To create an AutoDock configuration file for docking molecules to the CB1 receptor using the provided residues and their coordinates, you can use the following template:

```
# AutoDock Configuration File

[receptor]
receptor_file = cb1_receptor.pdbqt

[ligand]
ligand_file = ligand.pdbqt

[docking]
ligand_atom_types = A C HD N NA OA SA
receptor_atom_types = A C HD N NA OA SA

[bindingsite]
bindingsite_center_x = <center_x>
bindingsite_center_y = <center_y>
bindingsite_center_z = <center_z>
bindingsite_size_x = <size_x>
bindingsite_size_y = <size_y>
bindingsite_size_z = <size_z>

[exhaustiveness]
exhaustiveness = 8
```

Replace `<center_x>`, `<center_y>`, `<center_z>`, `<size_x>`, `<size_y>`, and `<size_z>` with the appropriate values for the binding site coordinates and size.

For example, using the coordinates provided for each residue:

For Residue F200:
- `<center_x>` = 39.115
- `<center_y>` = 35.254
- `<center_z>` = 309.278

For Residue H264:
- `<center_x>` = 35.217
- `<center_y>` = 38.083
- `<center_z>` = 330.111

For Residue W279:
- `<center_x>` = 32.475
- `<center_y>` = 39.468
- `<center_z>` = 315.546

You can also adjust the `exhaustiveness` parameter as needed, which controls the thoroughness of the docking search.

Save the configuration file with the desired name, such as `autodock.conf`, and make sure to replace `cb1_receptor.pdbqt` with the filename of the CB1 receptor's PDBQT file.

With this configuration file, you can run AutoDock using the `autodock.conf` file as a parameter to specify the docking settings and the receptor-ligand files.