If you have created a P1 cif file for a crystal that turns out to have a rather low space group number, the space group number nor the Hermann-Mauguin name contains sufficient information to determine the crystal unambiguously. FINDSYM will write additional information. Unfortunately, cif2cell cannot smoothly read that information. This shows up via this kind of error message:

```
***Warning: Space group operation check failed for Hall symbol Unknown (H-M symbol
P21/m2/m2/a).
Traceback (most recent call last):
   File "/home/max/.local/bin/cif2cell", line 490, in <module>
        cd.primitive()
   File "/home/max/.local/lib/python3.6/site-packages/cif2cell/uctools.py", line
293, in primitive
        self.getCrystalStructure(reducecell=True)
   File "/home/max/.local/lib/python3.6/site-packages/cif2cell/uctools.py", line
432, in getCrystalStructure
   eqsites = SymOpsHall[self.HallSymbol]
```

In order to circumvent that problem, a manual intervention is needed to modify the cif file that results from FINDSYM. Based on an example, this example tells you how.

We start from a P1 cif file for a TiPt-crystal:

```
# generated using pymatgen
data TiPt
_symmetry_space_group_name_H-M 'P 1'
_cell_length_a 4.62768884
_cell_length_b 2.79714039
_cell_length_c 4.88491870
_cell_angle_alpha 90.00000000
_cell_angle_beta 90.0000000
_cell_angle_gamma 90.00000000
_symmetry_Int_Tables_number 1
_chemical_formula_structural TiPt
_chemical_formula_sum 'Ti2 Pt2'
_cell_volume 63.23183050
 cell formula units Z
loop
 symmetry equiv pos site id
  symmetry equiv pos as xyz
1 'x, y, z'
loop
 atom site type symbol
 _atom_site label
 atom site symmetry multiplicity
 atom site fract x
 _atom_site fract y
 atom site fract z
 atom site occupancy
 Ti TiO 1 0.250000 0.500000 0.700620 1
 Ti Ti1 1 0.750000 0.500000 0.299380 1
  Pt Pt2 1 0.250000 0.000000 0.189705 1
  Pt Pt3 1 0.750000 0.000000 0.810295 1
```

If we run this through FINDSYM, this is the result:

```
cell length c 4.8849187000
cell angle alpha 90.0000000000
cell angle beta 90.0000000000
cell angle gamma 90.0000000000
cell volume
              63.2318301747
_symmetry_space_group_name_H-M "P 21/m 2/m 2/a"
_symmetry_Int_Tables_number 51
_space_group.reference_setting '051:-P 2a 2a'
_space_group.transform_Pp_abc a,b,c;0,0,0
loop_
_space_group_symop_id
_space_group_symop_operation xyz
1 x, y, z
2 x+1/2,-y,-z
3 - x, y, -z
4 -x+1/2, -y, z
5 -x,-y,-z
6 -x+1/2, y, z
7 x,-y,z
8 x+1/2, y, -z
loop_
atom site label
_atom_site_type_symbol
atom site symmetry multiplicity
atom site Wyckoff label
_atom_site_fract x
atom site fract y
_atom_site_fract_z
_atom_site_occupancy
_atom_site_fract_symmform
Til Ti 2 f 0.25000 0.50000 0.70062 1.00000 0,0,Dz
Pt1 Pt 2 e 0.25000 0.00000 0.18970 1.00000 0,0,Dz
```

The (correct) information from FINDSYM that cif2cell will not understand, is this block:

```
_symmetry_space_group_name_H-M "P 21/m 2/m 2/a" _symmetry_Int_Tables_number 51 _space_group.reference_setting '051:-P 2a 2a' _space_group.transform_Pp_abc a,b,c;0,0,0
```

Replacing these lines by the following ones, will work for cif2cell:

```
_symmetry_space_group_name_Hall '-p_2a_2a'
_symmetry_Int_Tables_number 51
```

How can we obtain these lines?

- The one with _symmetry_Int_Tables_number can just stay as it is.
- The keyword _symmetry_space_group_name_H-M has to be changed to symmetry space group name Hall.
- Go to http://cci.lbl.gov/sginfo/hall_symbols.html, and scroll down to the bottom where there is a long list of space groups, Hermann-Mauguin symbols and Hall symbols. Search the space group number in the first column (in our example: 51):

```
51 P m m a -P 2a 2a
51:ba-c P m m b -P 2b 2
51:cab P b m m -P 2 2b
```

Read in the cif file from FINDSYM the <code>_space_group.transform_Pp_abc</code> value: it starts with 'a,b,c'. Search that sequence in the lines for space group 51. The regular order 'abc' will not be explicitly mentioned, so "51" is equivalent to "51:abc", and that's the line we need here. Read the Hall symbol in the last column: "-P 2a 2a". This should be the string you read in <code>_space_group.reference_setting</code>, which is indeed the case. Hence, it is this Hall symbol which you have to fill out after <code>_symmetry_space_group_Hall</code>.

With these two new lines replacing the four old ones, cif2cell will correctly read your cif file.