



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 6, 2024 – 01:47 AM EDT

PDB ID : 1OVL  
Title : Crystal Structure of Nurr1 LBD  
Authors : Wang, Z.; Liu, J.; Walker, N.  
Deposited on : 2003-03-26  
Resolution : 2.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtrriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

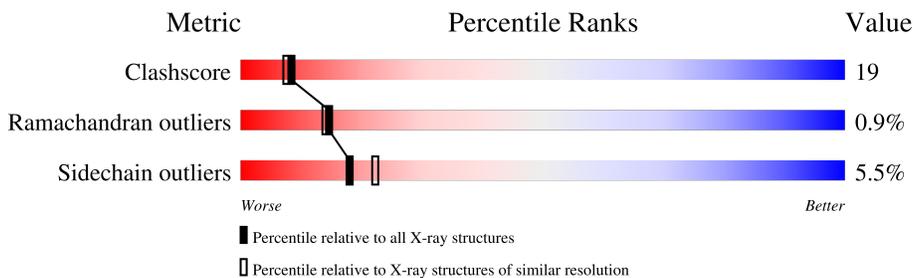
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	180529	6634 (2.20-2.20)
Ramachandran outliers	177936	6560 (2.20-2.20)
Sidechain outliers	177891	6561 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ .

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	271	59% 23% • 16%
1	D	271	52% 30% • 15%
2	B	271	63% 22% • 13%
2	C	271	52% 28% • 17%
2	E	271	58% 30% • 8%
2	F	271	55% 26% • 18%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	BR	E	815	-	-	X	-

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 11703 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Orphan nuclear receptor NURR1 (MSE 414, 496, 511).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	228	1819	1169	310	331	7	2	0	0	0
1	D	230	1834	1178	312	335	7	2	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	496	MSE	MET	modified residue	UNP P43354
A	511	MSE	MET	modified residue	UNP P43354
D	496	MSE	MET	modified residue	UNP P43354
D	511	MSE	MET	modified residue	UNP P43354

- Molecule 2 is a protein called Orphan nuclear receptor NURR1 (MSE 496, 511).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
2	B	236	1881	1206	319	346	7	3	0	0	0
2	C	226	1803	1160	304	330	6	3	0	0	0
2	E	250	1992	1271	346	365	7	3	0	0	0
2	F	223	1784	1149	301	325	6	3	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	414	MSE	MET	modified residue	UNP P43354
B	496	MSE	MET	modified residue	UNP P43354
B	511	MSE	MET	modified residue	UNP P43354
C	414	MSE	MET	modified residue	UNP P43354

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Chain	Residue	Modelled	Actual	Comment	Reference
C	496	MSE	MET	modified residue	UNP P43354
C	511	MSE	MET	modified residue	UNP P43354
E	414	MSE	MET	modified residue	UNP P43354
E	496	MSE	MET	modified residue	UNP P43354
E	511	MSE	MET	modified residue	UNP P43354
F	414	MSE	MET	modified residue	UNP P43354
F	496	MSE	MET	modified residue	UNP P43354
F	511	MSE	MET	modified residue	UNP P43354

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total K 1 1	0	0
3	B	3	Total K 3 3	0	0
3	D	2	Total K 2 2	0	0
3	E	1	Total K 1 1	0	0
3	F	1	Total K 1 1	0	0

- Molecule 4 is BROMIDE ION (three-letter code: BR) (formula: Br).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	4	Total Br 4 4	0	0
4	B	1	Total Br 1 1	0	0
4	C	1	Total Br 1 1	0	0
4	D	4	Total Br 4 4	0	0
4	E	7	Total Br 7 7	0	0
4	F	2	Total Br 2 2	0	0

- Molecule 5 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total I 1 1	0	0

- Molecule 6 is water.

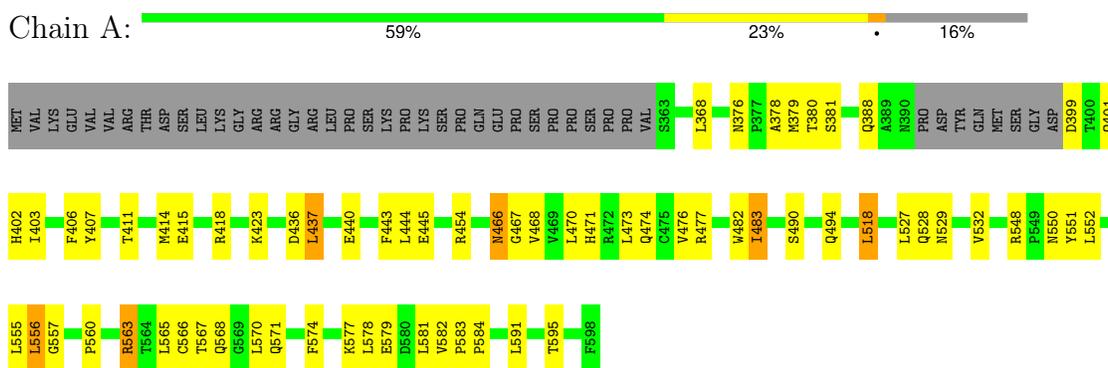
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	88	Total O 88 88	0	0
6	B	100	Total O 100 100	0	0
6	C	68	Total O 68 68	0	0
6	D	107	Total O 107 107	0	0
6	E	114	Total O 114 114	0	0
6	F	85	Total O 85 85	0	0

