Dear Prof. Perez-Mato,

Thank you once again for taking the time to handle these manuscripts. Here are the responses to the three referees of manuscript PZ5072 with a summary of the changes we made to the manuscript:

Reviewer 1's comments:

Title: Molecular Crystal Global Phase Diagrams III: Sufficient parameter space determination
Author(s): J.B. Keith,a+ and R.B. McClurg

This manuscript comprises part III of a multi-article series by the authors. The first paper was published in Acta Cryst. A60, pp 621-636 (2004), and the second is currently under review.

If we place center of mass of a single molecule at the origin, a pair of molecules have a total of nine positional and orientational degrees of freedom. Ignoring their separation distance, eight of these dofs are orientational. In summarizing the relevant portion of the 2004 Acta Cryst A paper, they demonstrated the utility of expressing the intermolecular potential (IP) as a linear combination of triple products of two Wigner functions (one for each molecule) and one spherical harmonic. The Wigner functions form an orthogonal basis for expanding the single-molecule potential and the spherical harmonics form an orthogonal basis for expanding the intermolecular-orientational components of the IP. The expansion coefficients of the total expansion are considered to be functions of the intermolecular distance. The authors further argue that when working with a molecule of a specific point symmetry, it greatly simplifies the expansion if we work with symmetry-adapted linear combinations of Wigner functions.

In this context, the authors then ask the question, how many expansion coefficients does one need to achieve a sufficiently rich parameter space for stabilizing all of the observed molecular structures studied in their previous manuscript (part II of the series)? Because the IP expansion is infinite over the manifold (i.e. L) indices of the Wigner functions that span the SO(3) space, this question seems impossible to answer at first. But the authors point out that distortions of the molecular structures relative to the idealized references lattices can be decomposed into symmetry-adapted order parameters that are classified according to the point-group irreps involved in breaking the molecular site symmetry. For each structure of interest, they identified the relevant molecular point-group irreps involved in the distortion. They also point out that for a given manifold of SO(3) and a given point group G, there will be specific irreps of G capable of producing a distortion with the same symmetry as the basis functions of the the selected manifold. Inspecting each manifold one at a time, one eventually reaches a minimum manifold that contains one of the point-group irreps involved in the distorted molecular structure. For each distortion of interest, the authors authors identified the minimal manifold that contains at least one route to stabilizing the observed distortion. This is a very clever simplifying assumption, though we are not able to verify that this minimal manifold

will be sufficient in practice to realize real distortions in a wide-range
of molecular crystals. Using these arguments, the authors find that their
test structures never require more than $L Â«= 4$, which requires only 15
symmetry-unique expansion coefficients as opposed to thousands. This is
their main result. Thankfully, they stopped at 39 pages and did not
actually generate a 15-parameter global phase diagram!

We took point-group-irrep decompositions of SO(3) in Table 1 at face value
and checked the minimal manifold results in Table 2, which was computed
correctly. We assume that the results in Tables 5-7 were also computed
correctly, but did not check.

The basic approach taken by the authors appears to be technically sound
and innovative. The selection of cited literature is adequate and the
choice of journal is probably OK. Being unfamiliar with the molecular
packing literature, we are not in a position to assess the relative
importance of this work. While the manuscript feels very long, we were
unable to identify a section or sections that could be conveniently
ommitted or moved to the supplementary material; another reviewer might be
able to accomplish this. Based on the novelty of the application and the
correctness of the analysis, the work appears to be suitable for
publication in Acta Cryst A in its current form.

Response:

This is a fairly accurate assessment and we thank the referee for taking time to review it.

