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Supplementary Information - GIGA: A Versatile Genetic Algorithm for Free and Supported Clusters and Nanoparticles in the Presence of Ligands

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1 GA Analysis Tool

In the following, the GA analysis tool is described. The purpose of the analysis algorithm is to provide a fast, handy and thorough analysis of all structural motifs found during the GO independent of the specific quantum chemical software used for local minimisations. Therefore, the analysis software consists of three sub-programs, written in object oriented Python: **Extraction**, **Analysis1** and **Analysis2**. With **Extraction**, all information of the cluster structures generated during the GO are extracted, **Analysis1** is used for automatic grouping of different cluster structures according to structural and energy criteria, **Analysis2** is used for automatic visualisation and checking of the results of **Analysis1** as well as for automatic documentation of the results.

Extraction

The purpose of the **Extraction** class is: i) extraction of the quantum chemical output calculation in an uniform format with and fix units ($[r] = \text{\AA}$, $[E] = \text{eV}$) independent of the quantum chemical backend used; ii) to save space on the hard disk, since typical quantum chemical output files of a local optimisation are in the range between 1 MB and 80 MB and the files generated with the **Extraction** program are smaller than 1 kB. The **Extraction** class iterates through all generated quantum chemical outputs (all cluster structures) and extracts information such as the final coordinates, the energy in eV, the CPU time taken, the number of the cluster structure (*strucNr*). With this information, for each cluster three small ASCII files are generated: *clusterName_strucNr.energy*, *clusterName_strucNr.xyz*, *clusterName_strucNr_aligned.xyz*. All the extracted information is saved for each cluster structure in the *clusterName_strucNr.energy* files and are used in the **Analysis1** program. The two geometry files only differ in the orientation of the cluster. The files *clusterName_strucNr.xyz* contain the cluster in the same orientation as in the corresponding quantum chemical output. In *clusterName_strucNr_aligned.xyz* the cluster is aligned in a distinct, specified way: first the cluster is transformed so its

center of mass (CoM) is at the origin. Then the cluster is rotated so that the most distant atom (with respect to the CoM) lies on the x-axis; second a rotation around the x-axis is performed so that the z component of the second most distant atom (with respect to the CoM) vanishes. The generated geometry files are used for cluster structure visualisation in the **Analysis2** program.

Analysis1

In **Analysis1**, the assignment of the individual cluster structure into different geometry motifs takes place. First the data from all .energy files are imported into an array and arranged in order of ascending energy. Then an iterative process is performed. Starting with the GM, all cluster structures in the array are compared to the GM structure according to a structural *diff* (relative value) criterion and an energetic criterion *Ediff* (in eV). Regarding the structural criterion, all atomic distances (taking into account the element types) within two clusters are compared and if the relative deviation exceeds *diff* then the two structures are considered to be different. The energetic criterion *Ediff* is the maximum allowable energy difference (in eV) between two cluster structures for them to be assigned to the same geometry group. According to *Ediff* and *diff* all generated cluster structures are grouped into several geometry groups. The first group (*GroupNr 1*) exhibits the GM geometry. Additionally the moment of inertia eigenvalues are calculated for each cluster structure, since they can be used as additional structural comparison criteria. Four different output ASCII files are generated by **Analysis1**: *AllClusters*, *AllClusters_Ordered*, *ErrorList* and *results*. *ErrorList* contains all structures, which are not converged. All groups with the lowest and highest energy structure within each group are listed in *results*. The geometry group, total Energy and the *strucNr* of all generated cluster structures ordered according to the *strucNr* are specified in *AllClusters_Ordered*. The *strucNr* of all clusters, the assigned geometry group and moment of inertia eigenvalues are written in *AllClusters*. This file is ordered according to the assigned groups (*GroupNr*) and all cluster geometries within each group are listed in ascending energy order.

Analysis2

Analysis2 provides a selection menu with different automatic vi-

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sualisation analysis modes to check and, if necessary, correct the clustering results of **Analysis1**. A screenshot of the selection menu is shown in Fig. 1. During this process, the user should note the *strucNr* of each cluster representing a new geometry. At the end of the analysis process, all extracted *strucNr* are passed as input to the program and an Excel output file is generated.

