584 19.580  
30 19.246 18.943

31  
32 6 20.427 17.595 17.579 17.776 16.090 17.184 16.232 17.175 17.884 18.151 18.451  
33 18.526 17.925

34  
35 7 27.190 23.252 23.132 23.247 20.786 22.475 21.026 22.531 23.320 23.617 23.942  
36 24.091 23.283

37  
38 8 25.736 23.234 23.400 23.631 21.432 22.834 21.734 22.892 23.695 23.991 24.311  
39 24.439 23.463

40  
41 9 28.360 27.707 28.038 28.020 26.845 27.157 26.834 27.232 27.814 27.949 28.076  
42 27.887 27.130

43  
44 10 27.282 23.806 24.137 24.522 23.121 23.736 23.412 23.760 24.604 24.927 25.284  
45 25.389 24.247

46  
47 11 29.602 27.098 27.339 27.663 25.173 26.638 25.692 26.735 27.749 28.100 28.483  
48 28.603 27.331

49  
50 12 28.300 24.607 25.288 25.817 23.907 24.903 24.168 24.928 25.908 26.281 26.695  
51 26.828 25.600

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53 13 31.322 26.038 25.682 25.982 23.770 25.080 23.679 24.994 26.105 26.480 26.892  
54 27.127 25.812

55  
56 14 26.955 28.215 29.159 29.484 27.671 28.703 27.641 28.698 29.438 29.691 29.960  
57 29.921 28.774



1												
2												
3	15	38.580	32.211	31.716	31.563	29.541	30.414	29.954	30.541	31.412	31.728	32.059
4		32.095	30.895									
5												
6	16	32.951	29.107	30.118	30.821	27.616	29.349	27.675	29.338	30.846	31.341	31.864
7		32.030	29.876									
8												
9	17	39.436	32.386	31.616	31.504	29.055	30.412	29.349	30.500	31.428	31.789	32.165
10		32.223	31.050									
11												
12	18	38.846	32.124	31.370	31.421	29.735	30.514	30.033	30.491	31.434	31.845	32.301
13		32.497	31.289									
14												
15	19	34.446	31.501	31.568	31.658	31.136	31.050	31.535	31.171	31.680	31.856	32.035
16		31.921	31.296									
17												
18	20	40.432	34.025	33.515	33.484	31.173	32.367	31.607	32.463	33.414	33.801	34.203
19		34.209	32.911									
20												
21	21	36.349	31.334	31.987	32.518	29.081	31.041	29.131	31.024	32.534	33.028	33.554
22		33.769	31.736									
23												
24	22	30.458	31.199	32.828	33.583	30.854	32.470	30.888	32.452	33.654	34.004	34.373
25		34.425	32.819									
26												
27	23	36.096	33.310	33.848	34.301	31.558	33.115	32.012	33.103	34.386	34.841	35.325
28		35.526	33.786									
29												
30	24	36.023	34.906	35.625	35.949	33.377	34.847	33.567	34.991	35.989	36.305	36.630
31		36.601	35.294									
32												
33	25	35.060	34.864	35.762	36.078	32.408	34.784	32.336	34.742	35.971	36.311	36.655
34		36.809	35.302									
35												
36	26	38.476	35.859	36.325	36.574	32.490	35.015	32.358	34.970	36.428	36.857	37.296
37		37.471	35.549									
38												
39												
40	27	35.800	36.540	37.506	37.837	34.459	36.519	34.445	36.501	37.712	38.047	38.386
41		38.484	36.898									
42												
43	28	32.848	36.546	38.136	38.474	36.271	37.229	35.860	37.121	38.184	38.418	38.637
44		38.619	37.046									
45												
46	29	40.728	37.575	38.519	39.121	35.176	37.563	35.180	37.455	39.158	39.725	40.328
47		40.524	38.243									
48												
49	30	38.128	38.310	39.337	39.950	38.566	39.038	39.057	39.162	40.035	40.327	40.655
50		40.537	39.345									
51												
52	31	40.861	38.087	38.396	38.813	35.750	37.635	35.872	37.637	38.913	39.363	39.848
53		39.993	38.494									
54												
55	32	42.455	39.882	40.580	40.923	37.095	39.302	37.061	39.264	40.787	41.248	41.717
56		41.865	39.747									
57												
58	33	44.519	40.230	40.696	40.938	37.535	39.413	37.578	39.415	40.740	41.176	41.633
59												
60												

1													
2													
3													
4		41.751	39.918										
5		34	45.592	41.848	42.275	42.456	39.310	40.939	39.375	40.939	42.276	42.683	43.101
6			43.156	41.209									
7													
8		35	48.047	47.186	48.581	49.397	47.785	48.156	48.482	48.327	49.538	49.870	50.234
9			50.241	48.492									
10													
11		36	56.316	52.093	52.673	52.903	50.476	51.661	50.542	51.683	52.822	53.259	53.713
12			53.627	52.334									
13													
14		37	54.432	53.090	53.850	54.066	50.532	52.485	50.233	52.407	53.813	54.277	54.755
15			54.813	52.881									
16													
17		38	61.648	58.243	59.353	60.085	56.173	58.296	56.571	58.316	60.109	60.745	61.433
18			61.591	59.008									
19													
20		39	71.576	66.527	67.270	68.055	64.475	66.578	65.098	66.666	68.381	69.070	69.842
21			70.053	67.740									
22													
23			Cysteine										
24													
25		1	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
26			0.000										
27													
28		2	10.076	7.357	7.447	7.644	6.632	7.278	6.603	7.162	7.725	7.962	8.232
29			7.592										
30													
31		3	7.566	7.867	8.538	8.912	7.091	8.333	7.143	8.135	8.911	9.241	9.597
32			8.657										
33													
34		4	13.235	11.619	11.577	11.644	10.796	11.150	10.474	10.889	11.388	11.616	11.865
35			11.960	11.136									
36													
37		5	9.442	9.357	10.086	10.650	9.102	10.029	9.055	9.902	10.710	10.992	11.299
38			10.185										
39													
40		6	10.840	11.348	12.203	12.640	10.906	12.164	10.696	11.991	12.680	12.986	13.323
41			13.411	12.497									
42													
43		7	13.192	10.855	11.611	12.129	10.243	11.493	10.169	11.267	12.189	12.582	13.022
44			13.164	11.981									
45													
46		8	13.974	13.775	14.540	15.108	13.113	14.584	13.121	14.392	15.156	15.504	15.887
47			16.079	15.033									
48													
49		9	13.664	13.923	15.093	15.749	13.431	14.970	13.538	14.872	15.810	16.212	16.659
50			16.830	15.562									
51													
52		10	14.932	14.701	15.681	16.228	13.605	15.295	13.412	14.914	16.143	16.653	17.203
53			17.421	15.645									
54													
55		11	14.918	14.021	14.897	15.428	14.280	14.865	14.244	14.695	15.412	15.754	16.141
56			16.219	15.151									
57													
58		12	20.548	17.654	17.861	18.003	15.928	17.118	15.984	17.035	17.805	18.155	18.528
59													
60													

