

IN YOUR OWN WORDS AND NO MORE THAN THREE LINES: WHAT IS:

1) A Diffraction Pattern

A diffraction pattern is indicative of the way in which light propagates when passed through a narrow aperture. When light is passed through a slit, it comes out the other side in the form of a series of circular waves, which constitutes the diffraction pattern of light of a specific wavelength.

2) An Electron Density Map

An electron density map gives an indication of the location of electrons in the atoms of a molecule. An electron density map is created through X-ray diffraction experiments, and the X-rays are scattered by the electrons in the sample, giving rise to an electron density map.

3) The meaning of Resolution in Crystallography

Resolution of a crystal refers to the smallest distance between two particles that can be observed through experimental results. Low resolution is better as it indicates that particles that are very close to each other can also be observed as separate entities.

4a) Resolution of 1JSF

1.15 Angstrom

4b) Resolution of Your Structure

2.4 Angstrom

4c) Resolution of 1B9O (below)

1.15 Angstrom

5a) Website IMAGE showing the resolution for 1JSF

1JSF X-ray 1.15 A 19-148

1JWR X-ray 1.40 A 19-148

1JSF	X-ray	1.15	A	19-148
1JWR	X-ray	1.40	A	19-148

5b) Website for 5a

UniProt

5c) Website IMAGE showing the resolution for Your Structure

EMBL-EBI Protein Data Bank in Europe
Bringing Structure to Biology

PDBe > 3v6p X-ray diffraction 2.4Å resolution

5d) Website for 5c

Protein Data Bank - EBI

5e) Website IMAGE showing the resolution for 1B90

EBI Search

Search results for 1B90 / Gene & protein summaries for 1B90 / Protein Structure summary for 1B90

Gene & protein summary for 1B90

ORGANISMS: human (*Homo sapiens*)

HUMAN ALPHA-LACTALBUMIN, LOW TEMPERATURE FORM [View in PDBe](#)

Method: X-ray diffraction

Experiment: Resolution: 1.15Å, R-Factor: 11.9%, Free R-Factor: 16.2%

5f) Website for 5e

EBI Search

6) Image showing the alignment of Your Structure TO that of 1JSF

The screenshot displays the PyMOL Molecular Graphics System interface. The main window shows a protein structure rendered in red ribbons, with a green ribbon structure overlaid for alignment. The command window at the top left contains the following text:

```
ObjectMolecule: Read secondary structure assignments.  
ObjectMolecule: Read crystal symmetry information.  
Symmetry: Found 4 symmetry operators.  
CmdLoad: "C:/Users/mariy/Desktop/Transtutors/8_3_19_Bioinformatics 2/pdb1b9o.ent" loaded as "pdb1b9o".  
Match: read scoring matrix.  
Match: assigning 373 x 130 pairwise scores.  
MatchAlign: aligning residues (373 vs 130)...  
ExecutiveAlign: 9 atoms aligned.  
Executive: RMS = 3.358 (9 to 9 atoms)  
Executive: object "aln_pdb3v6p_to_pdb1jsf" created.
```

The PyMOL Viewer window at the bottom right shows the following legend:

all	A	S	H	L	C
pdb1jsf 1/1	A	S	H	L	C
pdb3v6p 1/1	A	S	H	L	C
pdb1b9o 1/1	A	S	H	L	C
aln_pdb3v6p_to_p	A	S	H	L	C

The bottom right corner of the PyMOL Viewer window displays the following mouse control information:

```
Mouse Mode 3-Button Viewing  
Buttons L M R Wheel  
& Keys Rota Move MovZ Slab  
Shft +Box -Box Clip MovS  
Ctrl +/- PKAt PK1 MvSZ  
CtSh Sele Orig Clip MovZ  
SnglClk +/- Cent Menu  
Db1Clk Menu - PKAt  
Selecting Residues  
State 1/ 1
```

7) Image showing the alignment of 1B9O TO that of 1JSF

The PyMOL Molecular Graphics System


File Edit Build Movie Display Setting Scene Mouse Wizard Plugin Help

```

Executive: object "aln_pdb3v6p_to_pdb1jsf" created.
Match: read scoring matrix.
Match: assigning 123 x 130 pairwise scores.
MatchAlign: aligning residues (123 vs 130)...
ExecutiveAlign: 114 atoms aligned.
ExecutiveRMS: 11 atoms rejected during cycle 1 (RMS=1.93).
ExecutiveRMS: 5 atoms rejected during cycle 2 (RMS=1.09).
ExecutiveRMS: 3 atoms rejected during cycle 3 (RMS=0.83).
ExecutiveRMS: 4 atoms rejected during cycle 4 (RMS=0.75).
Executive: RMS = 0.689 (91 to 91 atoms)
Executive: object "aln_pdb1b9o_to_pdb1jsf" created.
PyMOL>

```

PyMOL Viewer
 for Educational Use Only



all	A	S	H	L	C
pdb1jsf 1/1	A	S	H	L	C
pdb3v6p 1/1	A	S	H	L	C
pdb1b9o 1/1	A	S	H	L	C
aln_pdb3v6p_to_p	A	S	H	L	C
aln_pdb1b9o_to_p	A	S	H	L	C

```

Mouse Mode 3-Button Viewing
Buttons L M R Wheel
& Keys Rota Move MovZ Slab
Shft +Box -Box Clip MovS
Ctrl +/- PKAt Pk1 MvSZ
CtSh Sele Orig Clip MovZ
SnglClk +/- Cent Menu
DblClk Menu - PKAt
Selecting Residues
State 1/ 1

```

PyMOL>

8a) rms For Your structure aligned TO 1JSF

3.358

8b) rms For 1B9O aligned TO 1JSF

0.689