Fig. 2 and Fig. 3 illustrate several geometry groups found with the analysis tool for the example of $[\text{Cd}_3\text{Se}_3(\text{H}_2\text{S})_3]^+$ obtained with optimisation mode **a** (optimisation from scratch at the PBE level of theory using Quantum Espresso as the quantum chemical software package).

jupyter GA_Analysis_program Last Checkpoint: 01/28/2019 (unsaved changes)

File Edit View Insert Cell Kernel Widgets Help

GIGA and MEGA GAAnalysis written by Marc Jäger

Main informations:
System name: Cd3Se3S3H6
Analysis parameter: Ediff = 0.2 diff = 0.2
4380 structures have been generated
The GM is in structure number 410 with total energy -6926.626

Please insert one of the following modes:

- [1] Show GA convergence
- [2] Show geometry group abundance
- [3] Show moments of inertia distribution
- [4] Show GM
- [5] Show all found group geometries for Emin in results...txt file
- [6] Show all found group geometries for Emin and Emax in results...txt file
- [7] Show all Cluster within one group with largest deviation in energy and moments of inertia (Emax, dIx, dIy, dIz, dIges)
- [8] Show Emin structure of a specified group
- [9] Show the structure of specified a OutputfileNr
- [10] Show all final pool structures
- [11] Show the max. 4 structures with largest dIges within one group together with the Emin structure of this group
- [12] Enter exit to leave this menu and to continue

Insert mode (that is number without brackets)

Fig. 1 Selection menu of **Analysis2** for automatic visualisation of the results of **Analysis1**.