1												
2												
3		18.596	17.344									
4												
5	13	17.195	15.602	16.338	16.814	15.573	16.172	15.605	15.924	16.755	17.098	17.478
6		17.571	16.426									
7												
8	14	19.451	17.734	18.338	18.658	16.399	17.802	16.178	17.611	18.495	18.902	19.331
9		19.382	18.056									
10												
11	15	18.296	17.976	19.063	19.835	17.486	18.847	17.456	18.631	19.805	20.242	20.716
12		20.874	19.091									
13												
14	16	21.248	19.766	20.565	21.085	19.653	20.469	19.983	20.373	21.168	21.559	21.996
15		22.183	21.090									
16												
17	17	20.079	19.257	20.818	21.631	18.682	20.404	18.233	20.221	21.613	22.108	22.637
18		22.748	20.597									
19												
20	18	24.603	22.413	22.775	23.131	20.745	22.301	21.054	22.209	22.966	23.331	23.717
21		23.815	22.582									
22												
23	19	21.855	22.425	23.392	23.787	21.231	22.881	21.308	22.833	23.769	24.147	24.547
24		24.590	23.219									
25												
26	20	24.211	21.670	22.169	22.716	21.199	21.844	21.258	21.563	22.567	23.016	23.510
27		23.701	22.257									
28												
29	21	25.520	24.775	25.269	25.485	23.178	24.621	22.937	24.409	25.378	25.793	26.241
30		26.306	24.919									
31												
32	22	21.481	23.400	25.069	25.767	22.295	24.583	21.745	24.290	25.627	26.068	26.525
33		26.678	24.753									
34												
35	23	23.851	23.820	25.091	25.650	22.564	24.495	22.349	24.313	25.491	25.908	26.353
36		26.482	24.726									
37												
38	24	26.436	24.506	25.908	26.840	23.735	25.557	23.658	25.404	26.818	27.346	27.912
39		28.101	25.944									
40												
41	25	28.717	26.284	27.187	27.931	25.637	26.919	25.463	26.525	27.890	28.506	29.189
42		29.489	27.570									
43												
44	26	28.606	27.236	27.852	28.130	26.669	27.167	26.706	27.102	28.051	28.320	28.608
45		28.548	27.191									
46												
47	27	26.460	27.254	28.593	29.300	25.911	28.195	25.919	28.000	29.163	29.554	29.965
48		30.131	28.397									
49												
50	28	23.604	27.270	29.067	29.786	26.630	28.785	26.430	28.611	29.710	30.107	30.526
51		30.678	29.035									
52												
53	29	31.828	30.277	30.843	31.265	28.647	30.145	28.809	29.987	31.095	31.578	32.088
54		32.250	30.591									
55												
56	30	30.864	31.617	32.517	32.738	30.271	31.722	30.027	31.609	32.668	32.959	33.255
57		33.272	31.852									
58												
59												
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3 31 30.159 29.720 30.970 31.661 29.540 30.538 29.492 30.433 31.644 32.029 32.437  
4 32.414 30.702

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6 32 35.572 34.402 34.427 34.319 32.569 33.460 32.523 33.335 34.052 34.294 34.541  
7 34.425 33.640

8  
9 33 29.725 29.850 31.247 32.096 29.727 31.149 29.759 31.136 32.171 32.593 33.053  
10 33.192 31.531

11  
12 34 33.774 34.119 35.096 35.481 32.335 34.298 32.370 34.201 35.383 35.713 36.043  
13 36.116 34.510

14  
15 35 38.007 36.764 36.684 36.507 35.584 35.863 35.851 36.100 36.366 36.410 36.429  
16 36.156 35.658

17  
18 36 31.115 35.123 36.236 36.353 34.400 35.362 33.930 35.084 36.028 36.255 36.469  
19 36.441 35.026

20  
21 37 39.659 38.595 39.452 39.721 38.675 39.036 38.627 38.922 39.601 39.854 40.114  
22 39.882 39.203

23  
24 38 37.948 37.161 38.666 39.540 35.853 38.154 35.744 37.952 39.622 40.298 41.034  
25 41.253 38.844

26  
27 39 36.497 38.646 40.355 41.064 37.220 39.622 36.727 39.220 40.737 41.324 41.956  
28 42.159 39.823

29  
30 40 37.290 37.264 39.000 40.004 37.112 38.674 37.569 38.639 40.072 40.598 41.177  
31 41.382 39.212

32  
33 41 45.268 43.632 43.383 43.123 41.172 41.839 40.555 41.500 42.627 42.969 43.309  
34 43.270 41.456

35  
36 42 42.399 41.762 43.243 44.143 40.871 42.570 40.522 42.197 43.933 44.622 45.371  
37 45.623 42.850

38  
39 43 44.406 43.541 45.185 46.231 42.432 44.544 42.588 44.363 46.204 46.920 47.693  
40 47.968 45.271

41  
42 44 44.518 44.482 45.727 46.512 43.991 45.411 44.712 45.494 46.706 47.216 47.781  
43 47.929 46.218

44  
45 45 47.650 49.257 50.010 50.233 47.384 48.754 46.917 48.361 49.719 50.134 50.556  
46 50.639 48.491

47  
48 46 44.881 46.301 48.255 49.188 45.371 47.722 45.681 47.647 49.193 49.752 50.362  
49 50.554 48.440

50  
51 47 53.198 52.145 53.442 54.386 51.180 52.865 51.340 52.619 54.397 55.136 55.952  
52 56.193 53.622

53  
54 MAD

55  
56 1 2.342 1.936 1.232 0.816 3.032 1.773 2.998 1.853 0.851 0.488 0.123  
57 1.410

1  
2  
3 MaxAD

4  
5 1 7.212 4.427 2.783 1.998 5.578 3.475 5.509 3.605 1.796 1.057 0.334  
6 2.774  
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12 =====  
13 =====  
14  
15 Geometries (xyz format, in Angstrom)  
16  
17 -----  
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19 GLYCINE

20 glycine\_1 -455.33935359386 a.u.

