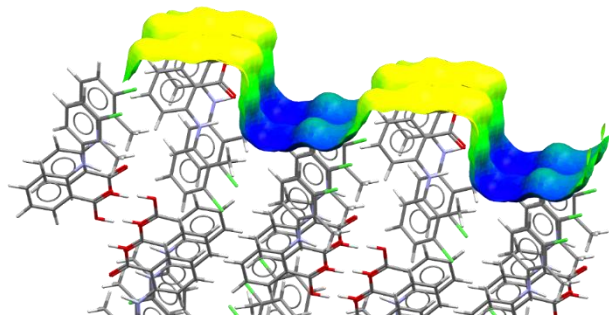


# Surface Analysis with CSD-Particle Tools in Mercury

Developed using  
2022.2 CSD Release



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## Introduction

This workshop shows you how to use functionality from the CSD-Particle suite to visualize and analyse the mechanical and chemical properties of molecular crystals. It uses quick computational models and algorithms, alongside data from the Cambridge Structural Database (CSD), to provide both qualitative and quantitative analyses of particle shape as well as surface and bulk properties. Such features are found under the CSD-Particle menu in Mercury.

Before beginning this workshop, ensure that you have a registered copy of the CSD installed on your computer. Please contact your site administrator or workshop host for further information.

## Objectives

In this workshop you will learn how to:

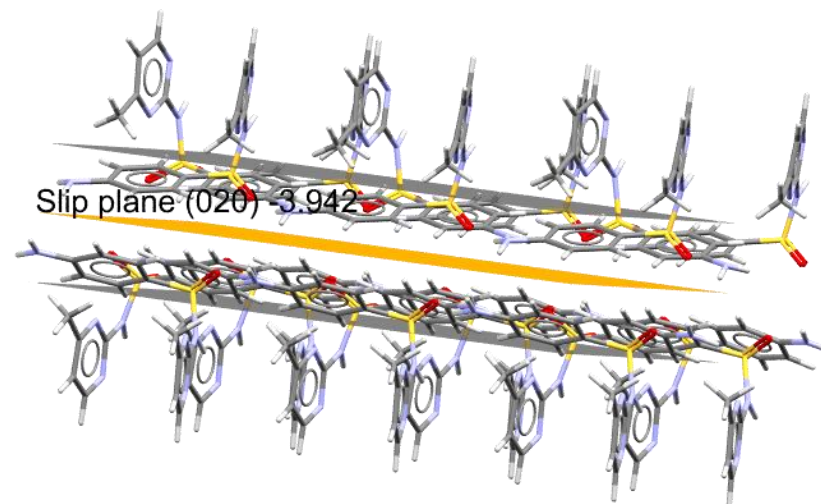
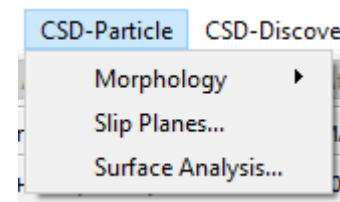
- Identify and analyse potential slip planes.
- Analyse particle surfaces.
- Calculate Full Interaction Maps on surfaces.

During the Virtual Workshop Try One part, work on one of the examples – you can pick the one on the components you are the most interested in. If you finish early, you may start a new example (if you have done example 1 or example 2, we suggest you then try example 3), or you can return to any of the examples at another time.

**Note:** The words in *Blue Italic* in the text are reported in the [Glossary](#) at the end of this handout.

## Pre-required skills

The following exercises assume you have a working knowledge of the basics of visualizing structures with Mercury, namely, how to display and manipulate structures from a 3D coordinates file. Familiarity with Full Interaction Maps (FIMs) would also be helpful in understanding the FIMs on Surface part of Example 3.



*Example of potential slip plane in CSD Entry SLFNMA02.*

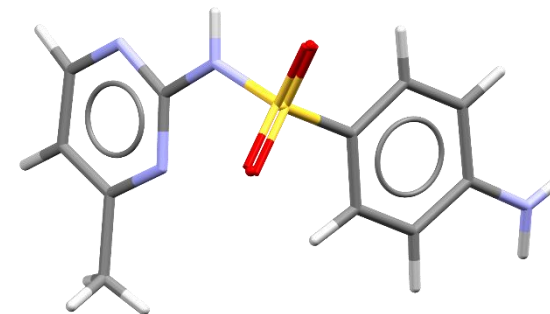
## Materials

There are no additional materials required for this workshop.

## Example 1. Slip Planes analysis to investigate elastic properties

In this example, we will focus on two polymorphs of sulfamerazine to investigate their different tableability and properties. In particular, our focus will be on CSD Entries SLFNMA02 and SLFNMA01, respectively displaying plastic and elastic behaviours based on experimental data. We will use the [Slip Planes](#) tools to try and understand where the slip planes might indicate elastic or plastic behaviour.

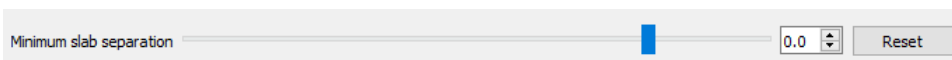
The Slip Planes tool shows potential slip planes based on the separation of the slabs.



A molecule of 2-p-Aminobenzene-sulfonamido-4-methylpyrimidine from CSD Entry SLFNMA02.

### Calculation of potential slip planes

1. Open Mercury by double-clicking the Mercury icon on the desktop.
2. In the *Structure Navigator* on the right-hand side of the Mercury interface type the refcode SLFNMA02 to bring up the first [polymorph](#) of sulfamerazine that we are going to investigate, i.e. the [plastic](#) one.
3. From the top-level menu select **CSD-Particle** > **Slip Planes...** to launch the *Slip Planes* window.
4. Observe that the [minimum slab separation](#) is set to 0.0 Å. To start the calculation, click **Calculate** at the bottom of the *Slip Planes* window.



**1** Mercury icon

**2** Structure Navigator showing SLFNMA02 selected

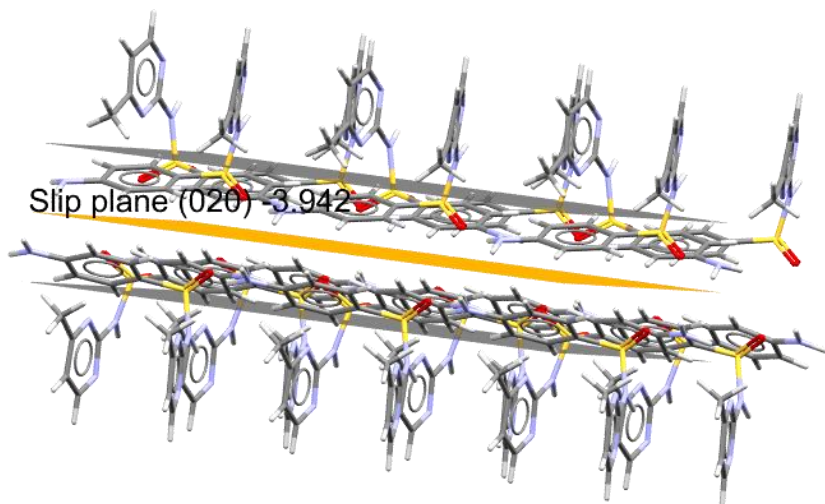
Crystal Structures	Spacegroup
SLFNMA	Pca21
SLFNMA01	Pbca
SLFNMA02	Pn21a
SLFNMA03	P21/c
SLFNMA04	Pna21

**3** CSD-Particle > Slip Planes...

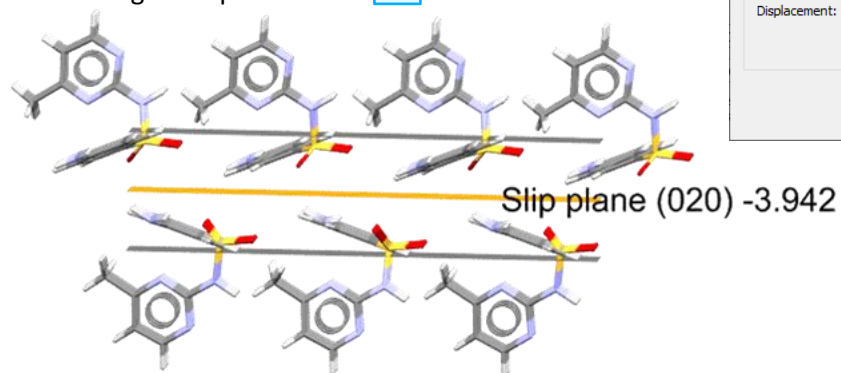
**4** Slip Planes window with Calculate button highlighted

5. You will see that the table is now populated with an entry representing a potential slip plane with a slab separation of 1.561 Å. Observe the values in the table.

6. Click now on the entry in the table to visualize the planes in the Mercury visualizer. Note that this will also open the *Packing and Slicing* window.



7. You can rotate the structure to see the alignment of molecules around the slip plane. You can see that there is a significant separation between the two slabs with potential slips in directions parallel to the plane. This structure has a high likelihood of having a slip plane and it is indeed the one indicated as plastic in the literature. Structures with such features might be preferable when compression of the particle is involved.



5

	Orientation	Slab separation	Repeat distance	Offset	H-bonded	Perpendicular planes
1	(020)	1.561	10.977	-3.942	yes	

6

Slip Planes... SLFNMA02

Minimum slab separation: 0.0 [Reset]

Status: Calculation completed

	Orientation	Slab separation	Repeat distance	Offset	H-bonded	Perpendicular planes
1	(020)	1.561	10.977	-3.942	yes	

H-bond dimensionality: 3D network

Packing and Slicing

Packing

Show cell axes

Label cell axes

Pack a: 0.0 1.0 +0.5

b: 0.0 1.0 +0.5

c: 0.0 1.0 +0.5

Reset 2x2x2 3x3x3

Include atoms

... that Fit

... in molecules whose Centroids fit

... in molecules where Any atom fits

... in molecules where All atoms fit

Slicing

Show slice

Select plane: Slip plane (020) -3.942 [Show plane]

New... Edit... Delete [Show bounds]

Depth: 5.00

Area: 20.00

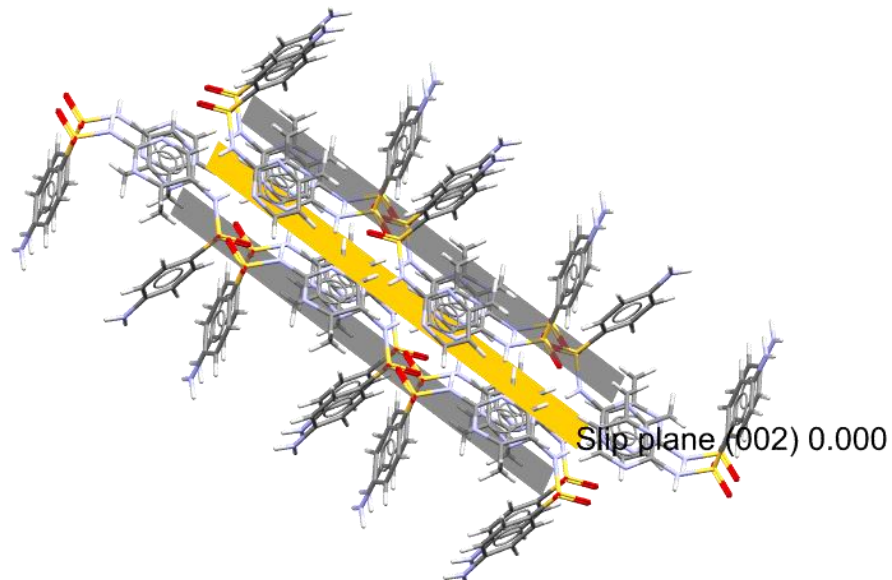
Displacement: 0.00

Reset

OK

7

8. We will now compare this structure with the *elastic* polymorph. Open another Mercury window by clicking on the icon again (on macOS, open a terminal window and run this command: `open -n -a "/Applications/CCDC/CSD_2022/mercury.app`) and in the *Structure Navigator* on the right-hand side of the Mercury interface type the refcode SLFNMA01.
9. If you have previously closed the *Slip Planes* window, re-open it from the top-level menu and select **CSD-Particle > Slip Planes...** as in **Step 3** above.
10. To start the calculation, click **Calculate** as in **Step 4** above. You will see that nothing has happened. The reason for this is that in this structure there are no potential slip planes with the minimum slab separation selected (0.0 Å).
11. Reduce the minimum slab separation by dragging the slider until the value is set to -1.6 Å. You will see in the dialog box that a new row has appeared with a slab separation value of -1.053 Å.
12. Observe the values in the table and then click on the row to visualize the plane in the structure. You will notice that for this polymorph the slabs are closer with more interlocked molecules compared to the structure analysed before. The potential slip plane appears more corrugated.