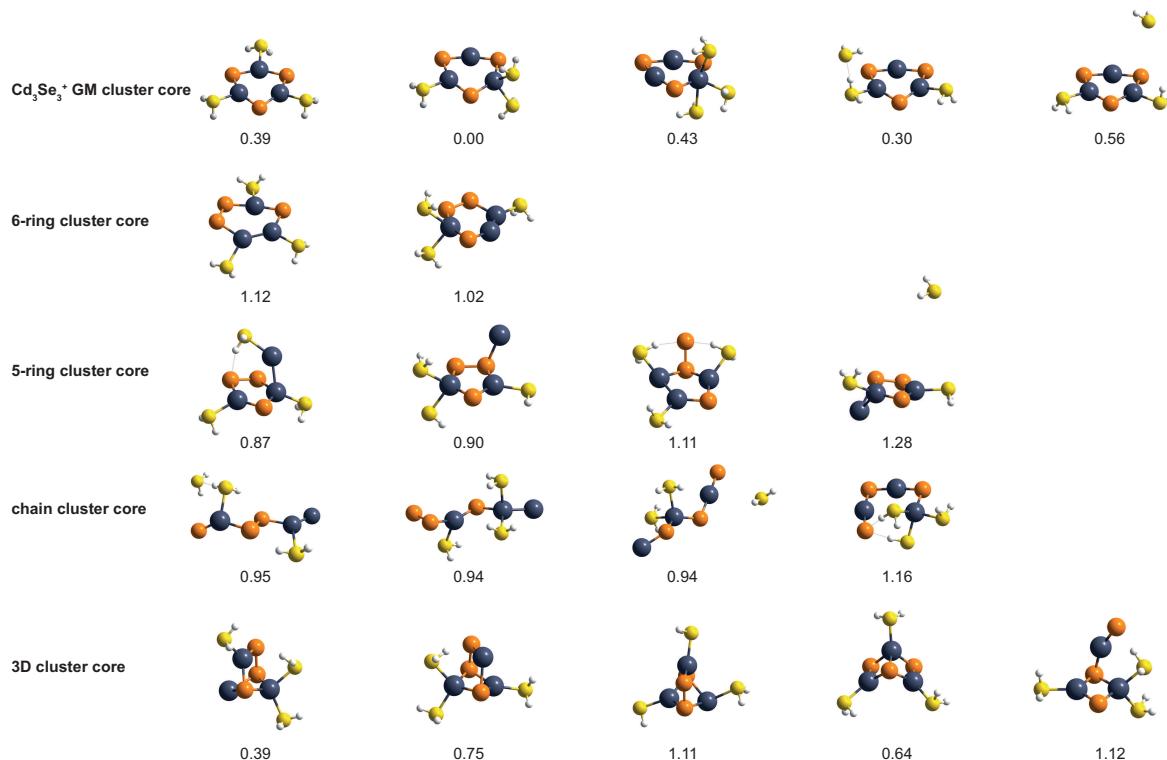


Fig. 2 [Cd₃Se₃(H₂S)₃]⁺ structural motifs with intact ligands. Relative energies are in eV.

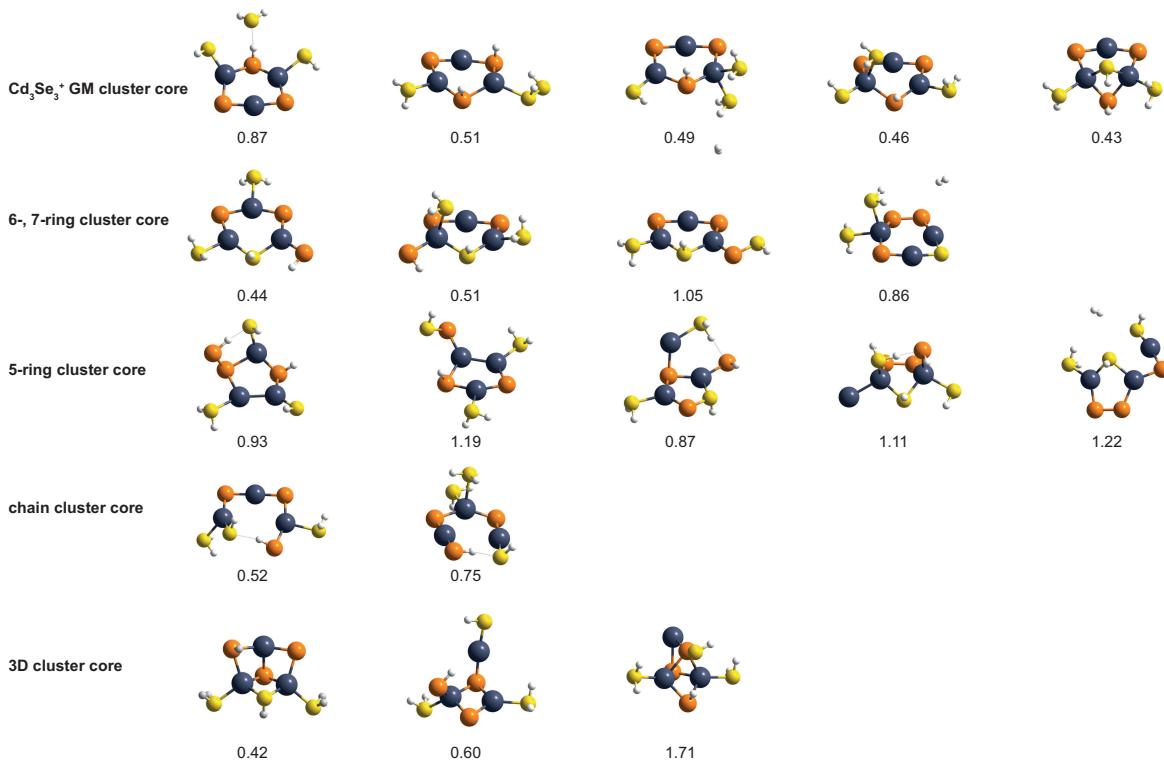


Fig. 3 [Cd₃Se₃(H₂S)₃]⁺ structural motifs where ligand dissociation occurs. Relative energies are in eV.