21  
22  
23 C 3.033948 0.370630 0.782112

24 C 1.802176 0.176200 -0.078235

25  
26 O 1.443213 1.023317 -0.915523

27  
28 H 2.905568 1.288005 1.374728

29  
30 H 3.227794 -0.476299 1.455992

31  
32 H 3.899914 0.514703 0.119925

33  
34 N 1.111247 -0.986642 0.108032

35  
36 C -0.095431 -1.292651 -0.659826

37  
38 C -1.342397 -0.616305 -0.075338

39  
40 O -2.228810 -1.261832 0.504760

41  
42 H 1.378305 -1.602044 0.866193

43  
44 H 0.073761 -0.960981 -1.696110

45  
46 H -0.262854 -2.376884 -0.636398

47  
48 N -1.378961 0.732275 -0.243586

49  
50 C -2.451943 1.520840 0.348622

51  
52 H -0.553035 1.176987 -0.642171

53  
54 H -3.426608 1.141059 0.010760

55  
56 H -2.426858 1.467394 1.448811  
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2  
3 H -2.335331 2.564465 0.029241  
4  
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6

7 glycine\_2 -455.33656092531 a.u.  
8

9 C 3.408842 0.915890 0.000064  
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11 C 2.340217 -0.161251 0.000005  
12

13 O 2.612265 -1.371075 0.000060  
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15 H 4.041608 0.780273 0.889226  
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17 H 4.041946 0.780036 -0.888820  
18

19 H 2.991492 1.933220 -0.000146  
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21 N 1.048372 0.279676 -0.000106  
22

23 C -0.049249 -0.659777 -0.000081  
24

25 C -1.356984 0.129111 -0.000043  
26

27 O -1.382383 1.368707 -0.000024  
28

29 H 0.800691 1.264838 -0.000066  
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31 H -0.001905 -1.315939 -0.886760  
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33 H -0.001854 -1.315948 0.886590  
34

35 N -2.490703 -0.622673 -0.000073  
36

37 C -3.805383 0.011417 0.000114  
38

39 H -2.412975 -1.631614 0.000163  
40

41 H -3.927408 0.644016 -0.891310  
42

43 H -4.571278 -0.774406 -0.000424  
44

45 H -3.927709 0.643093 0.892160  
46  
47

48 ALANINE

49 alanine\_1 -494.53336002632 a.u.  
50

51 C -3.077696 -0.614096 0.770471  
52

53 C -1.837634 -0.380064 -0.068647  
54

55 O -1.529867 -1.134105 -1.009779  
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7	H	-0.418053	1.087624	-1.706102
8				
9	H	-3.434930	-1.856102	0.610141
10				
11	H	-3.645462	-1.038336	-0.960056
12				
13	H	-3.013635	-2.722515	-0.901347
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15				
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17	serine_35	-569.58463816	a.u.	
18				
19	C	-3.288880	-0.819234	-0.424296
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21	C	-1.834561	-0.580782	-0.051986
22				
23	O	-1.335686	-1.137270	0.936529
24				
25	H	-3.509933	-1.888000	-0.302829
26				
27	H	-3.918624	-0.257450	0.282748
28				
29	H	-3.536420	-0.503888	-1.448592
30				
31	N	-1.164516	0.271937	-0.893674
32				
33	C	0.142348	0.937899	-0.751922
34				
35	C	1.405317	0.081023	-0.532562
36				
37	O	2.486328	0.545880	-0.935722
38				
39	C	0.117762	2.083065	0.264366
40				
41	O	-0.098032	1.521891	1.562812
42				
43	H	-1.718366	0.618575	-1.667605
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45	H	-0.005626	2.230308	2.214423
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47	H	0.330248	1.405866	-1.731468
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49	H	1.087749	2.606181	0.199183
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51	H	-0.694833	2.783892	-0.004221
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53	N	1.275501	-1.106357	0.093797
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55	C	2.468403	-1.880646	0.412939
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57	H	0.387657	-1.279798	0.578270
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3 H 3.069236 -2.027101 -0.495502  
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5 H 3.094490 -1.364113 1.158551  
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7 H 2.154320 -2.855487 0.807996  
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11 serine\_36 -569.58518761 a.u.  
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13 C 3.128904 -1.010278 -0.318829  
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15 C 1.710453 -0.470511 -0.328149  
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17 O 0.897950 -0.749991 -1.212976  
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19 H 3.511581 -1.008899 -1.347981  
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21 H 3.803833 -0.430807 0.328313  
22  
23 H 3.098277 -2.052231 0.036123  
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25 N 1.388661 0.347566 0.735073  
26  
27 C 0.009553 0.752931 1.005775  
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29 C -0.964353 -0.406390 0.692525  
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31 O -0.902710 -1.443946 1.361609  
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33 C -0.329581 2.119451 0.408988  
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35 O -0.261770 2.054098 -1.025550  
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37 H 2.035157 0.358927 1.514630  
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39 H -0.395503 2.947728 -1.370621  
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41 H -0.071339 0.875571 2.099667  
42  
43 H -1.342684 2.408299 0.744201  
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45 H 0.399447 2.853530 0.794747  
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47 N -1.906393 -0.165856 -0.265592  
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49 C -2.708460 -1.297052 -0.725632  
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51 H -1.610513 0.511778 -0.966400  
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53 H -3.204952 -1.761969 0.135790  
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55 H -3.467296 -0.928192 -1.428505  
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57 H -2.078738 -2.055896 -1.219069  
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serine\_37 -569.58191740 a.u.