**8**

Crystal Structures	Spacegroup
SLFNMA	Pca21
SLFNMA01	Pbc
SLFNMA02	Pn21a
SLFNMA03	P21/c
SLFNMA04	Pna21

**11**

Minimum slab separation: -1.6 Å [Reset]

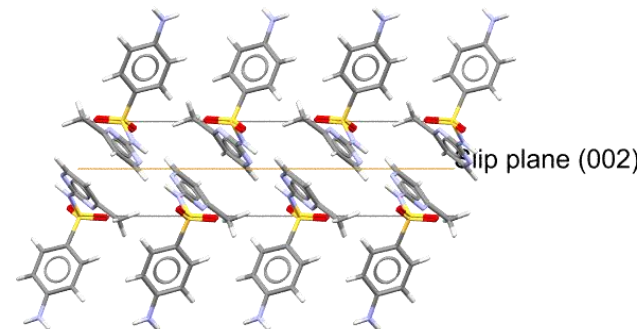
Slip Planes... SLFNMA01

Minimum slab separation: -1.6 Å [Reset]

Status: Calculation completed

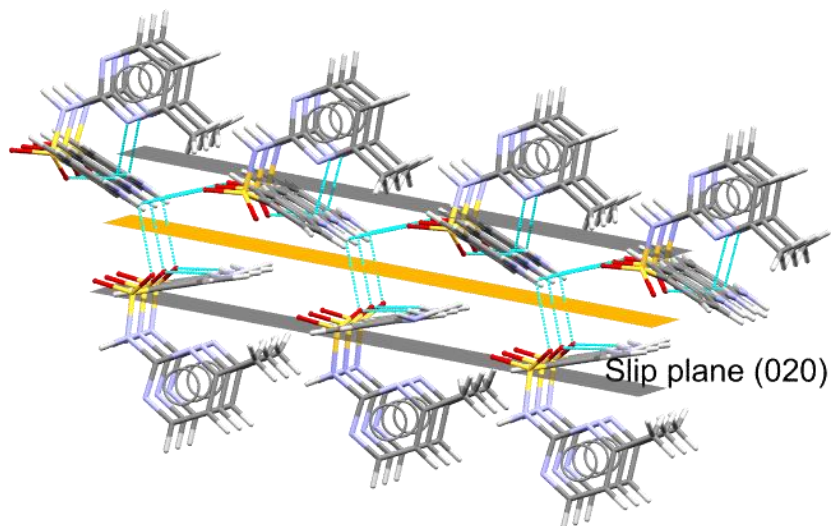
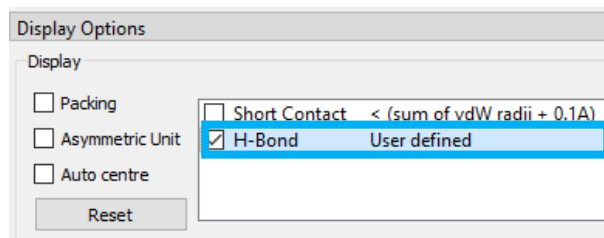
	Orientation	Slab separation	Repeat distance	Offset	H-bonded	Perpendicular planes
1	(002)	-1.053	11.442	0.000	yes	

H-bond dimensionality: 3D network [Analyse Surface] [Export...] [Calculate] [Close]



## Hydrogen bonds analysis

- For both structures, we will explore the [hydrogen bonds](#) network. Hydrogen bonds are indeed really important for the stability of the structure. At the bottom of the Slip Planes window, you will see *H-bond dimensionality: 3D network*; and in the table, under *H-bonded* you can read “yes”, which means that there are hydrogen bonds across the defined slip plane.
- Visualize hydrogen bonds by turning on H-Bonds in the *Display Options* box at the bottom of the Mercury interface.



Hydrogen bonds for the plastic deforming polymorph, CSD Entry SLFNMA02

Slip Planes... SLFNMA02

Minimum slab separation 0.0 Reset

Status: Calculation completed

Orientation	Slab separation	Repeat distance	Offset	H-bonded	Perpendicular planes
1 (020)	1.561	10.977	-3.942	yes	

H-bond dimensionality: 3D network

Slip Planes... SLFNMA01

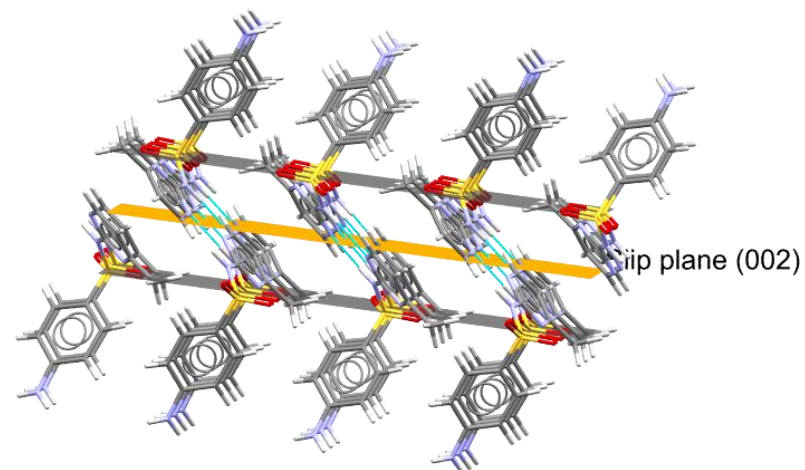
Minimum slab separation -1.6 Reset

Status: Calculation completed

Orientation	Slab separation	Repeat distance	Offset	H-bonded	Perpendicular planes
1 (002)	-1.053	11.442	0.000	yes	

H-bond dimensionality: 3D network

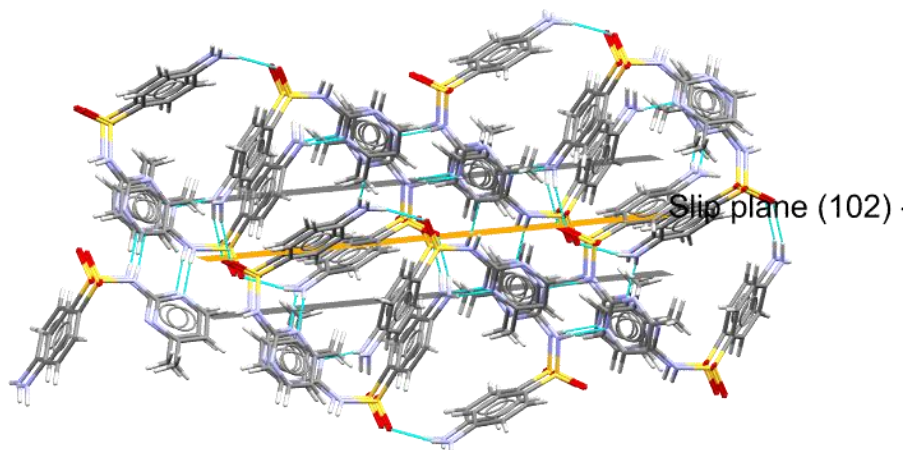
Analyse Surface Export... Calculate Close



Hydrogen bonds for the elastic deforming polymorph, CSD Entry SLFNMA01

## Exploring more potential slip planes

15. Go back to the Mercury window with CSD Entry SLFNMA01.
16. To bring up more potential slip planes, drag the cursor at the top of the *Slip Planes* window to lower the minimum slab separation until a value of -4.0 Å. A total of 7 planes will populate the table.
17. If you explore the potential planes, by clicking on each entry, you will notice that plane (102) is very interlocked and connected so it seems very unlikely to be a slip plane. It is thus important to analyse in detail the potential planes.



18. You will also notice that the column with [perpendicular planes](#) is now populated and informs of which other potential slip planes are about perpendicular to the one in analysis. This might help assess where in an elastic system there might be a flexible crystal.

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Slip Planes... SLFNMA01

Minimum slab separation

Status: Calculation completed

	Orientation	Slab separation	Repeat distance	Offset	H-bonded	Perpendicular planes
1	(002)	-1.053	11.442	0.000	yes	(02-1), (10-2), (102)
2	(02-1)	-2.631	5.670	0.000	yes	(002), (10-2), (102)
3	(021)	-2.631	5.670	-2.835	yes	(002), (10-2), (102)
4	(020)	-2.973	5.852	0.000	yes	(002), (10-2), (102)
5	(020)	-3.909	5.852	-2.926	yes	(002), (10-2), (102)
6	(10-2)	-3.958	7.144	0.000	yes	(002), (02-1), (102)
7	(102)	-3.958	7.144	-3.572	yes	(002), (02-1), (10-2)

H-bond dimensionality: 3D network

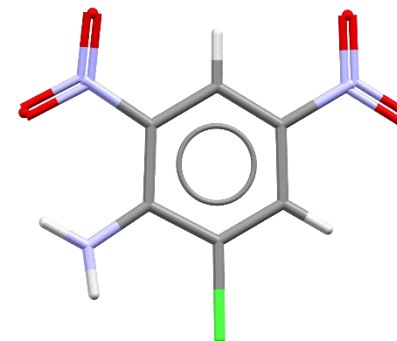
## Conclusion

In this example, we explored an elastic and a plastic polymorph of sulfamerazine. Using the Slip Planes tool from CSD-Particle, we were able to investigate the location and properties of potential slip planes and consider how these could be related to the experimentally determined plastic or elastic properties.



## Example 2. Slip planes analysis to investigate plastic properties of polymorphs

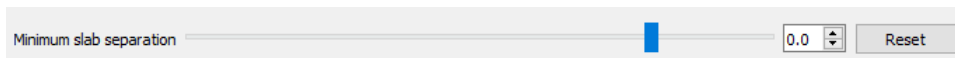
In the previous example, we looked at polymorphs that have different elastic properties: one plastic and the other elastic. In this example, we will look at polymorphs that exhibit similar plastic behaviours, however, one is more compressible than the other due to the type of planes observed.



6-Chloro-2,4-dinitroaniline molecule from CSD Entry UCECAG02.

### Calculation of potential slip planes

1. Open Mercury by double-clicking the Mercury icon on the desktop.
2. In the *Structure Navigator* on the right-hand side of the Mercury interface type the refcode UCECAG02 to bring up the first polymorph that we are going to investigate.
3. From the top-level menu select **CSD-Particle > Slip Planes...** to launch the *Slip Planes* window.
4. Observe that the minimum slab separation is set to 0.0 Å. To start the calculation, click **Calculate** at the bottom of the *Slip Planes* window.



**1**

**2**

**3**

**4**

Structure Navigator

UCECAG02 Find

Crystal Structures	Spacegroup
UCECAG01	P21/c
UCECAG02	P21
UCECAG03	P-1
UCECAH	P41
UCECAI	P-1
UCECAJ	P21/n
UCECAK	P21/c

CSD-Particle CSD-Discover

Morphology

Slip Planes...