Reviewer 2's comment:

Comments to manuscript Ms.No. pz5072; "Molecular Crystal Global Phase
Diagram III ..." by AJ. B. Keith and R. B. McClurg

The authors address the issue of constructing generic phase diagrams for
certain classes of chemical systems, where certain parameter sets are
derived that allow the characterization of the several possible phases in the
system. They find that a relatively small number is sufficient to do so for
the purpose of their phase diagram construction.
The work appears to have been done correctly, although the presentation is
not necessarily always very clear for the un-initiated. Since such generic
phase diagrams can be quite useful when trying to interpolate between
different "boundary" systems, I think that the work should be of sufficient
general interest to warrant publication once the issues and questions
mentioned below have been addressed.
I also noticed that part II of this sequence of manuscripts is still in the
process of evaluation. The authors and the editor might want to consider to
expand the part-II-manuscript by including some of the work presented in
this part-III-manuscript. They could then move the main body of the part-
III-manuscript reviewed here to a large technical supplementary material,
while including more details for those readers who want to implement the
authors' procedure themselves.

Response:

We use the following abbreviations:
GPD I: Molecular crystal global phase diagrams I: Method of construction, (with J.A. Mettes and R.B. McClurg), Acta Cryst. A 60, 621-636, 2004
GPD II: Molecular crystal global phase diagrams II: Reference lattices (with R.B. McClurg), submitted to Acta Crystallographica A, 2009
GPD III: this work

First, we apologize Reviewer 2 did not get access to GPD II--our intention was to specify that the manuscripts be reviewed together, or at least that the reviewers of GPD III be given a copy of GPD II. Unfortunately such specifications sometimes are "lost in translation" while transmitting the papers to various staff members. And yes, originally this work and GPD II were together, but the resulting length of each manuscript (and its supplementary material) was such that a division was absolutely necessary (GPD II and its supplementary material are 63 pages!). We apologize again for Reviewer 2 not having direct access to GPD II.

Reviewer 2's comment:
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1. Quite generally, the authors should explain what they mean by "global phase diagrams", even though this is the third paper in a sequence. Here they should make the connection to the physics community where generic phase diagrams have a long-standing tradition. Just consider the many studies of Ising-models characterized by a small set of interaction parameters, where generic phase diagrams with critical points etc. are derived, and where both the general topology of the phase diagram and the quantitative values of the various critical points are correlated with the region of parameter space chosen.

Response:

This is a good point. We have tried to explain the concept of Global Phase Diagrams (GPDs) from the standpoint of binary fluid mixtures, but a connection to the physics community and especially some of the many Ising-type models would be useful. This has been added as a discussion point. We have also added figures of actual GPDs near the introduction to better convey the general idea.

Reviewer 2's comment:
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2. What about metastable compounds? Can the authors deduce anything in this regard?

Response:

Yes, that is one of the purposes of GPDs in general. They allow one to enumerate polymorphs and help elucidate whether a given structure is metastable or not. This can be done by examining the vicinity in parameter space for other crystallographic phases, or my calculating the coefficients and seeing if the observed metastable phase is near to the calculated one in nu-space.

Reviewer 2's comment:
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3. Equation 1: Where is "l" in the formula, and what is its meaning?

Response:

The "l" is a parameter that indexes the spherical harmonics intervening the Wigner functions. It ranges from $|li - lj|$ to $li + lj$ and is essentially a product of the mathematics--forming a complete basis set over SO3 x S2 x SO3. These functions have been used extensively in the quantum chemistry literature (see the paper by van der Avoird referenced on page 8), and this has allowed some physical insight into the meaning of "l". For instance, all electrostatic forces are present in the $\nu_{\{li,l,lj\}}$ where $l = li + lj$.

Reviewer 2's comment:
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4. Equation 2: If someone wants to follow the authors prescription in
practice, more information is necessary. Please, give a more complete
version of this equation in the appendix including ranges for mi, ni in the
summation.