C	-3.448036	-0.344564	-0.374990
C	-2.067579	-0.117312	0.213981
O	-1.856220	0.649850	1.155911
H	-3.948946	0.627191	-0.482656
H	-3.420352	-0.856961	-1.347981
H	-4.033544	-0.950370	0.333526
N	-1.034945	-0.815241	-0.386210
C	0.278519	-0.858125	0.257787
C	0.939590	0.527594	0.331762
O	1.677284	0.837070	1.267507
C	1.149593	-1.821887	-0.556702
O	2.390796	-1.966897	0.127289
H	-1.286792	-1.578661	-1.006624
H	2.988924	-2.474568	-0.437233
H	0.201738	-1.210573	1.299345
H	0.624539	-2.795018	-0.634847
H	1.290441	-1.408890	-1.572572
N	0.726851	1.327695	-0.763051
C	1.183755	2.713781	-0.717124
H	-0.096990	1.110952	-1.313221
H	2.254866	2.728948	-0.477342
H	1.025182	3.171529	-1.702782
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serine\_38 -569.57795927 a.u.

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C	2.065133	-0.756007	0.077880

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7 H 2.301669 -1.993627 -1.725141  
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9 H 3.747013 -1.072906 -1.201064  
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11 N 0.829548 -0.379125 -0.408442  
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13 C -0.060751 0.494068 0.342427  
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15 C -1.436883 -0.162293 0.505221  
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19 C -0.157711 1.888221 -0.283546  
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21 O 1.148016 2.463572 -0.228556  
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23 H 0.520605 -0.759589 -1.294602  
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25 H 1.095024 3.368113 -0.566158  
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27 H 0.375001 0.586315 1.347696  
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29 H -0.503670 1.819779 -1.334835  
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31 H -0.891331 2.485805 0.289024  
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33 N -2.172442 -0.282018 -0.649916  
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35 C -3.512169 -0.862667 -0.599564  
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37 H -1.909784 0.268300 -1.457784  
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39 H -3.460397 -1.851761 -0.125035  
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41 H -4.201879 -0.235396 -0.013122  
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43 H -3.888815 -0.967942 -1.625446  
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## CYSTEINE

cysteine\_1 -892.21081947086 a.u.

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52 C -1.705008 -1.313294 0.063364  
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56 H -2.718237 -3.179529 -0.149367  
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3 H -3.032565 -2.016087 -1.456741  
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7 N -0.358239 -1.117616 0.006890  
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9 C 0.327371 -0.108090 0.807715  
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11 C 0.238126 1.293364 0.164326  
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13 O 1.241303 1.917042 -0.224971  
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15 C 1.782348 -0.525004 1.040149  
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17 S 2.681147 -0.977895 -0.500053  
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19 H 0.208275 -1.609646 -0.680558  
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21 H 2.610078 0.269090 -1.021316  
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23 H -0.196100 -0.063949 1.779520  
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25 H 2.322010 0.287929 1.544295  
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27 H 1.809625 -1.424789 1.673800  
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29 N -1.023164 1.778410 0.075788  
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31 C -1.278214 3.070030 -0.550455  
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35 H -0.717473 3.862809 -0.033882  
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37 H -0.966190 3.061603 -1.606209  
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39 H -2.353453 3.279909 -0.487142  
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43 cysteine\_2 -892.20733413107 a.u.  
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45 C -3.779963 -1.000497 0.125086  
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47 C -2.552638 -0.167719 -0.188375  
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57 N -1.352565 -0.699240 0.196431  
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5 C 1.009726 -1.055123 -0.017833  
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7 O 0.800504 -2.187716 0.449573  
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9 C 0.091440 1.194582 0.785608  
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11 S 1.272374 2.441199 0.126578  
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15 H 0.468274 2.854183 -0.879441  
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17 H -0.187717 0.343966 -1.185900  
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19 H -0.878258 1.684709 0.941265  
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21 H 0.493774 0.871713 1.758979  
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23 N 2.231351 -0.644850 -0.440111  
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25 C 3.397387 -1.506892 -0.273791  
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27 H 2.344417 0.336802 -0.680404  
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29 H 3.617403 -1.680981 0.791061  
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33 H 4.257597 -1.023032 -0.753620  
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37 cysteine\_3 -892.20737742594 a.u.

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39 C 3.453412 -1.281508 0.523441  
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41 C 2.215467 -0.757578 -0.175347  
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43 O 2.279015 -0.126889 -1.244419  
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45 H 3.980631 -1.956834 -0.166067  
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47 H 4.118577 -0.433174 0.740149  
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53 C -0.249306 -0.560703 -0.136710  
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55 C -0.480714 0.899623 0.294913  
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57 O -1.222700 1.198054 1.246003  
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3 C -1.390105 -1.459657 0.328725  
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5 S -2.980843 -1.028295 -0.473449  
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7 H 1.018575 -1.417538 1.368160  
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9 H -3.136455 0.129468 0.206984  
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11 H -0.147099 -0.611156 -1.231629  
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15 H -1.509875 -1.397143 1.420737  
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17 N 0.218742 1.806260 -0.432477  
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19 C 0.221985 3.214254 -0.052476  
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21 H 0.930343 1.436487 -1.062197  
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23 H -0.813087 3.564270 0.060312  
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27 H 0.718843 3.789427 -0.844161

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31 cysteine\_4 -892.20640260508 a.u.