Surface Analysis...

Slip Planes

Minimum slab separation 0.0 Reset

Status

Orientation	Slab separation	Repeat distance	Offset	H-bonded	Perpendicular planes

H-bond dimensionality:

Analyse Surface Export...

Calculate Close

5. You will see that the table is now populated with entries representing potential slip planes with the value of slab separations. You will also notice that the Perpendicular planes have also been populated. Perpendicular planes might help assess where in a system there might be a flexible crystal. Observe the values in the table.

5

	Orientation	Slab separation	Repeat distance	Offset	H-bonded	Perpendicular planes
1	(001)	2.190	13.275	0.000	no	(101), (01-1)
2	(101)	0.501	6.882	0.000	yes	(001), (01-1)
3	(01-1)	0.071	3.532	-2.116	yes	(001), (101)
4	(011)	0.071	3.532	-0.350	yes	(001), (101)

6. Click now on the first entry in the table to visualize the planes in the Mercury visualizer. Note that this will also open the *Packing and Slicing* window. You can move the Area slider to adjust the views in the main Mercury window.

6

Slip Planes... UCECAG02

Minimum slab separation: 0.0 [Reset]

Status: Calculation completed

	Orientation	Slab separation	Repeat distance	Offset	H-bonded	Perpendicular planes
1	(001)	2.190	13.275	0.000	no	(101), (01-1)
2	(101)	0.501	6.882	0.000	yes	(001), (01-1)
3	(01-1)	0.071	3.532	-2.116	yes	(001), (101)
4	(011)	0.071	3.532	-0.350	yes	(001), (101)

H-bond dimensionality: 2D sheet

Packing and Slicing

Packing

Show cell axes

Label cell axes

Pack

a: 0.0 [1.0] + 0.5

b: 0.0 [1.0] + 0.5

c: 0.0 [1.0] + 0.5

2x2x2

3x3x3

Reset

Include atoms

... that Fit

... in molecules whose Centroids fit

... in molecules where Any atom fits

... in molecules where All atoms fit

Slicing

Show slice

Select plane: Slip plane (001) 0.000 [Show plane]

New... Edit... Delete [Show bounds]

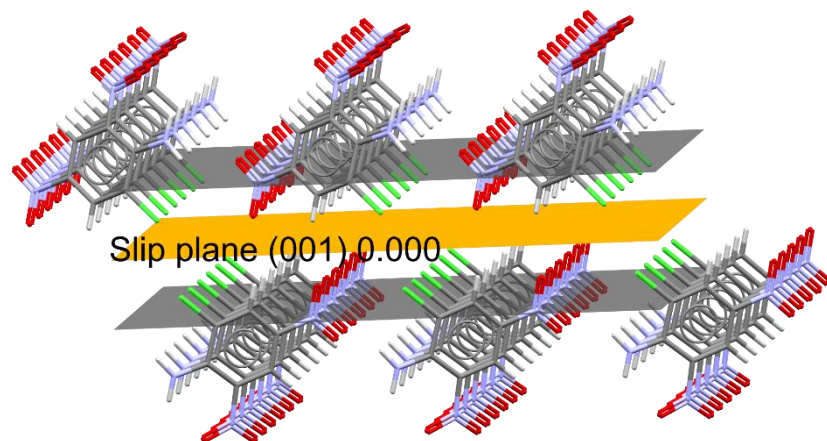
Depth: 5.00

Area: 20.00

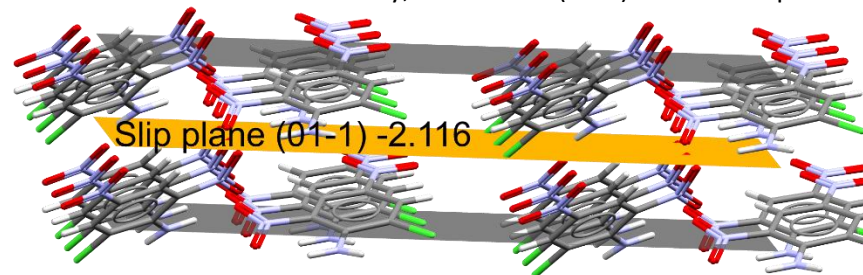
Displacement: 0.00

Reset

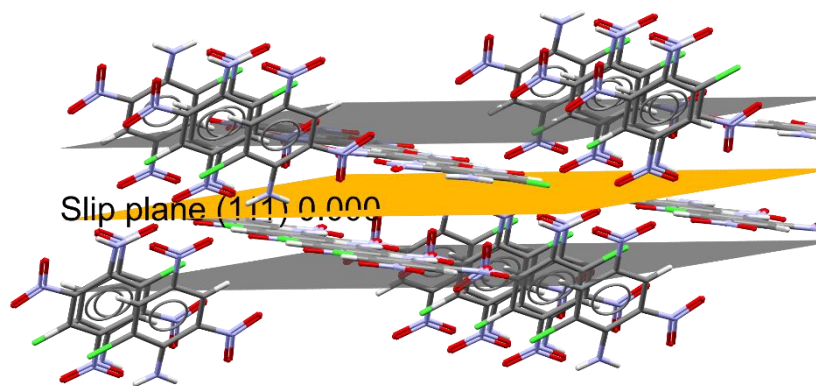
OK



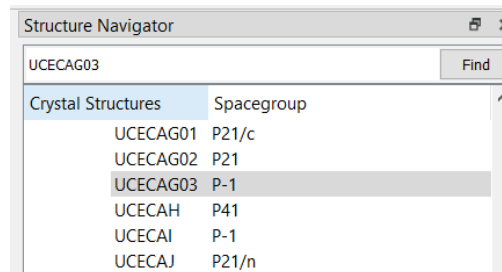
7. You can rotate the structure to see the alignment of molecules around the slip plane. You can see that there is a significant separation between the two slabs with potential slips in directions parallel and perpendicular to the plane. This structure has a high likelihood of having a slip plane. Structures with such features might be preferable when compression of the particle is involved. You can also view a different entry; orientation (01-1) to view the planes.



8. We will now compare this structure with the other polymorph. In the *Structure Navigator* on the right-hand side of the Mercury interface type the refcode UCECAG03.
9. If you have previously closed the *Slip Planes* window, re-open it from the top-level menu by selecting **CSD-Particle > Slip Planes...** as in **Step 3** above.
10. To start the calculation, click **Calculate** as in **Step 4** above. You will see the table populated with two entries. You will notice that there are no perpendicular planes observed in this structure
11. Observe the values in the table and then click on each row to visualize the plane in the structure. You will notice that for this polymorph there are no perpendicular planes, only parallel ones. We can say that this polymorph is less likely to be flexible than the other.



8



10

Slip Planes... UCECAG03

Minimum slab separation: 0.0 Reset

Status: Calculation completed

	Orientation	Slab separation	Repeat distance	Offset	H-bonded	Perpendicular planes
1	(111)	1.262	6.372	0.000	yes	
2	(110)	0.840	7.086	-3.543	yes	

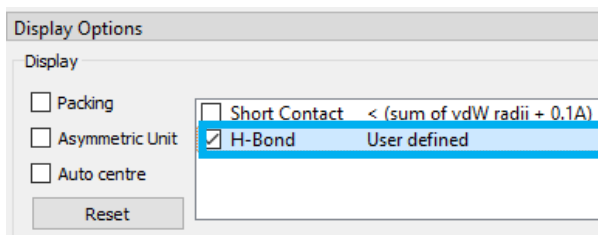
H-bond dimensionality: 2D sheet

Analyse Surface Export... Calculate Close

## Hydrogen bonds analysis

12. For both structures, we will explore the hydrogen bonds network. Hydrogen bonds are indeed really important for the stability of the structure. At the bottom of the Slip Planes window, you will see *H-bond dimensionality: 2D sheet* for both structures. In the table for UCECAG02, under *H-bonded* you can read “no” for the first entry, which means that there are no hydrogen bonds across the plane. However, the other entries do exhibit hydrogen bonding for both structures

13. Visualize hydrogen bonds by turning on H-Bonds in the *Display Options* box at the bottom of the Mercury interface.



Slip Planes... UCECAG02

Minimum slab separation: 0.0 [Reset]

Status: Calculation completed

	Orientation	Slab separation	Repeat distance	Offset	H-bonded	Perpendicular planes
1	(001)	2.190	13.275	0.000	no	(01), (01-1)
2	(101)	0.501	6.882	0.000	yes	(01), (01-1)
3	(01-1)	0.071	3.532	-2.116	yes	(01), (101)
4	(011)	0.071	3.532	-0.350	yes	(01), (101)

H-bond dimensionality: 2D sheet

---

Slip Planes... UCECAG03

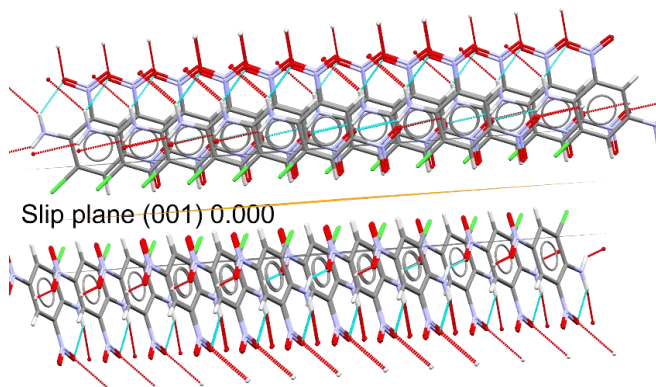
Minimum slab separation: 0.0 [Reset]

Status: Calculation completed

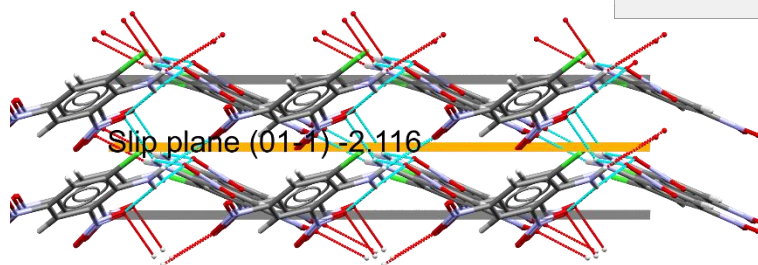
	Orientation	Slab separation	Repeat distance	Offset	H-bonded	Perpendicular planes
1	(111)	1.262	6.372	0.000	yes	
2	(110)	0.840	7.086	-3.543	yes	

H-bond dimensionality: 2D sheet

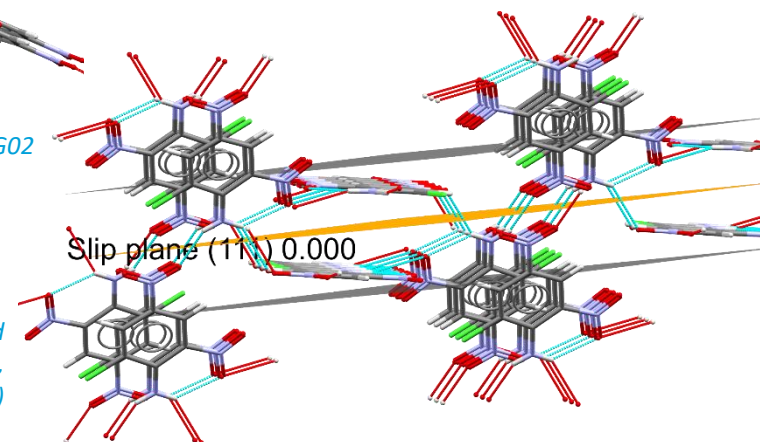
Analyse Surface Export... Calculate Close



No hydrogen bonds for the first plane, the one with (001) orientation, in CSD Entry UCECAG02



Hydrogen bonds for the (01-1) orientation in CSD Entry UCECAG02



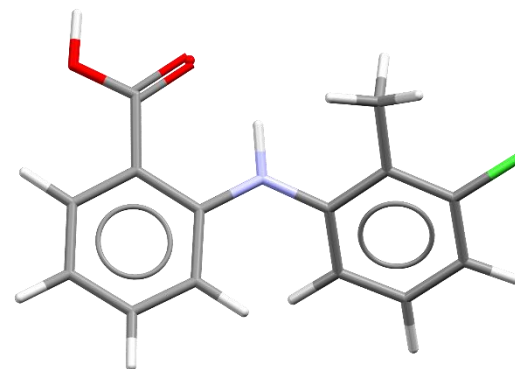
Hydrogen bonds for the second polymorph, CSD Entry UCECAG03, shown for the potential slip plane (111)

## Conclusion


In this example, we used the *Slip Planes* tool from CSD-Particle to investigate polymorphs with similar behaviours, where one is more compressible than the others. We studied the potential slip planes in both polymorphs to investigate such properties.