Response:

   This has been done. If Reviewer 2 wants to understand this work well enough to reproduce it, we would whole-heartedly endorse a thorough reading of GPD I and its supplementary material. It is an exposition of the thermodynamic procedures and how hard it is to tease a solution out of the mean field equations without having some idea of what phase one is looking for so one can seed the solutions with each possibility. In quantum mechanics it is more or less known the electrons will be somewhat like their hydrogen equivalents so the numerical seed into the self-consistent mean-field equations of DFT or Hartree-Fock is more or less like hydrogen. However, in statistical mechanics, the new rotational average could be *anything* -- certain molecules could be ordered (i.e. a non-zero $<U_{\{lmn\}}>$ average)...others could be disordered (i.e. $<U_{\{lmn\}}> = 0$), and sometimes partially ordered (i.e. some $<U_{\{lmn\}}>$'s = 0 and others not). Sometimes, some of the molecules in a unit cell are disordered while others are ordered. Also, it is unknown how big the new unit cell will be. In the new figures added to the manuscript, one can see the initial fcc unit cell has expanded to 2, 3, 4, or 32 molecules in a unit cell with a completely new setting. Fortunately group theory allowed us to look through all the isotropy subgroups of the high temperature reference phase and use these as seeds in the mean field self-consistent equations.

Reviewer 2's comment:
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5. Page 10, top: Is the assumption justified that including only pairwise
interactions among nearest neighbors is sufficient?

Response:

This is an assumption which, to a first approximation, is probably adequate for most van der Waals crystals (the majority of molecular crystals). It would be good to include second-neighbor interactions, particularly when starting from reference lattices which are not a sphere packing as discussed in GPD II. However, this of course leads to greater computational cost and worse, more axes on the GPD! Thus we feel the current approach is adequate, but subsequent studies including more rich potentials such as second-neighbor or many-body effects as perturbations on a given direction in nu-space would certainly be interesting. See GPD I for a more thorough explanation of this point with various references for a quantitative justification.

Reviewer 2's comment:

Page 11: Equation 5: What is A, what is V? (A = free energy at T = 0?, V = potential energy / total energy?)

Response:

Yes, that is more or less right..."A" is the free energy (at any temperature) and V is the potential energy (since kinetic energy would be 0 at T=0). Thus the zero point energy is implicitly included in V, etc.

Reviewer 2's comment:

Page 13: First paragraph: There are very many paths between two space
groups (probably infinitely many for a macroscopic system, where one can
play with reducing/adding translational symmetry). Why did the authors
pick the ones they present?

Response:

   Overall scheme: According to previous work (see GPD I), studies show most molecules pack like spheres in the Cambridge Structural Database (CSD). So the idea is to choose sphere packings as translationally-fixed "reference lattices" from which additional rotaitonal symmetry-breaking may occur. On page 13 we demonstrate how this may be done for the subset of tetrahedral molecules in the CSD with an fcc reference lattice (see GPD II for why this reference lattice was chosen for these molecules).
   There were a few surprising results from this exercise. The first was a discovery of some intriguing phase transition mechanisms for molecules which actually go through a transition from an fcc disordered phase to a lower-temperature ordered phase such as adamantane (225a->114a). In this transition, the centers of mass of the adamantane molecule apparently stay fixed while the molecules suddenly become rotationally ordered. Amazingly, this happens through a coupled IR. Transitions from a coupled IR are thought to be uncommon in the physics community, I believe. The other transitions through coupled IRs are not as remarkable perhaps because they are nonphysical. Another discovery was that symmetry breaking pathways may be a useful way to explore packing space, compared to the "brute force" approach commonly used in crystal structure prediction pathways where a molecule is randomly oriented/positioned and operated on by the space group operations of all 230 space groups, then energy-minimized, then compared to each other to remove duplicates (i.e. different domains) and finally sorted to find the lowest-energy phase (this is a simplification--see the literature for a more complete description). But to get back to the point, space group IR symmetry-breaking removes duplicates by enumerating all possible domains so we only have to calculate the energy of one of them.
   So, to answer the question, the pathways shown in that table and similar ones in the supplementary material are simply a demonstration of the ways to get from the orientationally disordered reference phase to the observed orientationally ordered phase. In most cases we simply listed the output from ISOTROPY, although in a few cases we had to truncate the results as noted in the supplementary material.

Reviewer 2's comment:

Page 15, top: The restrictions in the allowed ISs appear rather strong - even
if Z' Â«= 1 for many structures, one should allow for a richer sample space of
structures.

Response:

They are somewhat strong and could be extended to Z' > 1. Keep in mind this is but a demonstration of approximately how many parameters one needs to consider in constructing GPDs for a certain class of molecules so an overly large candidate library has not been utilized.