### 3 Residue-property plots [i](#)

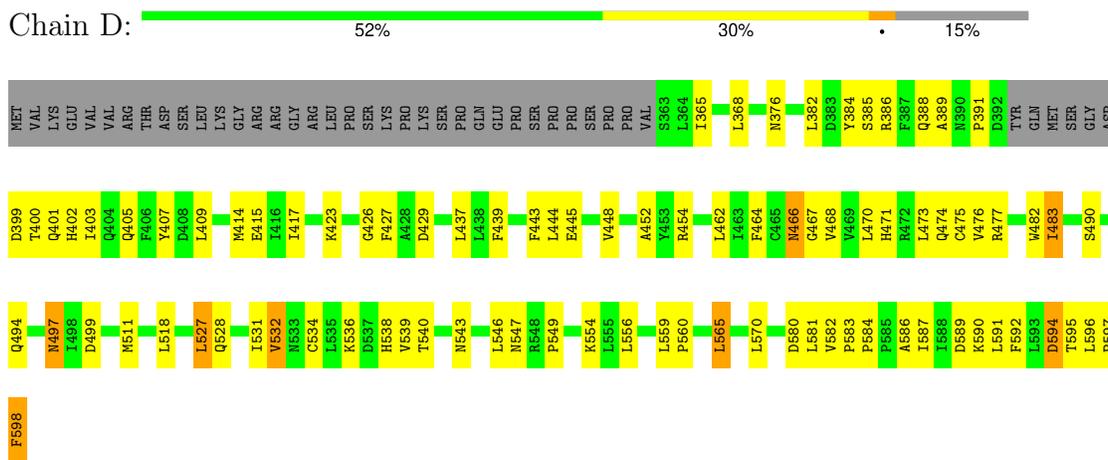
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

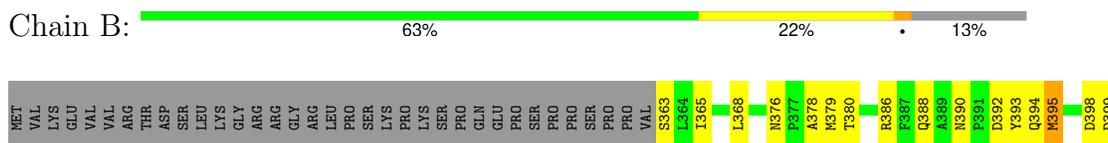
- Molecule 1: Orphan nuclear receptor NURR1 (MSE 414, 496, 511)

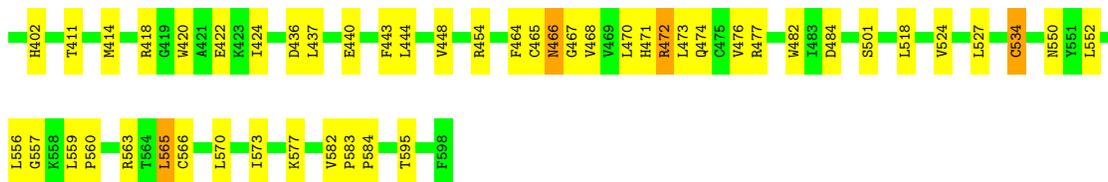


- Molecule 1: Orphan nuclear receptor NURR1 (MSE 414, 496, 511)

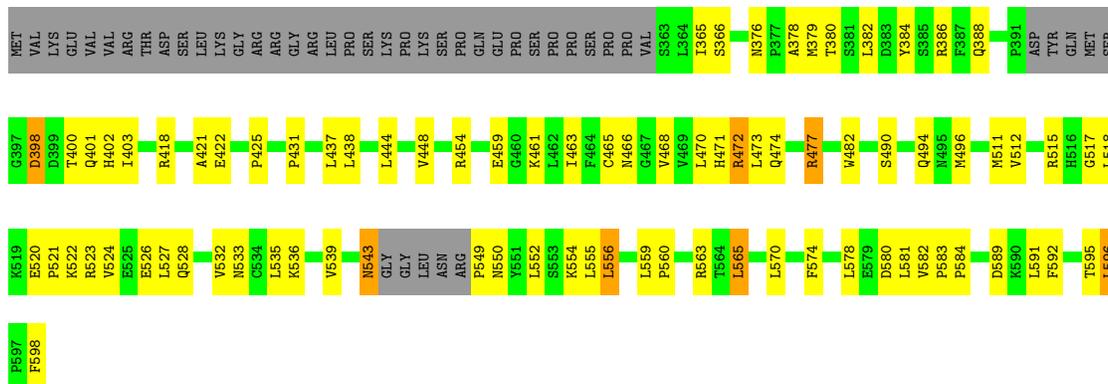


- Molecule 2: Orphan nuclear receptor NURR1 (MSE 496, 511)