## Example 3. Surface Analysis

In this example, we will employ tools from the *Surface Analysis* feature in CSD-Particle to investigate two different surfaces of a 2-(3-chloro-2-methylanilino)benzoic acid crystal. The two surfaces under investigation are the (110) and the (020). By calculating these two surfaces and analysing their properties and the chemistry on each surface, we will learn more about their activities.




CSD Entry KAXXAI10 2-(3-chloro-2-methylanilino)benzoic acid

1. Open Mercury by double-clicking the Mercury icon  on the desktop.
2. In the **Structure Navigator** toolbar type the refcode KAXXAI10.

### BFDH Morphology

3. We want to identify facets of interest in this morphology. We will first create the morphology using the [BFDH morphology](#) feature.
4. From the top-level menu select **CSD-Particle > Morphology > BFDH...** to generate the morphology. BFDH morphology uses the unit cell to create the morphology you see, therefore it does not account for the chemistry of the structure.
5. Rotate the structure to view the various facets that have been generated. For this exercise, we will explore two facets: (020) and (110). If you wish, explore options in the *Morphology* menu. Once you are ready to continue, close the *Morphology* menu and click the Reset button from the *Display Options* menu to return to the structure view.
6. The first surface that we will explore is the (110) facet.

**1** 

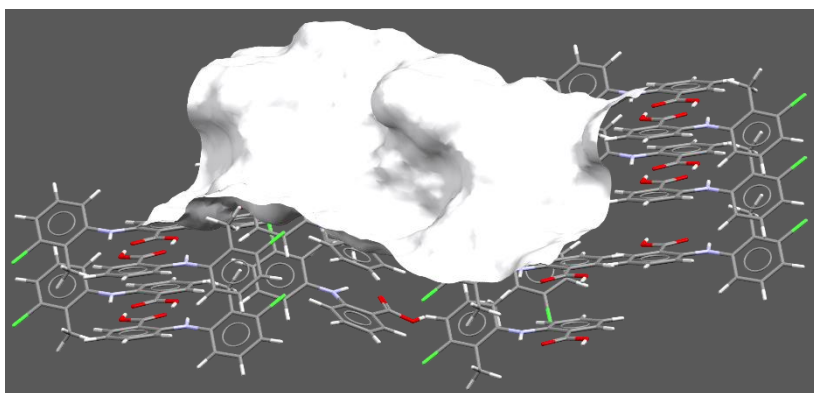
**2** Structure Navigator  
KAXXAI10 Find  
Crystal Structures Spacegroup  
KAXXAI10 P21/n  
KAXXAI11 P21/c

**4** CSD-Particle CSD-Discovery CSD Python  
Morphology BFDH...  
Slip Planes...  
Surface Analysis...

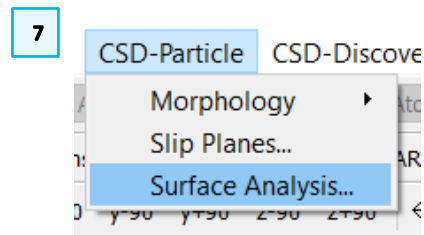
**5** Display Options  
Display  
 Packing  Short Contact < (sum of vdW radii + 0.15A)  
 Asymmetric Unit  H-Bond User defined  
 Auto centre  
Reset  
Press the left mouse button and move the mouse to rotate the structure

## Surface Analysis

- From the top-level menu select **CSD-Particle > Surface Analysis...** to open the Surface Analysis dialog. Since we are interested in the (110) surface, we want to enter those values in the *Select surface orientation (hkl) and offset (o)* section. Change the value for *h* and *k* to 1, and leave *l* and *o* as 0, then click **Calculate Surface**.
- You will notice that a surface has been generated and the *Results* section of the *Surface Analysis* dialog has been populated. Let us go through the sections to understand what they mean.



- The *Results* section begins with the structure refcode and the surface generated as (orientation)[offset], here KAXXA10(110)[0.00]. The **Density Info (count/Å<sup>2</sup>)** portion tells us about the chemistry on the surface that is in contact with the topology (the white surface that has been generated). The density of hydrogen bond acceptors is higher than hydrogen bond donors on the surface. Observe that the density of **Unsatisfied H-Bond Donors** is lower than the density of hydrogen bond donors as they are a subset of this group. You can then rotate the surface to view the aromatic bonds in contact with the surface. The **Topology Info** section describes the physical roughness of the generated surface. The **Rugosity** is the ratio of the surface area to the projected area, and **RMSD** is the root mean squared deviation of the height from the mean plane. **Skewness** describes whether the surface is dominated by peaks (value higher than 0) or by valleys (lower than 0). Finally, **Kurtosis** describes the



9

**Surface Analysis... KAXXA10**

**Analyse**

Select surface orientation (hkl) and offset (o)

h: 1 k: 1 l: 0 o: 0.00  Preview Slab

Show Advanced Options

Full Interaction Map **Calculate Surface**

---

**Results - KAXXA10 (110)[0.00]**

Density Info (count/Å<sup>2</sup>)

H-Bond Acceptors:	0.051	Aromatic Bonds:	0.158
H-Bond Donors:	0.025	Unsatisfied H-Bond Donors:	0.006

Topology Info

Surface Area (Å <sup>2</sup> ):	449.533	Projected Area (Å <sup>2</sup> ):	315.890
Rugosity:	1.423	RMSD:	1.444
Skewness:	0.060	Kurtosis:	2.236

**Display Options**

Surface colouring: Single colour

Opacity: (%) 100

Periodic View  Hide Molecules

Atom Properties

Charge  H-Bond Acceptors

Aromatic  H-Bond Donors

Unsatisfied H-Bond Donors

Reset Close

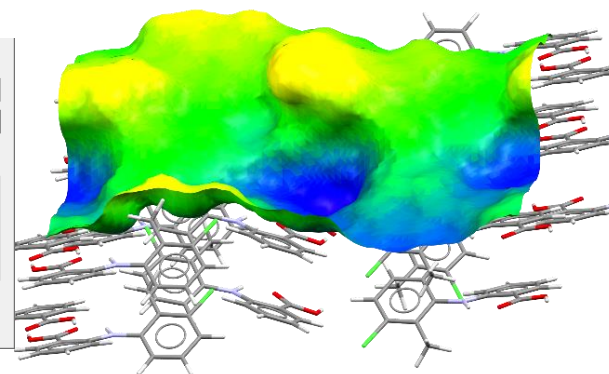
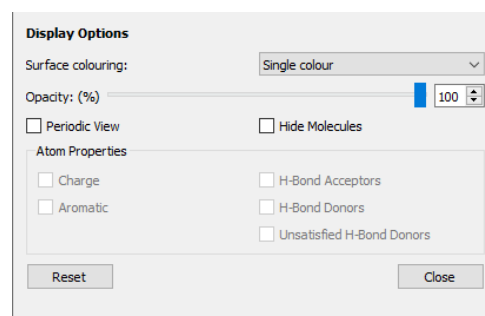
sharpness of the peak: values less than 3 signify a step-height change and values higher than 3 hint at a sharp peak.

10. The *Display Options* section of the **Surface Analysis** dialog allows us to generate more dynamic views of the surface. We will adjust the values here to change the surface views.

11. First, we will change the *Surface colouring* from *Single Colour* to *Topology* to get a better view of the height map of the surface. The areas closer to red are the peaks (note that in this case, we see a maximum of yellow), while the blue-purple areas are the valleys.

12. Next, select *Atom Properties* from the Surface Colouring menu. You will see that the surface is back to white and that it is now possible to tick the *Atom Properties* options below to visualise where specific chemistry is found on the surface. Explore the options to learn more about the surface. Tick H-Bond Acceptors (coloured red), H-Bond Donors (blue) and Aromatic (orange). We notice that what we observe on the surface is in line with the descriptors explored before. If Some areas show both red and blue, the dominant colour will be hydrogen bond acceptors. To get a better view of which atoms are contributing to the maps, you can reduce the opacity.

10



11

**Display Options**

Surface colouring:

Single colour

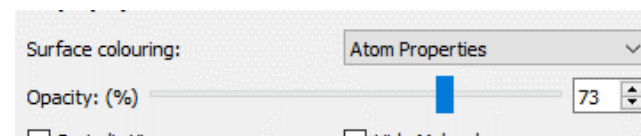
Opacity: (%)

 Periodic View

Single colour

Topology

Atom Properties

 Hide Molecules

12

**Display Options**

Surface colouring:

Opacity: (%)

 Periodic View

Atom Properties

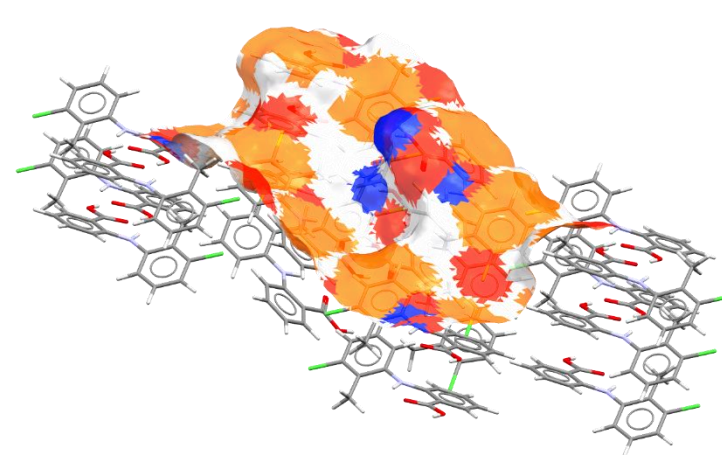
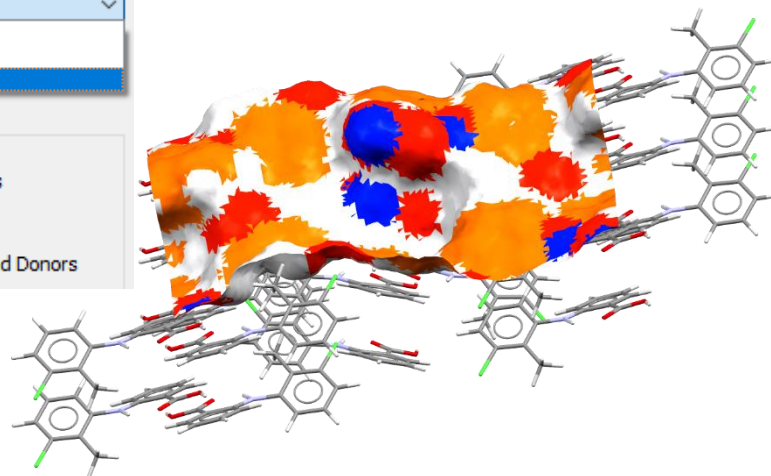
 Charge Aromatic

Atom Properties

Single colour

Topology

Atom Properties

 Hide Molecules H-Bond Acceptors H-Bond Donors Unsatisfied H-Bond Donors

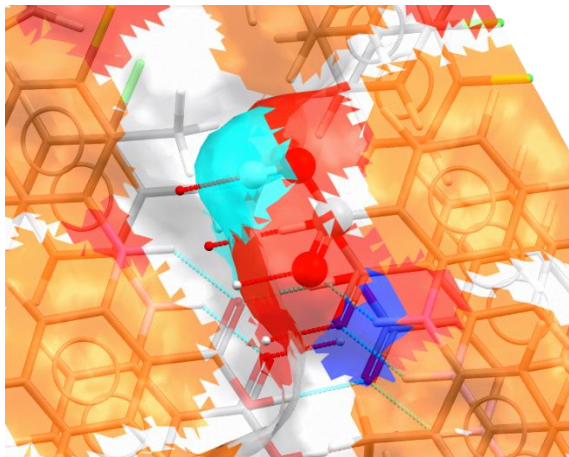


13. We will now visualise where hydrogen bond donors and acceptors are located by turning on H-Bonds in the *Display Options* box at the bottom of the Mercury interface.