32  
33 C -2.291869 -2.368868 -0.833364  
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35 C -1.726852 -1.292512 0.070467  
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37 O -2.453325 -0.612504 0.819979  
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39 H -2.796282 -3.119221 -0.206945  
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41 H -3.047684 -1.914303 -1.489990  
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43 H -1.521974 -2.862129 -1.443667  
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45 N -0.374682 -1.123872 0.024483  
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47 C 0.318058 -0.118470 0.823905  
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51 O 1.269319 1.864880 -0.225919  
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53 C 1.774584 -0.530576 1.043904  
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55 S 2.656412 -0.847426 -0.549478  
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9 H 1.815272 -1.443416 1.654074  
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11 N -1.001657 1.790519 0.077471  
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13 C -1.226843 3.078253 -0.567851  
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15 H -1.775986 1.218787 0.415187  
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17 H -0.644374 3.864488 -0.065454  
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19 H -0.918925 3.046218 -1.624405  
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21 H -2.296179 3.316595 -0.503977  
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25 cysteine\_5 -892.20648452460 a.u.  
26  
27 C 3.365309 -0.457956 -0.966367  
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29 C 2.306650 -0.508623 0.119937  
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31 O 2.545941 -0.919973 1.259138  
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33 H 3.871696 -1.432341 -1.011211  
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35 H 2.953812 -0.208472 -1.955245  
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37 H 4.114303 0.297748 -0.685406  
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39 N 1.047243 -0.085495 -0.267561  
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41 C 0.007599 0.170911 0.718670  
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43 C -1.302774 -0.564928 0.402333  
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45 O -2.383883 -0.185360 0.878618  
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47 C -0.263415 1.670818 0.881924  
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49 S -0.786072 2.457067 -0.698267  
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51 H 0.965721 0.437521 -1.137125  
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53 H -2.000968 1.862636 -0.724410  
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5 N -1.189550 -1.653609 -0.399459  
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9 H -0.267371 -1.897836 -0.739031  
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13 H -2.050574 -3.274650 -1.391310  
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19 cysteine\_6 -892.20587470359 a.u.  
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21 C 0.630535 3.168306 0.719844  
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23 C 0.092708 1.952937 -0.006196  
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25 O -0.690372 2.052903 -0.968863  
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27 H 1.281345 0.720300 1.118803  
28  
29 N 0.503515 0.738546 0.466546  
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31 C 0.223084 -0.492953 -0.272537  
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33 C -1.174454 -1.029581 0.112049  
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35 O -1.320801 -2.006065 0.862881  
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37 C 1.269952 -1.564344 0.030782  
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39 S 3.002304 -0.996643 -0.188787  
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41 H 2.871023 -0.603975 -1.476046  
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43 H -1.962230 0.549163 -0.891267  
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45 N -2.200983 -0.337961 -0.445065  
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47 C -3.576880 -0.638358 -0.066306  
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49 H -0.218887 3.759068 1.091712  
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23 H 4.381673 -1.257482 0.653973  
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25 H 3.583109 -1.747618 -0.877107  
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27 N 1.400071 -0.625846 -0.180282  
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29 C 0.159129 0.027205 0.192588  
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31 C -0.967196 -0.966732 -0.086905  
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33 O -0.880461 -1.789497 -1.013853  
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35 C -0.024274 1.314855 -0.639102  
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37 S -1.471709 2.333269 -0.146445  
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39 H 1.326807 -1.410762 -0.821606  
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41 H -2.404214 1.601387 -0.795068  
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13 O -0.630617 2.044038 -1.008023  
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15 H -0.256886 3.788183 1.015600  
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17 H 1.171159 2.901798 1.649942  
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19 H 1.248428 3.743788 0.068395  
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21 N 0.503318 0.733003 0.473793  
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23 C 0.227606 -0.510795 -0.249291  
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25 C -1.177173 -1.039704 0.111889  
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27 O -1.343899 -2.030771 0.839090  
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29 C 1.273842 -1.566086 0.094121  
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31 S 2.942421 -0.894069 -0.312602  
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33 H 1.153666 0.700979 1.251855  
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35 H 3.629099 -1.994624 0.062770  
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41 H 1.074607 -2.467631 -0.499881  
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43 N -2.188496 -0.320146 -0.436614  
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45 C -3.573585 -0.615598 -0.089866  
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47 H -1.934999 0.557461 -0.892877  
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56 cysteine\_9 -892.20471439220 a.u.  
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7	O	-0.681828	1.955005	-1.135035
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9	H	0.706373	0.818919	1.478874
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11	N	0.433370	0.815702	0.500816
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13	C	0.316083	-0.477656	-0.176940
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15	C	-1.046256	-1.115185	0.156028
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17	O	-1.166572	-2.032246	0.982722
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19	C	1.459990	-1.394285	0.244165
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21	S	3.089934	-0.823637	-0.378985
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23	H	2.986488	0.437990	0.094291
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25	H	-1.894842	0.278056	-1.062832
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27	N	-2.086424	-0.567853	-0.527118
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29	C	-3.456966	-0.965747	-0.226088
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31	H	-0.958969	3.636390	0.982417
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33	H	0.549065	3.040679	1.755867
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35	H	0.611758	3.946538	0.209557
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37	H	0.373439	-0.266883	-1.256405
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39	H	1.477481	-1.518234	1.337117
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25 H -0.562738 2.380873 0.345166  
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## ALANINE PEPTIDES

Tetrapeptide (extended)

44 C -1.7307169 -1.9998193 2.4398450  
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50 H 0.3399725 -1.1321307 1.1057528  
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52 N -0.4815890 -0.5546139 0.9193524  
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13	H	-1.1764994	0.3562927	-0.8156046
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15	H	-0.1251338	2.5918091	-0.4138146
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19	H	0.6558929	1.9666558	1.0649776
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31	C	2.3387540	-0.8315821	-3.7387636
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33	H	3.2183819	0.4169620	-2.2060526
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35	H	3.2732523	-0.9541708	-4.3048091
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37	H	2.2232795	-1.6947458	-3.0713953
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39	H	1.4994302	-0.8145745	-4.4482407
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41	H	4.4664927	1.2745949	-4.2320421
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49	O	5.9213548	1.6565450	-5.7116738
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13 H 6.2929684 2.8199577 -9.1082906  
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19 Tetrapeptide (alpha-helix)

20  
21 C -5.2517434 -2.0228398 0.7780798  
22  
23 C -4.8625137 -0.5517560 0.7325422  
24  
25 O -5.5925336 0.3304254 1.1814779  
26  
27 H -3.2468464 -1.0469982 -0.4047796  
28  
29 N -3.6131928 -0.3039855 0.1936698  
30  
31 C -3.1178851 1.0615508 -0.0685251  
32  
33 C -1.7262370 0.9878734 -0.7290987  
34  
35 O -1.4639211 1.5783618 -1.7734027  
36  
37 C -3.0555640 1.9271467 1.2022938  
38  
39 H -6.2949817 -2.1176460 0.4506971  
40  
41 H -4.6105689 -2.6679419 0.1636226  
42  
43 H -5.2045696 -2.3636619 1.8226802  
44  
45 H -3.7643212 1.5600933 -0.8077555  
46  
47 H -2.6139898 2.9036408 0.9575397  
48  
49 H -4.0642812 2.0735442 1.6015975  
50  
51 H -2.4399311 1.4514300 1.9803264  
52  
53 H -1.0743581 -0.1370730 0.8696851  
54  
55 N -0.8053020 0.2230847 -0.0443091  
56  
57 C 0.5751754 0.0423786 -0.4887049  
58  
59  
60