Reviewer 2's comment:

Page 16, beginning section 2.2.4: I really have a hard time following what
the authors are trying to do here. Please clarify and elaborate. Why do they
minimize atomic distances with respect to fractional coordinates (there
appears to be a comparison between quantities measured in Angstroms and

those which are dimensionless!)?

Response:

We apologize for jumping into this section without a smooth transition. The beginning of section 2.2 introduces the general plan, but there should be a few sentences reorienting the reader at each subsection. This has been added. The main point of this paper is to take a set of experimental lattices and attempt to deduce how many coefficients in our potential expansion are needed to adequately describe them (i.e. find a "spot" on our GPDs where they are the lowest-energy structure). To do this we need to know a set of Euler angles for each molecule in each experimental structure. There are a few complications in doing this (i.e. slight distortions in molecular form and center of mass), and section 2.2.4 attempts to explain them. None of the complications are terribly important and the section could be omitted. Certainly the detail about using fractional instead of Cartesian coordinates is non-essential so it has been omitted. However, for the sake of completeness, we have revised this section and retained it. The main point is the extraction of the Euler angles from the experimental structures using a least squares fitting procedure and their insertion into Eq. 1.

Reviewer 2's comment:

Page 17, equation 8: What are the units of the various potential
parameters?

Response:

They are unitless in this study because we scale the set of nu's to the unit sphere. It is only an exercise to see if we can find where in nu space the experimental structure is most stable.

Reviewer 2's comment:

Page 17, right after equation 8: The authors state that MEZDIE01
crystallizes in space group 2. Is that the outcome of their calculations, or is
this used as input to their calculations?

Response:

It is used as input to our study. From the orientation of the molecules we extract a set of Euler angles, input them to our potential, then search nu-space to see where that structure is the most stable in an effort to see how many nu's we need in our potential expansion.

Reviewer 2's comment:

Page 17, section 2.2.5: Where do the authors get the target structure and its
energy from? What is general, what is specific about the procedure
described in this section? What is really the predictive power of this
method? Please, make a clear list of the information that is used to derive
the parameters, and of the information one can deduce by a strict
application of the authors' rules afterwards.

Response:

   Each target structure comes from the subset of tetrahedral molecules in the CSD. How its energy is obtained (independent of nu) is the subject of section 2.2.4. The purpose of section 2.2.5 is to describe a method whereby one can find a point in nu-space where the target structure is the lowest-energy structure, extending nu-space as

necessary to higher manifolds. The technique to do this is perfectly general and can be applied to any molecule, not just tetrahedral molecules. The overall objective of this search is to find out whether a reasonably small number of nu's can describe real structures. We posited a small number was necessary in GPD I, and here we prove it. The final paper would be to calculate GPDs using the relatively small number of reference lattices from GPD II and using a small potential truncation as we have demonstrated here. Then, to connect the resulting set of GPDs with the real world, we would extract a set of nu parameters for each experimental structure from, say, ab initio data and see if we can "find" the experimental structure at the "correct" region of nu-space and at the correct temperature (this assumes the ab initio calc was perfect). This would be a rather large calculation since one has to do the equivalent of an MD or Monte Carlo calculation at each point in nu space and for each reference lattice. This is why we seek a faster statistical mechanics method, as remarked in page 27 in the original mauscript.

   Although the current test of nu-space is not designed to be predictive, the concept of a GPD in its final scenario should be valuable for the reasons remarked on page 5 and would have predictive power in the sense that it would provide some guidance to the synthetic chemist, for example, in how to perturb the molecular form to get a more desirable crystal structure. Or GPDs could provide rationalization and/or prediction of crystal polymorphs.