14. The next atom property to investigate is the [Unsatisfied H-Bond Donors](#). Tick the corresponding box in the *Atoms Properties* section of the **Surface Analysis** dialog to colour the matching areas in teal (light blue shade).

15. Observe that not all the H-bond donors (blue) areas became teal, as some of the donors are satisfied. As an example, observe the hydrogen bond donors in the images on the side and on your structure: you will notice that (a) is protruding out of the surface and has a hydrogen to donate hence it is unsatisfied, while (b) is part of a dimer and the hydrogen donor is satisfied within the structure. This is important because it allows us to explore which hydrogens are available for donation, for incoming molecules for example, and which donors are not available as they are already involved in hydrogen bonds with the bulk of the surface.

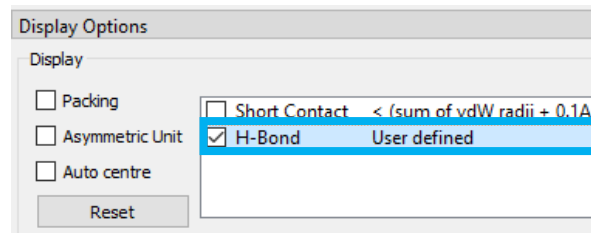
15a



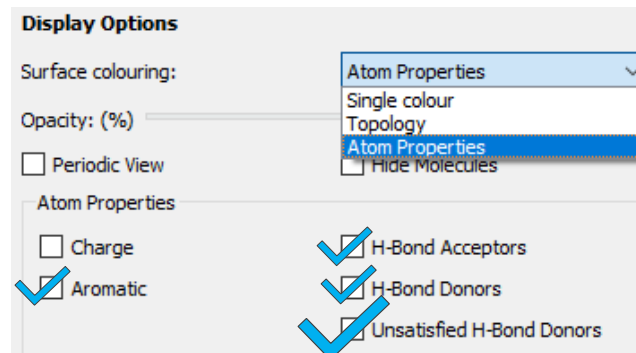
16. At the end of the analysis, turn off the hydrogen bonds by unticking the H-Bond box (opposite of **Step 13**).

17. The last atom's property that we will see in this example is the charge. In the *Atoms Properties* section of the **Surface Analysis** dialog, untick all the properties that you currently have on and tick only *Charge*.

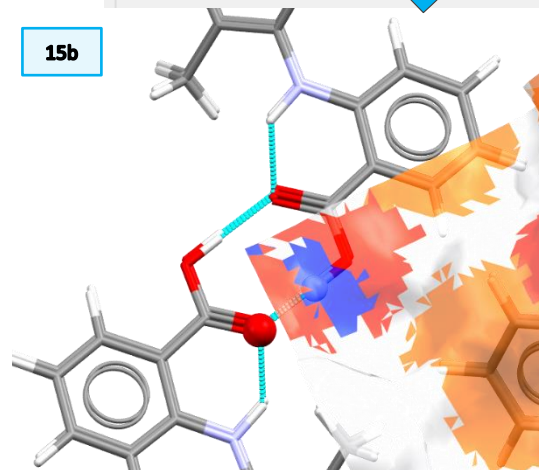
13



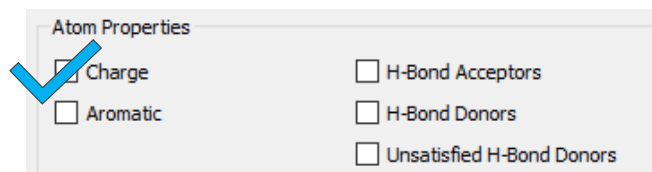
14



15b

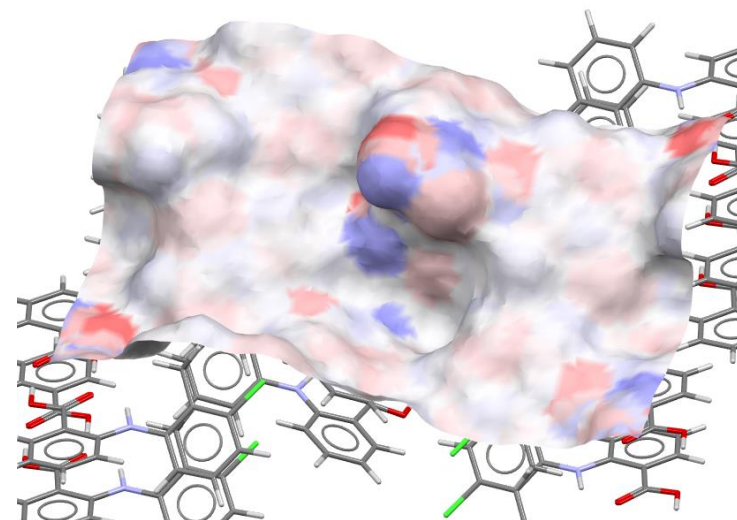


17



18. The surface is now coloured representing the *Gasteiger charges*. You can observe areas of positive charge (blue) and negative charge (red). **Bonus tip:** if you have calculated your own charges, you can import them into a mol2 file by modifying the charges column and when you do the surface analysis, it will overlay the charges that you have given.

19. **Bonus tip:** If you tick the box next to *Periodic View* in the **Surface Analysis** dialog, you will only see the molecules that are within the bounding box of the surface. You may export this representation for further calculations, for example with Molecular Dynamics, Quantum Mechanics, or other computational techniques.



19

**Display Options**

Surface colouring:

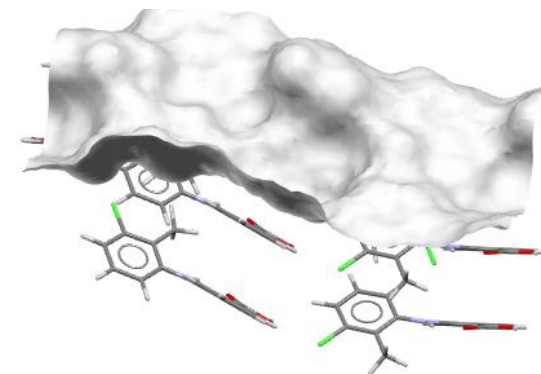
Opacity: (%)

Periodic View

Atom Properties

Charge

Aromatic



### FIMs on Surface

20. For the next part, we will study the Full Interaction Maps (FIMs) on Surface. We will start with the same surface analysed in the previous part of this example.

21. For this example, we will first untick all the options in the *Display Properties* section of the **Surface Analysis** dialog. Then, click the **Full Interaction Map** button at the top of the **Surface Analysis** dialog.

21

**Surface Analysis... KAXXAI10**

**Analyse**

Select surface orientation (hkl) and offset (o)

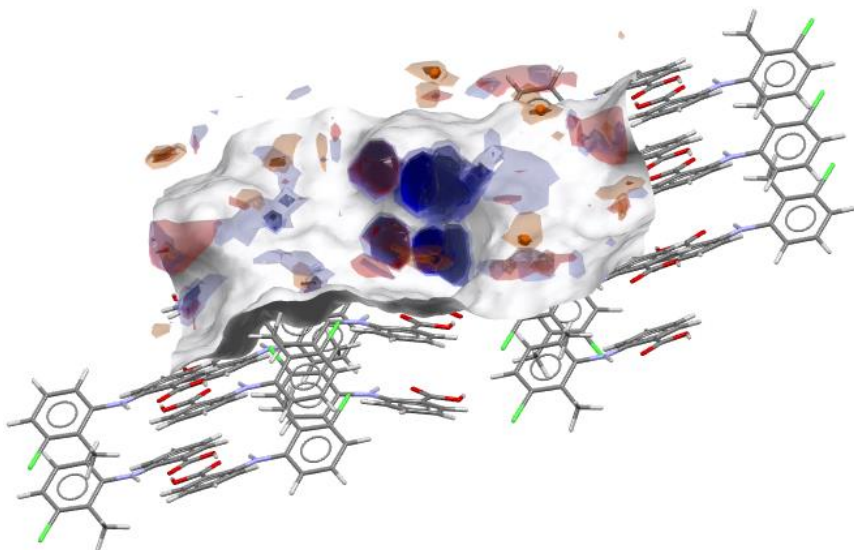
h: 1 k: 1 l: 0 o: 0.00  Preview Slab

Show Advanced Options

**Full Interaction Map** Calculate Surface

22. This will bring up the **Full Interaction Maps on Surface** window. For this example, we will keep the default settings and additionally, we will tick the *Generate hotspots in the map* box, and also select in the probes *Water Oxygen*. Then, click **Calculate Surface Maps**. A progress bar will appear.

23. FIMs have been generated on the surface and they show the likelihood of finding interactions of the selected probes on this surface. We can see maps and hotspots.



24. Let us investigate the maps. For ease of visualization, turn off the hotspots by going in the *Hotspots* tab and untick *All* above the *Visible* column.