1				
2				
3	C	0.8320892	-1.3386175	-1.1474921
4				
5	O	1.9299767	-1.6255600	-1.6274862
6				
7	C	1.5748296	0.2853630	0.6460407
8				
9	H	0.7306093	0.7793531	-1.2916747
10				
11	H	2.5927162	0.1043997	0.2795442
12				
13	H	1.5024151	1.3187428	1.0101867
14				
15	H	1.3903442	-0.3988468	1.4890283
16				
17	H	-1.1402482	-1.8183899	-0.8301867
18				
19	N	-0.2371053	-2.1786707	-1.1385930
20				
21	C	-0.3020475	-3.4272486	-1.8714773
22				
23	C	-1.7869380	-3.6163954	-2.2563637
24				
25	O	-2.6893041	-2.9937801	-1.6767274
26				
27	C	0.2240130	-4.6168323	-1.0456462
28				
29	H	-1.2182257	-4.9588337	-3.6846560
30				
31	N	-2.0199070	-4.5168943	-3.2440336
32				
33	C	-3.3540002	-4.8607962	-3.7221645
34				
35	H	0.3135974	-3.3248260	-2.7813050
36				
37	H	0.2042205	-5.5504236	-1.6266284
38				
39	H	1.2623667	-4.4172411	-0.7507604
40				
41	H	-0.3826724	-4.7565815	-0.1400023
42				
43	H	-4.0694367	-4.2025039	-3.2174844
44				
45	H	-3.4263386	-4.7057978	-4.8077443
46				
47	H	-3.6022480	-5.9065505	-3.4893921
48				
49				
50				
51	Hexapeptide (extended)			
52				
53	C	-0.3608532	-1.6602936	0.6496324
54				
55	C	-0.1276226	-0.5560681	-0.3627130
56				
57	O	-0.6332025	-0.5884094	-1.4949245
58				
59				
60				

1				
2				
3	H	1.1136119	0.4378538	0.9547199
4				
5	N	0.6655882	0.4785102	0.0434593
6				
7	C	0.9183939	1.6653896	-0.7855861
8				
9	C	2.0432127	1.3826641	-1.8183614
10				
11	O	3.1668942	1.9025595	-1.7305239
12				
13	C	1.2518372	2.8647625	0.0934572
14				
15	H	-1.4405553	-1.7411778	0.8344402
16				
17	H	-0.0308438	-2.6144382	0.2175455
18				
19	H	0.1539205	-1.5005216	1.6061688
20				
21	H	-0.0114654	1.8462696	-1.3484788
22				
23	H	1.3957978	3.7592300	-0.5247347
24				
25	H	0.4352338	3.0558902	0.8028889
26				
27	H	2.1887511	2.7007938	0.6438141
28				
29	H	0.7477894	0.1077843	-2.7435510
30				
31	N	1.6836146	0.5323857	-2.8110937
32				
33	C	2.6441820	-0.0159074	-3.7813257
34				
35	C	2.9052129	0.9682584	-4.9560747
36				
37	O	2.6590893	0.6709650	-6.1352698
38				
39	C	2.1639305	-1.3705320	-4.2885396
40				
41	H	3.6043398	-0.1265423	-3.2480599
42				
43	H	2.8886842	-1.7857816	-4.9990594
44				
45	H	2.0459071	-2.0703850	-3.4503032
46				
47	H	1.2059472	-1.2761816	-4.8172679
48				
49	H	3.6489079	2.2922453	-3.5813462
50				
51	N	3.4488557	2.1518179	-4.5813551
52				
53	C	3.7113546	3.2378847	-5.5347050
54				
55	C	5.0764346	3.0156435	-6.2388999
56				
57	O	6.0670616	3.7212666	-6.0045546
58				
59				
60				

1				
2				
3	C	3.6596470	4.5903524	-4.8345397
4				
5	H	2.9260912	3.1728707	-6.3057079
6				
7	H	3.8304095	5.3960568	-5.5592767
8				
9	H	2.6775127	4.7377128	-4.3651184
10				
11	H	4.4454649	4.6677181	-4.0713944
12				
13	H	4.2282191	1.4191696	-7.1967284
14				
15	N	5.0832175	1.9840880	-7.1221608
16				
17	C	6.3178694	1.5017346	-7.7554772
18				
19	C	6.6420725	2.3252622	-9.0346569
20				
21	O	6.5579031	1.8469197	-10.1691426
22				
23	C	6.2064926	0.0150805	-8.0722042
24				
25	H	7.1311247	1.6834701	-7.0336599
26				
27	H	7.1394001	-0.3453565	-8.5223731
28				
29	H	6.0109312	-0.5569795	-7.1547789
30				
31	H	5.4025361	-0.1718295	-8.7963133
32				
33	H	7.0371163	3.9398624	-7.8015823
34				
35	N	7.0364581	3.6029448	-8.7736644
36				
37	C	7.3528233	4.5441033	-9.8391315
38				
39	C	8.5474872	5.4037628	-9.3875122
40				
41	O	8.6185333	5.8621288	-8.2470668
42				
43	C	6.1558599	5.4501898	-10.1861235
44				
45	H	9.3690370	5.1932384	-11.2592796
46				
47	N	9.4824237	5.6454142	-10.3574375
48				
49	C	10.6466073	6.4905728	-10.1345023
50				
51	H	7.6123680	3.9350113	-10.7187164
52				
53	H	6.4075892	6.1408801	-11.0044347
54				
55	H	5.3047415	4.8317078	-10.5016124
56				
57	H	5.8641729	6.0424284	-9.3081541
58				
59				
60				

1  
2  
3 H 11.5798958 5.9257748 -10.2774155  
4  
5 H 10.6456082 7.3588508 -10.8106350  
6  
7 H 10.5980034 6.8434755 -9.0977057  
8  
9  
10