   Here is a list of the information used to derive the nus (in this study):
* experimental structure (atomic positions and unit cell) of each structure
* a minimal truncation of the U_{lmn} expansion--this can be done using subduction frequencies of the molecular point group in the Wigner funtions as explained in Sec. 2.2.2
* a reference lattice for each structure, derived using the methods of GPD II
* a list of candidate lattices with which to compare it, which was described in Sec. 2.2.3
When all these are applied to the minimization algorithm described in Sec. 2.2.5, we get results that will give us guidance about how many potential parameters are needed. The "rules" described in Sec. 3 are just a way of rationalizing our results from the minimization procedure (i.e. how close do we need to the global minimum do we have to be to have "found" it and what does the answer actually tell us about that point in nu-space). The overall result was all but 2 of the experimental structures seem to have a point in nu space that is representative of that family of potentials characterizing that molecule. The representative potential (RP) is not necessarily "the" potential for that molecule, but only used to find out if such a phase can be located on such a GPD. The actual nu coefficients can then be extracted using a type Fourier transform from ab initio data, for example, although be aware of the caveats described on page 21.

Reviewer 2's comment:

Page 18: A citation for genetic algorithms is Holland's work in the mid-
seventies.

Response:

Thank you--the citation has been added.

Reviewer 2's comment:

Page 20, second paragraph: Is there a connection to "real" energies of solids
or liquids? If so, how are these energies computed?

Response:

There is a connection and it is all in the nu's, or expansion coefficients of the potential. One way to compute the nus, demonstrated in Briels, W. J. (1980). J. Chem. Phys. 73, 1850–1861, for example, is to use the orthogonality of these functions and perform a type of "Fourier transform" on whatever model potential you might want, whether forcefield-based as in the Briels reference or ab initio. The intermolecular potential is then reproduced by Eq. 1 with the new set of nus. Be aware of the caveats on page 21, however.

Reviewer 2's comment:

Page 21: The authors refer to free energy calculations. I do not see any "free
energies" in their description: everthing seems to be just energy or some
proxy for the energy or a cost function.

Response:

Our apologies again that Reviewer 2 was unable to access GPD II. In that work and especially GPD I, we only
deal with the free energy. This point is summarized on pages 4-5 where we describe how the free energy is
minimized in the general method. To better convey that, we have included two figures from GPD I showing the
high temperature reference state as previously mentioned. However, in this paper we look at the low-T solutions
so energy is substituted for free energy from Eq. 5 on and that is why it is hard to find, but occasionally
referenced in the discussion.

Reviewer 2's comment:

Page 27: I realize that the authors imagine readers reading all their papers
in sequence, but that is not necessarily so. Thus, they should include at
least one generic phase diagram, at least in projection if the number of
parameters needed to describe it is too large. The number of parameters
might appear modest to the authors, but it still appears to be rather large.
How close are we to reality concerning the actual energies?

Response:

An excellent suggestion and an example to illustrate the concept at the beginning of the paper has been included
as mentioned. Regarding the energies, we assume Reviewer 2 is asking if the point in nu-space actually
corresponds to that from a given ab-initio or forcefield-based potential, we answer that it is unknown, but for this
study we did not try to find *the* set of nus that describe an observed strcture, but *a* set of nus where that
structure is more stable than the others. In short, we haven't been able to extract nu's from a real structure yet,
although publications are planned to do that (see Missaghi, M. N., Mettes, J. A. & McClurg, R. B. (2009). In
Preparation.).

Reviewer 3's comment:

The paper has a very desirable aim of obtaining a global phase diagram for molecular crystals using
a small number of reference lattices and a "modest number" of interaction potential parameters. As
such a more general discussion (sec 3) and condensed account of potential determination (sec 2)
would have been useful to the general reader. There exists a large volume of experimental crystal
structure data along with a large number of theoretical models. It is attractive to judge these models
after assessing their merits to find a classification that gives an hierarchy of their usefulness.
The authors use a small number of parameters to describe intermolecular potentials for constructing
the GPDs thereby aiming to enhance the utility of GPDs for materials design. The authors start from
a given lattice of a plastically crystalline, rotationally disordered state and examine the evolution of
the space groups of the new phases that appear as the temperature is changed for a fixed
intermolecular potential when single molecules are reduced to spheres. Such structures are
necessarily a subgroup of on of the reference lattices. The potential itself is obtained from

interaction between molecular orbitals of different molecules which are used as microscopic director belonging to S2 with two degrees of freedom. If one associates the orbital orientation with a spin, then this approach is concerned only with local orientational spin balance. Neither local orientational balances of momentum and angular momentum nor entropy nor long-range alignment tensor balances seem to be considered, as they have been done in the theory of liquid crystals. Consequently it does not seem that there is viability in the phase diagrams that are obtained for the various physical conditions,