25. Then, in the **Surface Analysis** dialog, tick again the atom properties *H-Bond Acceptors* and *H-Bond Donors*.

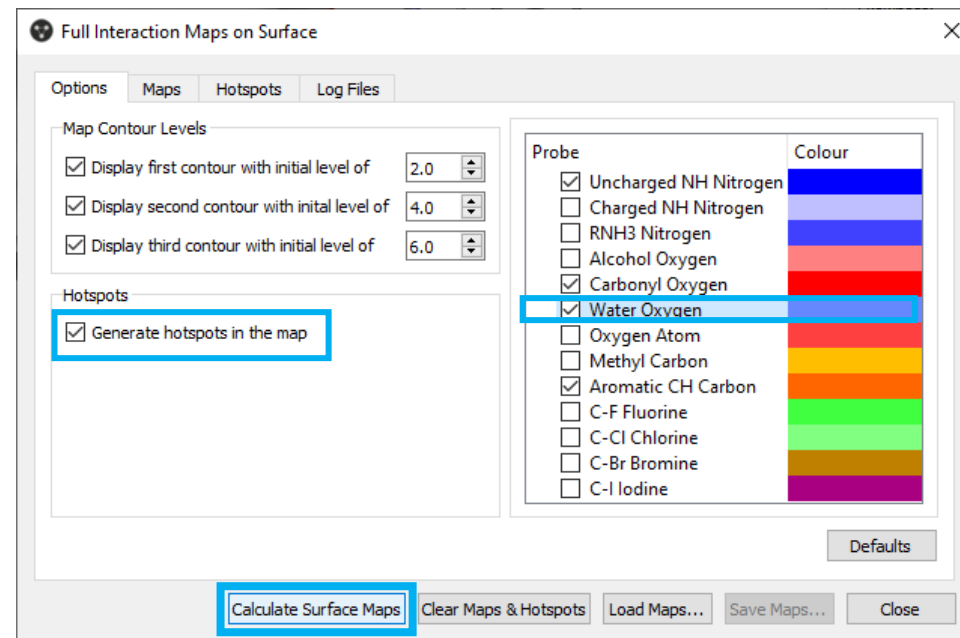
Atom Properties

Charge  H-Bond Acceptors

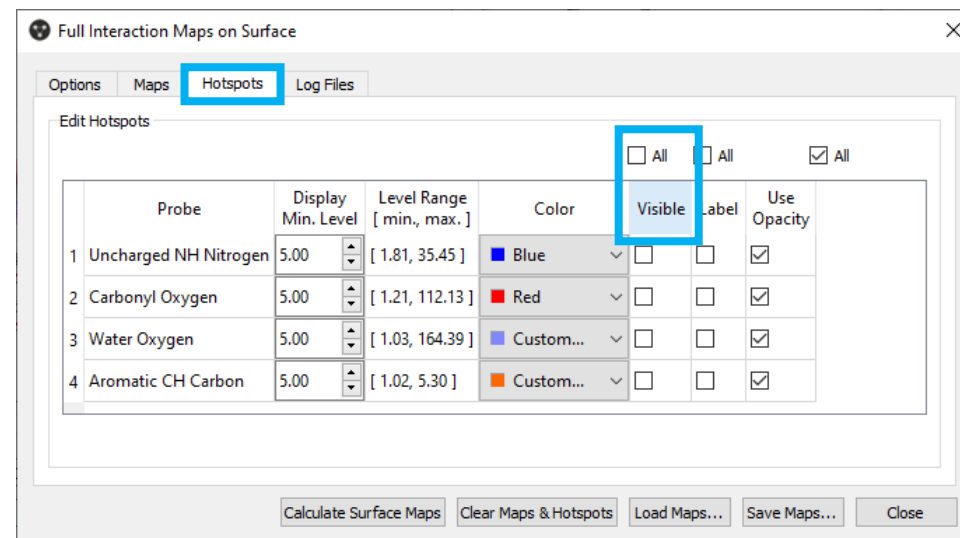
Aromatic  H-Bond Donors

Unsatisfied H-Bond Donors

22



24



26. Observe that red areas on the surface (H-bond acceptors) match blue areas in the FIMs (NH Nitrogen, H-bond donors), while blue areas on the surface (H-bond donors) correspond to red areas in the FIMs (Carbonyl Oxygen, H-bond acceptors).

27. You can continue the analysis by turning on the *Unsatisfied H-Bond Donors* property for the surface. You will see that the unsatisfied hydrogen bond donors have a likely acceptor area on the maps, while satisfied donors do not as having already formed a H-bond in the surface would make the formation of any other hydrogen bond at an unlikely angle.

28. We can then explore FIMs numerically. Go to the *Maps* tab and observe the values in the *Level Range* column. These values express how likely over random it is to find such interaction.

Full Interaction Maps on Surface

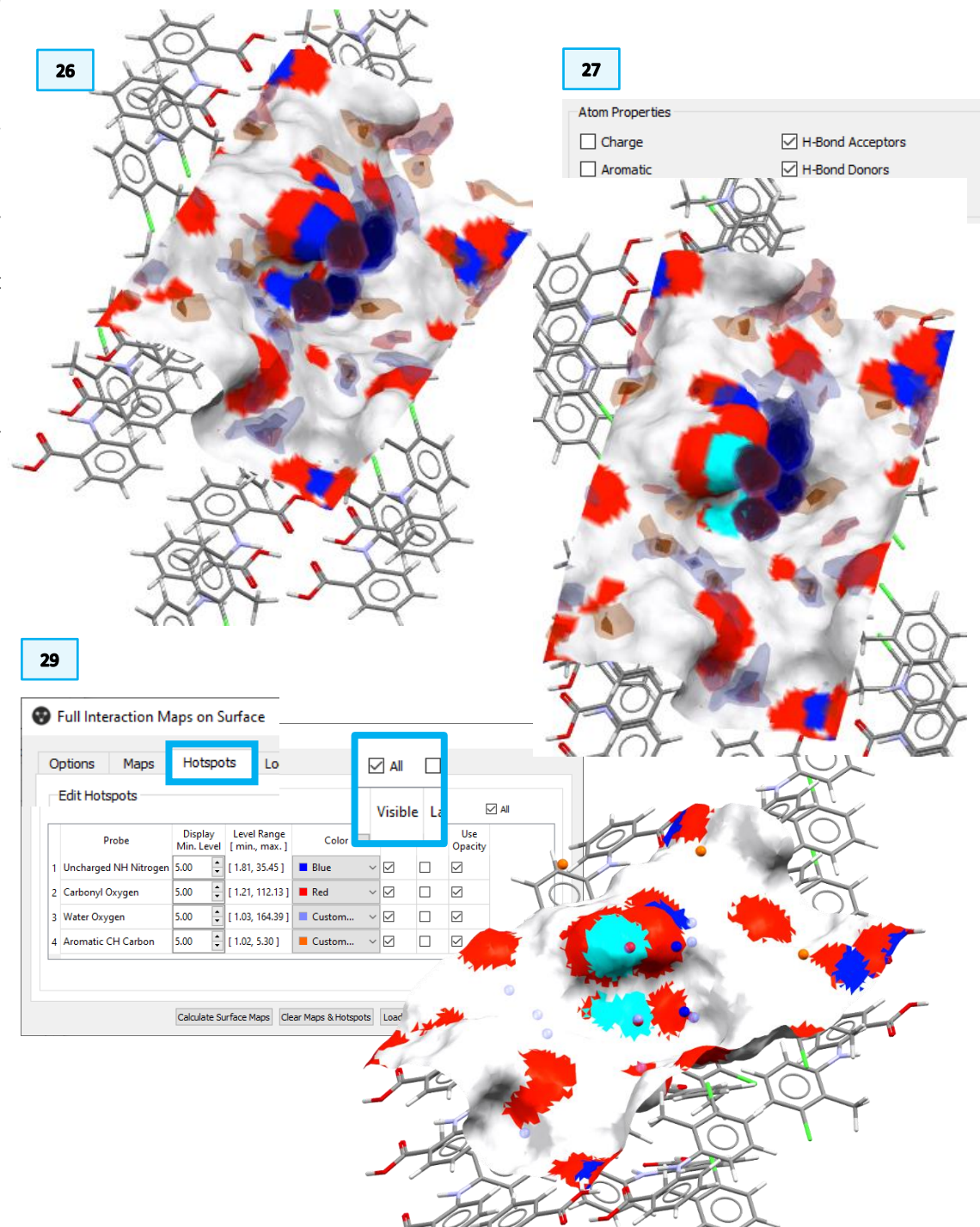
Options: **Maps** Hotspots Log Files

Edit Existing Contours

Probe	Level	Level Range [min., max.]	Color	Visible	Display Type	Opacity
1 Uncharged NH Nitrogen	2.00	[ 0.00, 35.45 ]	Blue	<input checked="" type="checkbox"/>	triangle	0.2
2 Uncharged NH Nitrogen	4.00	[ 0.00, 35.45 ]	Blue	<input checked="" type="checkbox"/>	triangle	0.5
3 Uncharged NH Nitrogen	6.00	[ 0.00, 35.45 ]	Blue	<input checked="" type="checkbox"/>	triangle	0.8
4 Carbonyl Oxygen	2.00	[ 0.00, 112.13 ]	Red	<input checked="" type="checkbox"/>	triangle	0.2
5 Carbonyl Oxygen	4.00	[ 0.00, 112.13 ]	Red	<input checked="" type="checkbox"/>	triangle	0.5
6 Carbonyl Oxygen	6.00	[ 0.00, 112.13 ]	Red	<input checked="" type="checkbox"/>	triangle	0.8
7 Water Oxygen	2.00	[ 0.00, 164.39 ]	Custom...	<input checked="" type="checkbox"/>	triangle	0.2
8 Water Oxygen	4.00	[ 0.00, 164.39 ]	Custom...	<input checked="" type="checkbox"/>	triangle	0.5
9 Water Oxygen	6.00	[ 0.00, 164.39 ]	Custom...	<input checked="" type="checkbox"/>	triangle	0.8
10 Aromatic CH Carbon	2.00	[ 0.00, 5.30 ]	Custom...	<input checked="" type="checkbox"/>	triangle	0.2

Calculate Surface Maps Clear Maps & Hotspots Load Maps... Save Maps... Close

29. We can now look in more detail at the *hotspots*. For ease of visualization, turn off the maps by unticking *All* above the *Visible* column. Then, move to the *Hotspots* tab and tick *All* above the *Visible* column.



30. As hotspots represent the areas of the highest likelihood of interactions, observe where they are located on the surface and which atom properties they correspond to. [What do you observe?](#)

### Comparison of different surfaces

31. Close the **Full Interaction Maps on Surface** window and click the **Reset** button in the *Display Options* menu at the bottom of the Mercury interface.

32. Since we are now interested in the (002) facet, in the **Surface Analysis** dialog we want to enter those values in the *Select surface orientation (hkl) and offset (o)* section. Change the value for *h* and *k* to 0, for *l* to 2, and leave *o* as 0.

33. **Bonus tip:** before calculating the slab, it is possible to preview it by ticking the *Preview Slab* option. You can tick *Show Advanced Options* to explore different visualization options, for example by changing *U* and *V* to 2 to obtain a 2x2 surface. Observe the surface, then untick both *Preview Slab* and *Show Advanced Options*.

34. Now click **Calculate Surface** as in **Step 7**.

35. At the bottom of the **Surface Analysis** dialog select *Topology* from the Surface Colouring menu. We can observe how the surface is different from the previous one; this is reflected also in the topology values. Compare these with the results obtained in **Step 9** for surface (110). In particular, we observe a negative value of the *Skewness* and a lower *Kurtosis* value, meaning that we have a surface resembling more a step function rather than a round peak.

Results - KAXXAI10 (020)[0.00]			
Density Info (count/Å <sup>2</sup> )			
H-Bond Acceptors:	0.055	Aromatic Bonds:	0.092
H-Bond Donors:	0.018	Unsatisfied H-Bond Donors:	0.018
Topology Info			
Surface Area (Å <sup>2</sup> ):	355.004	Projected Area (Å <sup>2</sup> ):	217.504
Rugosity:	1.632	RMSD:	1.883
Skewness:	-0.099	Kurtosis:	1.485

**31** Display Options

Display

Packing  Short Contact

Asymmetric Unit  H-Bond

Auto centre

Reset

**32** Surface Analysis... KAXXAI10

Analyse

Select surface orientation (hkl) and offset (o)

**33** h: 0 k: 2 l: 0 o: 0.00  Preview Slab

Show Advanced Options

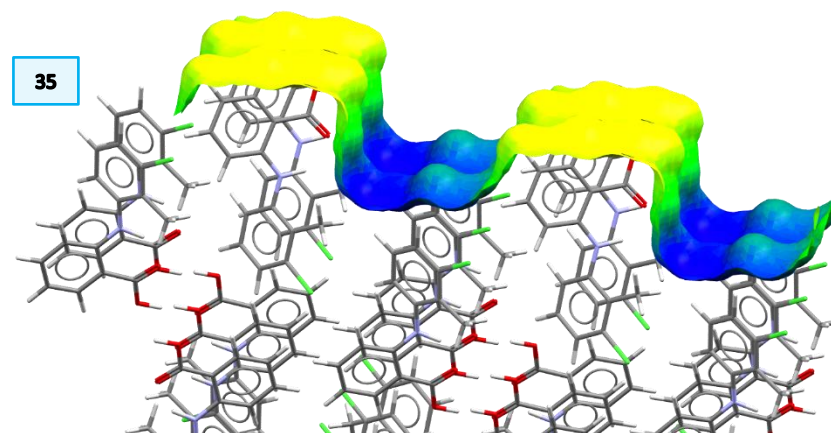
Size of Surface: U: 1 V: 1

Default values for the following settings have been optimised for small molecule organic systems.