11 Hexapeptide (alpha-helix)

12  
13 C -1.8566174 0.1013342 -1.9406248  
14  
15 C -0.6159223 0.8384601 -1.4770731  
16  
17 O -0.0408217 1.6717919 -2.1748291  
18  
19 H -0.7847461 -0.0470457 0.3731835  
20  
21 N -0.1532925 0.4972252 -0.2114070  
22  
23 C 0.8350031 1.3237120 0.4864251  
24  
25 C 2.1262977 0.5703329 0.8770376  
26  
27 O 2.9514878 1.0810749 1.6339012  
28  
29 C 0.2317379 2.0336121 1.7032682  
30  
31 H -1.6721523 -0.3443433 -2.9291980  
32  
33 H -2.1894172 -0.6807089 -1.2432468  
34  
35 H -2.6683791 0.8330278 -2.0611781  
36  
37 H 1.1506859 2.0733709 -0.2589486  
38  
39 H 1.0093333 2.6136293 2.2138784  
40  
41 H -0.5759802 2.7080001 1.3894721  
42  
43 H -0.1741294 1.3075339 2.4253439  
44  
45 H 1.6311483 -0.9320797 -0.4098080  
46  
47 N 2.3012168 -0.6625102 0.3077921  
48  
49 C 3.5930601 -1.3591072 0.4159509  
50  
51 C 3.7708568 -2.3936471 -0.7078489  
52  
53 O 4.7768092 -2.4192256 -1.4070539  
54  
55 C 3.7831743 -2.0094174 1.7979309  
56  
57 H 4.3929224 -0.6202898 0.2663661  
58  
59  
60

1				
2				
3	H	4.7582001	-2.5140905	1.8461581
4				
5	H	3.7524435	-1.2309259	2.5699467
6				
7	H	2.9942150	-2.7459844	2.0106728
8				
9	H	2.0708731	-3.3635589	-0.0808724
10				
11	N	2.7285183	-3.2972024	-0.8580411
12				
13	C	2.8919019	-4.5149742	-1.6671273
14				
15	C	1.8199460	-4.6737204	-2.7714605
16				
17	O	1.6536886	-5.7503863	-3.3444868
18				
19	C	2.9637108	-5.7710448	-0.7946527
20				
21	H	3.8503666	-4.3767379	-2.1940940
22				
23	H	3.0454878	-6.6573026	-1.4346774
24				
25	H	3.8351909	-5.7240078	-0.1282801
26				
27	H	2.0545032	-5.8837677	-0.1832286
28				
29	H	1.3207904	-2.7068747	-2.5343001
30				
31	N	1.1260131	-3.5406179	-3.0837727
32				
33	C	0.0703038	-3.5090196	-4.0983918
34				
35	C	0.0687065	-2.1310410	-4.8073730
36				
37	O	-0.9571256	-1.4494301	-4.9121580
38				
39	C	-1.3040347	-3.8524465	-3.5232059
40				
41	H	0.3478475	-4.2785249	-4.8380595
42				
43	H	-2.0667795	-3.8256912	-4.3116260
44				
45	H	-1.2747678	-4.8592363	-3.0865012
46				
47	H	-1.5992763	-3.1298349	-2.7501844
48				
49	H	2.0843882	-2.3666941	-5.2885405
50				
51	N	1.2744435	-1.7407302	-5.2958974
52				
53	C	1.4595059	-0.5220795	-6.0717129
54				
55	C	2.6441301	-0.7914453	-7.0248753
56				
57	O	3.4413066	-1.7099068	-6.8136647
58				
59				
60				

1				
2				
3	C	1.7365610	0.7024881	-5.1780155
4				
5	H	2.0391566	0.7889611	-8.1806001
6				
7	N	2.7494898	0.0710105	-8.0738173
8				
9	C	3.8488613	0.0275524	-9.0286965
10				
11	H	0.5356948	-0.3472868	-6.6474843
12				
13	H	1.8358314	1.6173242	-5.7804419
14				
15	H	0.9126422	0.8546859	-4.4686694
16				
17	H	2.6693302	0.5604624	-4.6144159
18				
19	H	3.4771353	-0.1394299	-10.0501367
20				
21	H	4.4310723	0.9606611	-9.0052481
22				
23	H	4.4986555	-0.8072828	-8.7438783

## Octapeptide (extended)

24				
25				
26				
27				
28				
29	C	-1.6015296	-1.8805714	2.3774044
30				
31	C	-1.5896908	-0.7306424	1.3785058
32				
33	O	-2.6094311	-0.1101131	1.0646801
34				
35	H	0.4556586	-1.0288983	1.0302893
36				
37	N	-0.3629157	-0.4451823	0.8465530
38				
39	C	-0.1794910	0.5369091	-0.2084299
40				
41	C	1.1185258	0.1575073	-0.9505692
42				
43	O	1.9276758	-0.6496631	-0.4719438
44				
45	C	-0.1122078	1.9732887	0.3469699
46				
47	H	-2.4978417	-1.7947855	3.0002755
48				
49	H	-1.6439709	-2.8405352	1.8406806
50				
51	H	-0.7068681	-1.8864723	3.0156836
52				
53	H	-1.0368833	0.4670951	-0.8989338
54				
55	H	-0.0087441	2.7105548	-0.4620455
56				
57	H	-1.0380597	2.1876806	0.8958275
58				
59				
60				