Response:

We use the following abbreviations:
GPD I: Molecular crystal global phase diagrams I: Method of construction, (with J.A. Mettes and R.B. McClurg), Acta Cryst. A 60, 621-636, 2004
GPD II: Molecular crystal global phase diagrams II: Reference lattices (with R.B. McClurg), submitted to Acta Crystallographica A, 2009
GPD III: this work

   Hmmmm, there may be a small misunderstanding. Judging from Reviewer 3's comments, we're not sure if the ideas behind our potential were clearly communicated. We'd like to clarify the potential is not based on a "microscopic director" description with only 2 degrees of freedom (such as the Axial Next Nearest Neighbor Ising model) but is based on a complete set of basis functions over SO3 x S2 x SO3 and has 8 degrees of freedom. However, since the positions of the molecules are fixed (for now) in their set of reference lattices, the S2 part of the potential has *no* degrees of freedom. Also, the orbital orientations have no association to this part (S2), or with each other ("spin balance"?), but each molecule is free to rotate in whatever way it chooses. Thus local orientational "balances of momentum" between molecules are unrelated to each molecule's angular momentum. According to the partition function, in fact, angular momentum for each molecule "integrates out", leaving only a temperature-dependent factor. Again, it appears Reviewer 3 may have misunderstood the potential to be Ising-like in nature, when in reality it is much more complex. Or we may be misunderstanding his/her comments. Regardless, to better clarify the nature of the potential, we have added two appendices giving an in-depth derivation.
   However, we thank Reviewer 3 for pointing out the general phenomenon in the literature of omission of entropic effects. Many studies on crystalline packing ignore these, even though they are non-negligible in molecular crystals, which frequently have melting points near room temperature. It is for this reason that in GPD I we introduced the full model which begins from elementary principles of statistical mechanics with free energetic/entropic effects fully included. It particularly focuses on the first set of phases forming after the initial symmetry is broken at higher temperatures. In GPD II we discuss the set of reference lattices appropriate to tetrahedral molecules, and in GPD III we discuss the low-temperature phases and as such, entropic effects are almost nonexistent and so are not necessary.
   We also note that, unlike liquid crystals, long-range alignment tensors are not necessary to describe most molecular crystals, which generally are fairly rigid on a global topology, despite a certain amount of local thermal disorder. Thus long range order is always present and material-wide strains do not influence the equilibrium thermodynamics or applications of molecular crystals like they do liquid crystals.

Reviewer 3's comment:

The effort of the authors in sec 2.2 for determining potential parameters to reproduce experimental structures may benefit from considerations of other models, notably the ANNNI (axial Next-Nearest-Neighbour Ising) which have rich phase diagrams including commensurate and incommensurate phases. By choosing a molecular orientation as the Ising spin the authors may compare their predictions with that from the ANNNI model. From the viewpoint of an emphasis as a review article it could perhaps be mandatory to make this comparison. The additional time spent could be worth the effort. One recognizes that the final space-group-determining step involves weak interactions that are many time within the error limits of the usual calculations. The mock version of

the ANNNI model has the advantage that it is completely solvable when reduced to a one-dimensional exercise. The conclusions of the present authors could be compared with those from the ANNNI models, for example.