Probe Radius: 1.2 Grid Spacing: 0.3

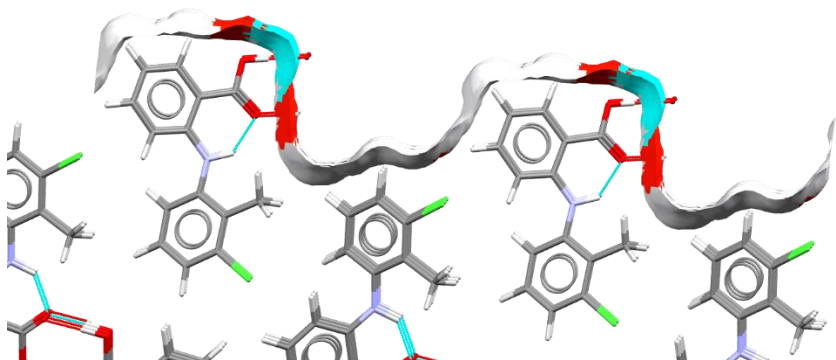
Thickness (W) Factor 1.60

Full Interaction Map Calculate Surface



36. Next, select *Atom Properties* from the Surface Colouring menu. Tick H-Bond Acceptors, H-Bond Donors, and Unsatisfied H-Bond Donors. Also, observe the *Density Info* values in the dialog (**Step 35**) and compare them with **Step 9** for surface (110). In particular, we observe that all the hydrogen bond donors are unsatisfied in this case; moreover, the unsatisfied H-bond donors count per Å<sup>2</sup> is higher than for the (110) surface, while the aromatic bonds density is lower.

37. Now turn on the hydrogen bonds as in **Step 13** to observe where potential hydrogen bonds could be formed on the surface.

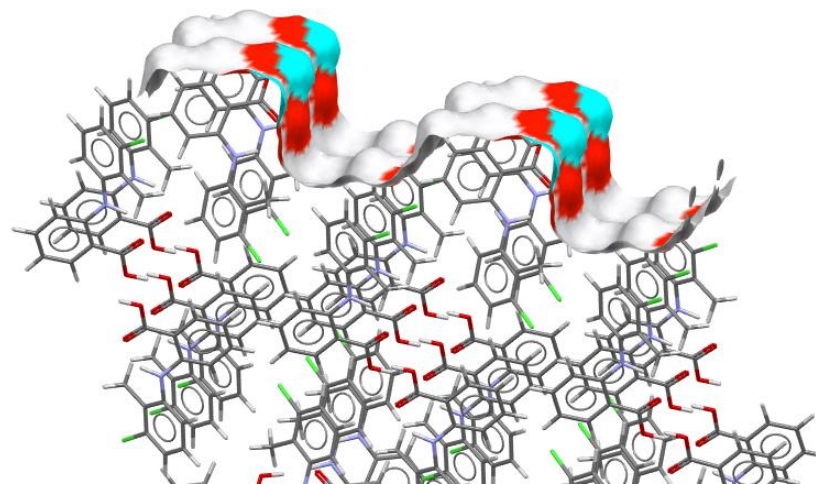


38. You may also observe the Gasteiger charges as in **Step 17** above.

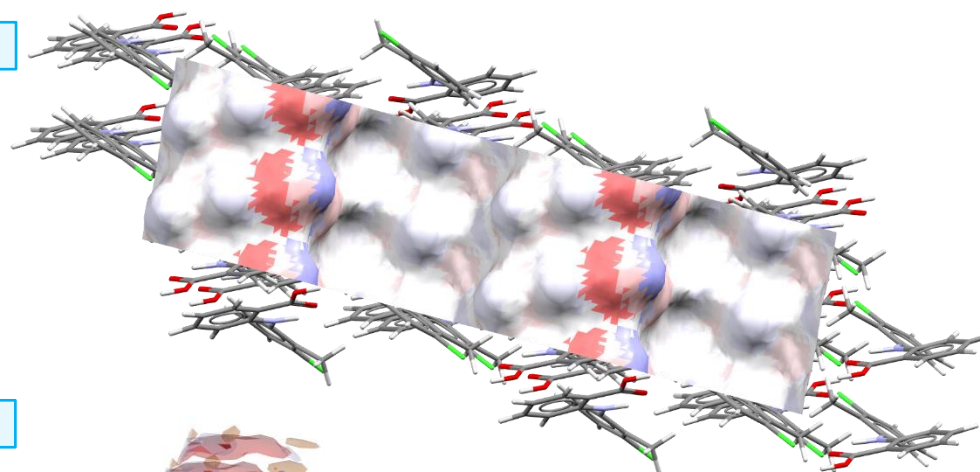
39. Next, we will generate FIMs on Surface, following **Steps 21 to 23** above.

40. Then, compare the values in the *Level Range* column of the table in the *Maps* tab with the ones obtained for surface (110) at **Step 28**. You will notice that in this case the values of the water oxygen and carbonyl oxygen are lower than in the previous case, suggesting a lower likelihood of interaction.

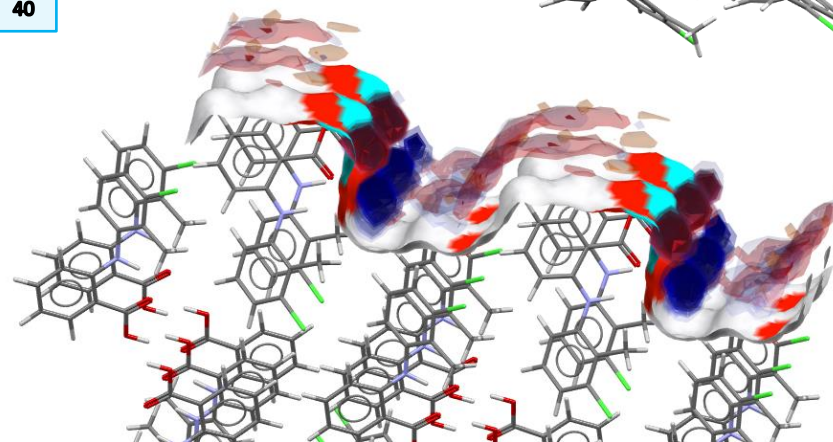
36



38

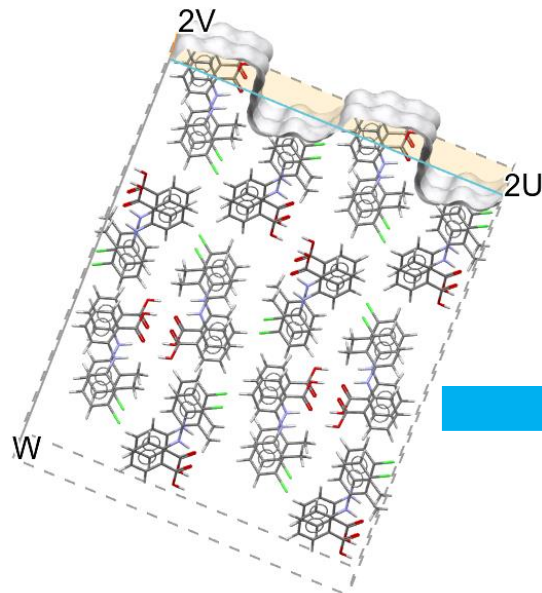


40



## Bonus Exercise

41. Clear the maps and close the **Full Interaction Maps on Surface** window.
42. Bring up again the preview slab, as done in **Step 33**. This time, change the offset to observe how that impact the surface terminations. We set the offset to 4 Å.



42

Surface Analysis... KAXXAI10

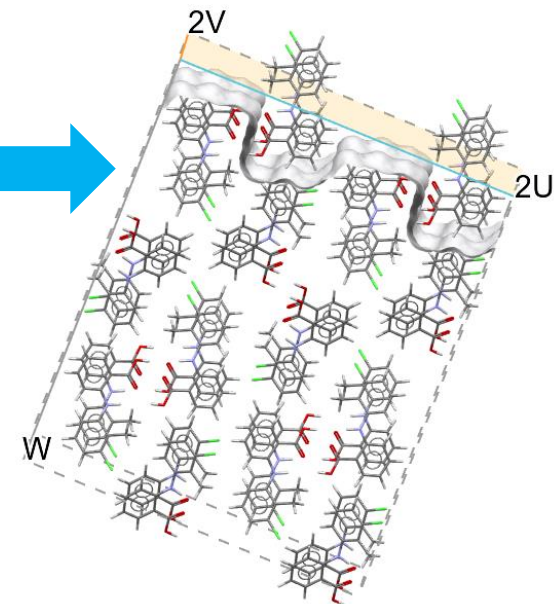
Analyse

Select surface orientation (hkl) and offset (o)

h: 0 k: 2 l: 0 o: 4.00

Preview Slab

Show Advanced Options



43. Click **Calculate Surface** to generate the surface and observe how its properties differ from the one without offset.

41

Full Interaction Maps on Surface

Options Maps Hotspots Log Files

Map Contour Levels

Display first contour with initial level of 2.0

Display second contour with initial level of 4.0

Display third contour with initial level of 6.0

Hotspots

Generate hotspots in the map

Probe

Probe	Colour
<input checked="" type="checkbox"/> Uncharged NH Nitrogen	Blue
<input type="checkbox"/> Charged NH Nitrogen	Light Blue
<input type="checkbox"/> RNH3 Nitrogen	Dark Blue
<input type="checkbox"/> Alcohol Oxygen	Light Green
<input checked="" type="checkbox"/> Carbonyl Oxygen	Red
<input checked="" type="checkbox"/> Water Oxygen	Orange
<input type="checkbox"/> Oxygen Atom	Yellow
<input type="checkbox"/> Methyl Carbon	Light Green
<input checked="" type="checkbox"/> Aromatic CH Carbon	Green
<input type="checkbox"/> C-F Fluorine	Light Green
<input type="checkbox"/> C-Cl Chlorine	Light Green
<input type="checkbox"/> C-Br Bromine	Light Green
<input type="checkbox"/> C-I Iodine	Light Green

Defaults

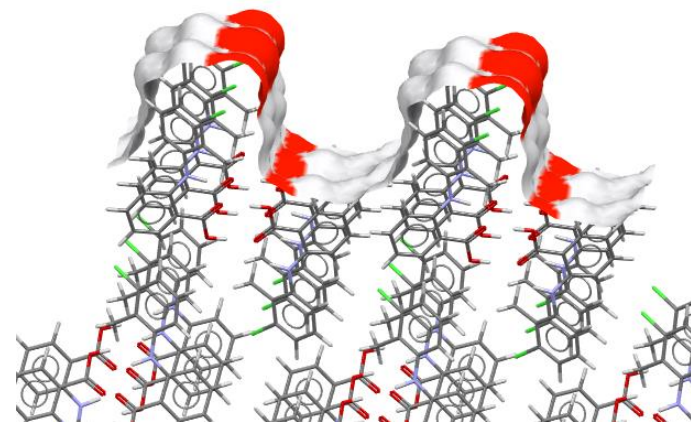
Calculate Surface Maps **Clear Maps & Hotspots** Load Maps... Save Maps... Close

44. Observe the chemistry and the properties: how does changing the terminations impact the properties of the surface? What does it mean?