1				
2				
3	H	0.7423157	2.0803974	1.0299777
4				
5	H	0.6506303	1.4733871	-2.5038881
6				
7	N	1.3119669	0.7847594	-2.1358599
8				
9	C	2.5276427	0.6390056	-2.9237133
10				
11	C	2.5803622	1.8540920	-3.8747794
12				
13	O	1.5727058	2.5395584	-4.0979809
14				
15	C	2.5523364	-0.6834855	-3.7136442
16				
17	H	3.3904430	0.6609613	-2.2378115
18				
19	H	3.4887864	-0.7862934	-4.2799114
20				
21	H	2.4747221	-1.5255520	-3.0143948
22				
23	H	1.7099749	-0.7244231	-4.4187203
24				
25	H	4.5947864	1.4836750	-4.2814716
26				
27	N	3.7822829	2.0825615	-4.4532108
28				
29	C	4.0017993	3.0977434	-5.4750496
30				
31	C	5.3102714	2.7037495	-6.1961988
32				
33	O	6.0905495	1.8786016	-5.6991653
34				
35	C	4.0973451	4.5142943	-4.8773453
36				
37	H	3.1590616	3.0665025	-6.1853032
38				
39	H	4.2357462	5.2659153	-5.6670283
40				
41	H	3.1694611	4.7438782	-4.3386000
42				
43	H	4.9439464	4.5806466	-4.1796563
44				
45	H	4.9024601	4.0383758	-7.7515172
46				
47	N	5.5418904	3.3356261	-7.3688287
48				
49	C	6.7739321	3.1809251	-8.1318552
50				
51	C	6.8272164	4.3793928	-9.1060793
52				
53	O	5.8233301	5.0736310	-9.3219788
54				
55	C	6.8269205	1.8408566	-8.8890685
56				
57	H	7.6258549	3.2303409	-7.4337131
58				
59				
60				

1				
2				
3	H	7.7727365	1.7372440	-9.4389300
4				
5	H	6.7508317	1.0140720	-8.1719565
6				
7	H	5.9968311	1.7716675	-9.6060509
8				
9	H	8.8297231	3.9797614	-9.5463669
10				
11	N	8.0208922	4.5872271	-9.7062894
12				
13	C	8.2344116	5.5960364	-10.7358215
14				
15	C	9.5282188	5.1865242	-11.4736300
16				
17	O	10.3026473	4.3482072	-10.9915355
18				
19	C	8.3504851	7.0139539	-10.1455658
20				
21	H	7.3820528	5.5678200	-11.4344996
22				
23	H	8.4850147	7.7613994	-10.9399236
24				
25	H	7.4320060	7.2549652	-9.5958989
26				
27	H	9.2069816	7.0755026	-9.4597313
28				
29	H	9.1279535	6.5496705	-13.0041748
30				
31	N	9.7525629	5.8208360	-12.6466286
32				
33	C	10.9785868	5.6640012	-13.4178378
34				
35	C	11.0588900	6.8969748	-14.3444767
36				
37	O	10.0769264	7.6332401	-14.5210763
38				
39	C	11.0003841	4.3498742	-14.2203810
40				
41	H	11.8321066	5.6692899	-12.7200418
42				
43	H	11.9440695	4.2406624	-14.7729617
44				
45	H	10.9046496	3.5016692	-13.5311966
46				
47	H	10.1694126	4.3231249	-14.9393564
48				
49	H	13.0357480	6.4413992	-14.8414239
50				
51	N	12.2537178	7.0944159	-14.9452741
52				
53	C	12.4856634	8.1405319	-15.9308424
54				
55	C	13.7511292	7.7163324	-16.7111764
56				
57	O	14.4710101	6.7967250	-16.3084263
58				
59				
60				

1				
2				
3	C	12.6550890	9.5246106	-15.2767141
4				
5	H	13.3539844	9.1700411	-18.0953314
6				
7	N	14.0068515	8.4372266	-17.8345002
8				
9	C	15.1824831	8.2211709	-18.6692389
10				
11	H	11.6200916	8.1724511	-16.6143716
12				
13	H	12.7903922	10.3102774	-16.0338891
14				
15	H	11.7563733	9.7630731	-14.6944967
16				
17	H	13.5287121	9.5317528	-14.6105597
18				
19	H	15.7486604	7.3902307	-18.2337197
20				
21	H	14.8913797	7.9584096	-19.6962512
22				
23	H	15.8196219	9.1173292	-18.6931048
24				
25				
26				
27	Octapeptide (alpha-helix)			
28				
29	C	-2.8430480	-2.3803383	3.9023715
30				
31	C	-3.0538594	-1.8363243	2.5035294
32				
33	O	-2.7836173	-2.4919837	1.4915857
34				
35	H	-3.8569117	-0.1003200	3.2723942
36				
37	N	-3.5583057	-0.5598854	2.4154666
38				
39	C	-4.0665677	-0.0190382	1.1489268
40				
41	C	-2.9781513	0.1647379	0.0729983
42				
43	O	-3.2931440	0.2072438	-1.1207359
44				
45	C	-4.7978553	1.3039449	1.3958417
46				
47	H	-3.5787775	-3.1779732	4.0794207
48				
49	H	-1.8470415	-2.8361068	3.9648552
50				
51	H	-2.9494038	-1.6242085	4.6915507
52				
53	H	-4.7616677	-0.7488252	0.7041859
54				
55	H	-5.1666415	1.7006690	0.4423677
56				
57	H	-5.6604154	1.1541580	2.0611183
58				
59				
60				

1				
2				
3	H	-4.1279579	2.0525977	1.8442321
4				
5	H	-1.5187619	0.1861333	1.5068839
6				
7	N	-1.6976340	0.2892916	0.5104867
8				
9	C	-0.5705616	0.4094077	-0.4107890
10				
11	C	-0.4052511	-0.8021026	-1.3554030
12				
13	O	0.2573997	-0.6656526	-2.3925774
14				
15	C	0.7260205	0.6646916	0.3631593
16				
17	H	-0.7663353	1.2529362	-1.0892194
18				
19	H	1.5610473	0.7455489	-0.3427813
20				
21	H	0.6610323	1.6026213	0.9326422
22				
23	H	0.9432099	-0.1607753	1.0581392
24				
25	H	-1.5759524	-2.0382463	-0.1599737
26				
27	N	-0.9962036	-1.9723041	-1.0035100
28				
29	C	-0.9045453	-3.1394802	-1.8810718
30				
31	C	-1.5550713	-2.9226893	-3.2641194
32				
33	O	-1.2128669	-3.6405593	-4.2140314
34				
35	C	-1.4960212	-4.3777593	-1.2012488
36				
37	H	0.1567165	-3.3149260	-2.1130279
38				
39	H	-1.4248723	-5.2318548	-1.8855582
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33	C	1.3989015	-3.6755369	-7.0373421
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35	C	0.5984915	-4.4755708	-8.0878659
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37	O	1.1001815	-5.4945528	-8.5978532
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