Response:

      This is a commendable idea and we thank Reviewer 3 for bringing it up. We were somewhat acquainted with the vast amount of Ising-type publications, but concluded an attempt to review the field adequately would inordinately shift the focus of this work and space would better be spent on the subject of the paper itself: finding a sufficient number of interaction parameters to represent real materials (especially since this work is already lengthy!). However, we have now included a section in the discussion outlining a comparison between molecular crystal GPDs and ANNNI-type models. We approach it in this manner because, although the scope of *this* work is narrow and specialized (parameter space), the *next* paper presenting a general computation with the full model from the high temperature reference state would be an ideal context in which to place these widely known ANNNI models. The caveats in such a comparison would be that molecular crystal GPD interactions are only nearest neighbor for now (justified by typical van der Waals molecule-molecule interactions--see GPD I), and the extra degree of freedom that comes from dealing with a complete three dimensional molecule rather than a one-dimensional spin makes "choosing a molecular orientation as the Ising spin" ambiguous since one would arbitrarily give the ANNNI models an extra degree of freedom somehow. However, we can probably attempt a qualitative comparison. One last issue with a direct comparison is that the two potentials are very different parametrically, leading to additional ambiguities in how to compare the typical J_1 and J_2 directional couplings from ANNNI with the 15 axes parameterizing a complete quantum mechanical basis set. This complete-set potential has the side effect of an extremely complex and computationally demanding solution technique in the general case discussed in GPD I. Thus Reviewer 3's good intentions at pointing toward the simplicity of solving ANNNIs as an impetus to make such a comparison may not be as profitable as one would hope for given the lack of a comparable methodology, which is of course lamentable! :)

Reviewer 3's comment:

Another point that requires mention/deliberation in the context of the focus of the general readership of the journal is the relation between the global phase diagram of essentially 3D liquids and that of the bulk molecular crystals especially in the context and as reflected in the local critical behavior of surfaces with or without defects separating the liquid and solid phase. Some mention of these aspects would be useful.

In my opinion, the advantages of methodology of the authors using interaction potentials obtained from orbital orientations, has to be examined in the context of those already available in the literature.

Response:

      This is an interesting point, and in initial drafts we attempted a connection with liquid structure on phase boundaries because it has such a large effect on polymorphism, a subject GPDs may help illuminate. We eventually elected to omit these considerations, supposing they were too large a subject to fully explore.
      However, on the positive prompting of Reviewer 3, we have added them again as part of the discussion (which is the best that can be done considering the narrow scope of this paper), and will form a larger section in our next paper which is devoted to the general application of GPDs. Regarding this point, there seem to be a few questions one might consider. First, what are the intersection lines on molecular crystal GPDs between solid GPDs and liquid GPDs?   Another question might be: how do surface free energies and kinetic effects (undercooling, seeding) affect crystal growth and therefore these solid-liquid phase boundaries? And finally: how do the presence of defects, both in the bulk and on solid/liquid surfaces, affect free energies and therefore phase boundaries? The preliminary answers to these questions might be the following:

1) One might expect each set of potential coefficients would have some temperature at which a liquid phase would be thermodynamically more stable than the solid phase listed on our GPD. A logical way to find this line would be to construct an equation of state based on our model's potential parameters. At higher temperatures one would expect to see other critical points/lines.

2) Surface free energies, crystal habit, growth rates, kinetic barriers, and external conditions (i.e. undercooling, seeding, etc.) would certainly have an effect on that initial transition line between liquid and solid. The best way to handle this would probably be to prescribe a set of crystallization conditions before calculating the intersection between liquid and solid GPDs, then include all such effects in that calculation.

3) Defects are an interesting subject in general and a complete description of their subtle effects on solid/ solid and solid/liquid free energy surfaces is probably beyond the scope of this response. In theory their effect could be included in an averaged way in each solid phase free energy by means of a Boltzmann factor-type expression (i.e. equilibrium fraction of vacancies proportional to $\exp(-f_v/kT)$ where f_v is the free energy of vacancy formation). For liquid/solid surfaces this would be more complex and depends on the particular method used to estimate melting temperatures, including all kinetic effects and external conditions.

 Once again, a summary of these considerations is now in the discussion on our final paper showing all parts of the model together with the data. Also, we reiterate we have included a more thorough discussion of other types of GPDs extent in the literature, such as the ANNNI models.

Thank you once again Prof. Perez-Mato for dealing with these rather lengthy issues,

Brandon Keith