Results - KAXXA110 (020)[4.00]			
Density Info (count/Å <sup>2</sup> )			
H-Bond Acceptors:	0.037	Aromatic Bonds:	0.129
H-Bond Donors:	0.018	Unsatisfied H-Bond Donors:	0.000
Topology Info			
Surface Area (Å <sup>2</sup> ):	420.815	Projected Area (Å <sup>2</sup> ):	217.504
Rugosity:	1.935	RMSD:	2.702
Skewness:	0.046	Kurtosis:	1.436

### Conclusion

In this example, we saw more in detail how to use tools from *Surface Analysis* from CSD-Particle to analyse two surfaces, namely the (110) and the (020), of a 2-(3-chloro-2-methylanilino)benzoic acid crystal. For each, we learnt how to investigate the chemistry and the topology of the surface and how to visualise such properties in the 3D visualiser in Mercury. We have also generated FIMs on each surface: FIMs allow us to quickly analyse where likely interactions are expected on the surface and which kind of chemistry we could expect. Changing the offset of the calculated surface also allows us to investigate how the activity of a surface would change.





## Conclusions

After this workshop you will be able to:

- Use the Slip Planes tool from CSD-Particle to explore the potential for slip planes, interesting, for example, to investigate elastic vs plastic behaviours.
- Calculate *hkl* surfaces and investigate their chemical and topological properties.
- Display different properties on the generated surface to visualize its potential activity and personalise the surface view to enhance clarity.
- Calculate Full Interaction Maps on such surface to quickly identify likely interactions.
- Visualise hydrogen bonds in Mercury.

## Next steps

If you have completed one of the three exercises proposed and still have time, you can start any of the other two exercises or try these components on one of your own structures. Or ask the tutors for more examples!

## Reading suggestions

You might find the following publications of interest:

- “Particle Informatics”: Advancing Our Understanding of Particle Properties through Digital Design, *Cryst. Growth Des.*, 2019, **19**, 9, 5258–5266 - <https://doi.org/10.1021/acs.cgd.9b00654>
- Elastically flexible molecular crystals, *Chem. Soc. Rev.*, 2021, **50**, 11725-11740 - <https://doi.org/10.1039/D1CS00469G>

## Glossary

### BFDH Morphology

Simulation of morphology using the Bravais Friedal Donnay Harker (BFDH) method. BFDH crystal morphology is an approximation based on crystallographic geometrical considerations. For a given structure, the BFDH algorithm will predict the habit or shape of a crystal using the corresponding unit cell and symmetry operator information.

### Elastic vs Plastic

An elastic material is a material that after compression can return to its initial shape and size once no more force is applied to it.

On the other hand, a plastic material would retain the deformation after the force has been removed.

### Gasteiger Charges

Gasteiger charges refer to partial charges calculated with the Marsili-Gasteiger method.

In Mercury, for atoms in a molecule increasing red colour represents an increasing positive charge and increasing blue colour represents an increasing negative charge. For surfaces instead, colouring by Charge colours the surface with a continuous scale from negative (red) to positive (blue).

### Hotspots

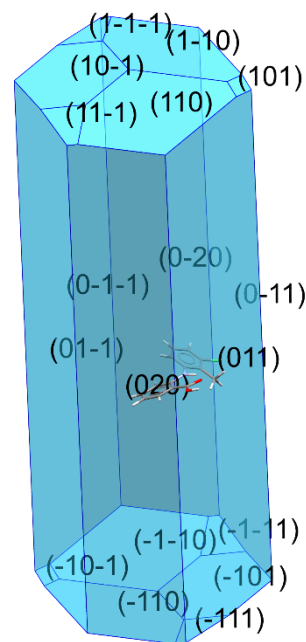
Hotspots represent the positions of the highest local density for each contour.

### Hydrogen Bonds

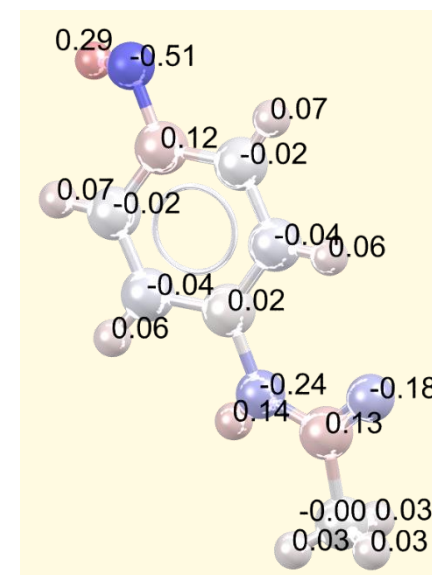
Hydrogen bonding occurs between donor-acceptor interactions precisely involving hydrogen atoms. The H-bonds interactions are classified as: strong (mostly covalent), moderate (mostly electrostatic) and weak (electrostatic). Their strength is observed to be between 12 and 30 kJ/mol.

### Kurtosis

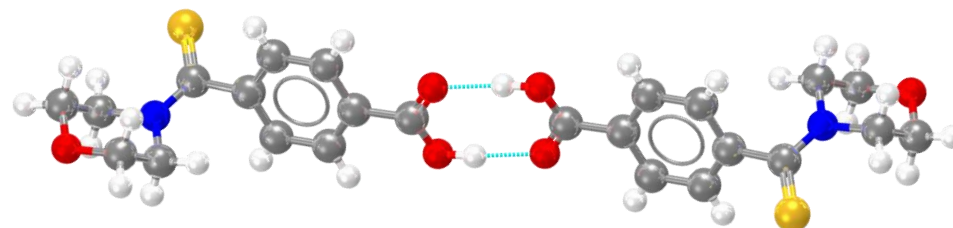
Kurtosis is a statistical characterisation of a dataset, such as surface topology, which measures the sharpness of height distribution and has a value of zero for a normal distribution. Positive values indicate a distribution with a sharp



*Example of BFDH Morphology for CSD Entry KAXXA10.*



*Molecule of paracetamol (CSD Entry HXACAN) with atoms coloured by Gasteiger charge, also expressed in the label.*



*In light blue, example of hydrogen bonds for refcode MULWIC.*

peak and long, “thick” tails. Negative values indicate a rounded peak with short, “thin” tails.

### Minimum Slab Separation

Potential slip planes will only be shown if the slab separation value is greater than the minimum slab separation which is 0 Å. The slab distance is the shortest distance between slabs of molecules on either side of this slip plane (Å).

### Offset

This is the value in Å of the distance to the calculated surface from the parallel Miller plane.

### Perpendicular Planes

The *Perpendicular Planes* column in the Slip Planes table contains a list of any potential slip planes  $>45^\circ$  from the given plane.

### Polymorph

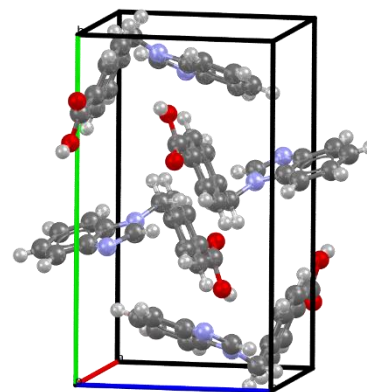
Polymorphism is the occurrence of two or more crystalline forms of the same substance. Where available, polymorph information can be displayed for Cambridge Structural Database (CSD) structures. Structures known to be polymorphic contain comments which include the word polymorph (when reported by the author), e.g., non-triboluminescent polymorph. There is also a CSD subset of polymorphic structures.

### Rugosity

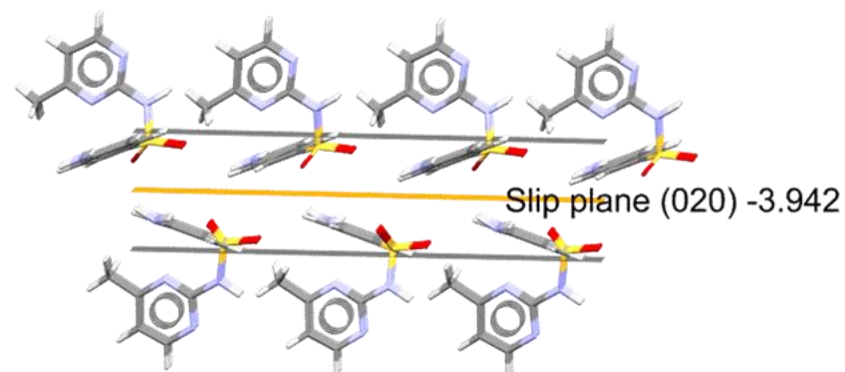
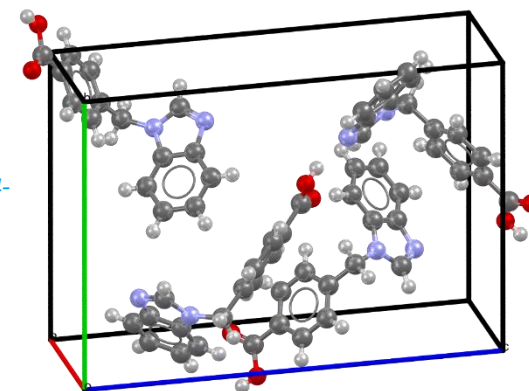
Rugosity is used to describe the roughness of the surfaces and is calculated as the surface area divided by the projected area.

### Skewness

Statistical characterisation of a dataset, such as surface topology. Skewness measures the lack of symmetry, so in the case of surface topology, equal peaks and valleys would have a skewness of 0. If the surface was mostly valleys, then the skewness would be a negative value close to -1 and if the value is higher than 0, then the surface was mostly dominated by peaks.



Example of polymorphic structures of 4-(1H-Benzimidazol-1-ylmethyl)benzoic acid: the monoclinic polymorph (CSD Entry ABADIS) at the top, and the orthorhombic polymorph (CSD Entry ABADIS01) on the right.



Example of potential slip plane in CSD Entry SLFNMA02.

### Slip Planes

Slip planes represent planes in a crystal structure along which a slip can take place.

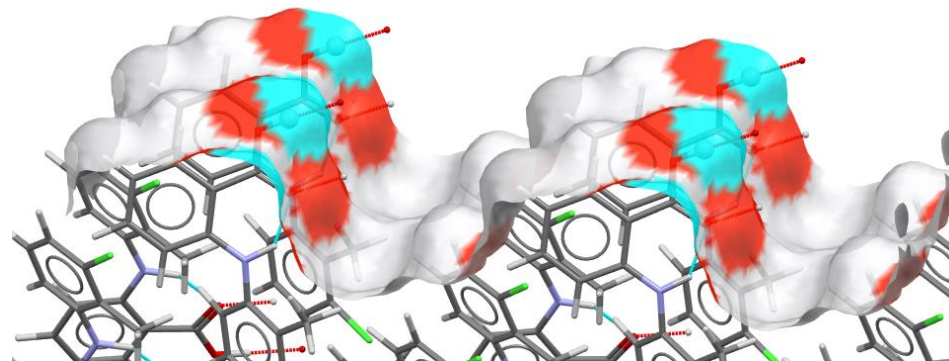
Please note that in CSD-Particle, the Slip Planes functionality identifies potential slip planes in a crystal structure.

### Root Mean Square Deviation (RMSD)

The root mean square deviation (RMSD) is a commonly used measure of the difference between two sets of values (usually comparing observed data to estimated data). The RMSD is defined as the square root of the mean squared error. In Mercury this is used to measure the geometric difference between packing features or packing patterns in crystal structures.

### Unsatisfied Hydrogen Bonds

Unsatisfied hydrogen bond donors are defined as those whose hydrogen atom is surface-terminating and not being used in an existing hydrogen bond. They are reported as unsatisfied hydrogen bond donor density (count/Å<sup>2</sup>).



*Example of unsatisfied H-bond donors on the (020) surface of CSD Entry KAXXAI10.*