2 Coordinates

All coordinates are given in Å.

bare Cd₃Se₃⁺
 Cd -0.151317880000 -0.942005430000 0.385045470000
 Cd 0.076601170000 1.287039780000 -1.426184050000
 Cd 1.535914140000 -0.373574290000 1.072359350000
 Se 2.390389030000 1.384933200000 -0.559370730000
 Se -2.273131930000 0.542177620000 -1.575073410000
 Se -0.113300530000 -1.886819150000 2.090367790000
 [Cd₃Se₃(H₂S)₃]⁺ Iso-I
 Cd 1.304584100000 1.410252650000 -0.785410130000
 Cd -0.640241600000 -1.496428240000 -1.265483080000
 Se 0.875542380000 -0.124522780000 -2.668089100000
 Cd -0.695349230000 0.108632590000 1.984557590000
 Se 0.732441520000 2.132040310000 1.611937290000
 Se -1.869661360000 -1.818691260000 0.952239160000
 S -1.232517750000 0.049207910000 4.688082590000
 H -2.502288240000 -0.393526230000 4.616892620000
 H -1.605119550000 1.332954310000 4.850832970000
 S -1.314746910000 -3.763602510000 -2.703363590000
 H -1.245495810000 -3.200665360000 -3.924557780000
 H -2.655758890000 -3.65804090000 -2.644835570000
 S 3.3393930000 3.154434620000 -1.483339900000
 H 3.149039110000 3.065315970000 -2.814200150000
 H 2.658186980000 4.315292830000 -1.389055590000
 [Cd₃Se₃(H₂S)₃]⁺ Iso-II
 Cd 0.732641310000 -0.884430280000 -1.764306270000
 Cd -1.617500190000 -0.795899200000 1.018501000000
 Cd 0.881523540000 1.690986080000 0.803653610000
 Se -0.972154790000 1.177748820000 2.358457350000
 Se 2.197797230000 1.076870290000 -1.308057490000
 Se -1.137862440000 -2.333895530000 -0.977444990000
 S 1.536641730000 -1.909803890000 -4.197248580000
 H 2.868131880000 -1.835531750000 -4.010457240000
 H 1.486141640000 -3.219453530000 -3.888270860000
 S -3.923179820000 -1.879617700000 2.098423880000
 H -3.704163160000 -1.465066630000 3.360723800000
 H -3.476066100000 -3.125043190000 2.347272780000
 S 2.187837270000 3.951839030000 1.721912800000
 H 1.121557240000 4.501040810000 2.334097170000
 H 0.205917700000 4.729255720000 0.630130330000
 [Cd₃Se₃(H₂S)₃]⁺ Iso-III
 Cd -1.68703330000 1.001702430000 -0.962479550000
 Cd 0.585188810000 -1.120327920000 1.462053030000
 Se 2.795838430000 -0.794135710000 0.306710290000
 Se -0.074407480000 1.805763730000 -2.656952830000
 Cd 1.624851550000 0.56207140000 -1.345599510000
 Se -1.9626600460000 -0.479970290000 1.089281330000
 S -4.157094690000 2.104355360000 -1.383416690000
 H -4.018030590000 2.321628100000 -2.705466770000
 H -4.866651580000 0.973917790000 -1.563410180000

Graphene slab
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[Pt₆/graphene]⁺ Structure B

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[Pt₆(H₂O)₂/graphene]⁺ Iso-I GM from scratch

Pt 9.517600000000 8.038258000000 7.336730000000
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Pt₄V₂ Iso-I PBE0/def-tzvp
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Pt -1.702593610000 0.301296860000 -1.515390590000
Pt 1.655406860000 1.591566650000 0.146800560000
V -0.766059920000 1.151908070000 0.663024920000
Pt 1.188657950000 -0.722921060000 1.201431920000
V 0.745865630000 -0.239317370000 -1.325253980000
Pt₄V₂ Iso-II PBE/def2-tzvp
V 0.045252010000 -0.505039540000 -0.114465430000
V -0.179472250000 1.995046520000 0.471624620000
Pt 0.235324720000 -2.579506640000 -0.537180110000
Pt -0.221914170000 1.148348290000 -1.758726890000
Pt 1.758677150000 0.682006340000 0.971508240000
Pt -1.734949350000 0.318514760000 1.180411790000