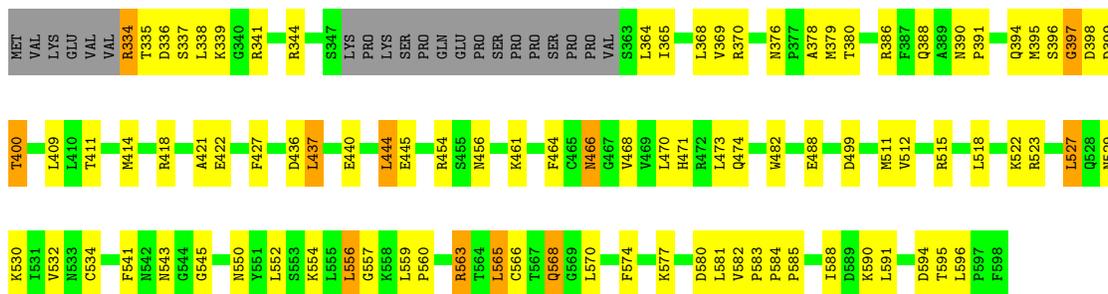




• Molecule 2: Orphan nuclear receptor NURR1 (MSE 496, 511)



• Molecule 2: Orphan nuclear receptor NURR1 (MSE 496, 511)



• Molecule 2: Orphan nuclear receptor NURR1 (MSE 496, 511)



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	80.38Å 80.38Å 227.37Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	500.00 – 2.20	Depositor
% Data completeness (in resolution range)	98.7 (500.00-2.20)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
Refinement program	CNX	Depositor
R, $R_{free}$	0.217 , 0.259	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	11703	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BR, IOD, K

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z  > 5$	RMSZ	# $ Z  > 5$
1	A	0.35	0/1854	0.54	0/2505
1	D	0.34	0/1870	0.56	0/2528
2	B	0.36	0/1918	0.56	0/2592
2	C	0.34	1/1837 (0.1%)	0.53	0/2480
2	E	0.35	0/2029	0.55	0/2737
2	F	0.33	0/1817	0.51	0/2452
All	All	0.35	1/11325 (0.0%)	0.54	0/15294

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	465	CYS	CB-SG	5.29	1.91	1.82

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1819	0	1837	70	0
1	D	1834	0	1848	80	0
2	B	1881	0	1887	57	0
2	C	1803	0	1815	81	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	1992	0	2007	82	0
2	F	1784	0	1801	61	0
3	A	1	0	0	0	0
3	B	3	0	0	0	0
3	D	2	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	A	4	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	4	0	0	1	0
4	E	7	0	0	2	0
4	F	2	0	0	0	0
5	B	1	0	0	1	0
6	A	88	0	0	11	0
6	B	100	0	0	4	0
6	C	68	0	0	2	0
6	D	107	0	0	4	0
6	E	114	0	0	4	0
6	F	85	0	0	5	0
All	All	11703	0	11195	420	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 19.

The worst 5 of 420 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:471:HIS:H	2:F:474:GLN:HE21	0.98	0.95
2:E:365:ILE:HG13	2:E:534:CYS:SG	2.10	0.91
2:B:388:GLN:HE21	2:B:390:ASN:H	1.21	0.89
2:C:472:ARG:HG3	2:C:472:ARG:HH11	1.40	0.87
2:E:563:ARG:HH11	2:E:563:ARG:HB2	1.38	0.87

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	224/271 (83%)	216 (96%)	7 (3%)	1 (0%)	30	34
1	D	226/271 (83%)	215 (95%)	8 (4%)	3 (1%)	10	8
2	B	234/271 (86%)	225 (96%)	5 (2%)	4 (2%)	7	5
2	C	220/271 (81%)	209 (95%)	11 (5%)	0	100	100
2	E	246/271 (91%)	236 (96%)	6 (2%)	4 (2%)	8	6
2	F	217/271 (80%)	209 (96%)	8 (4%)	0	100	100
All	All	1367/1626 (84%)	1310 (96%)	45 (3%)	12 (1%)	14	14

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	379	MET
2	B	465	CYS
2	E	395	MET
2	E	396	SER
2	B	379	MET

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	202/240 (84%)	191 (95%)	11 (5%)	18	23
1	D	204/240 (85%)	192 (94%)	12 (6%)	16	20
2	B	209/239 (87%)	198 (95%)	11 (5%)	19	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	201/239 (84%)	190 (94%)	11 (6%)	18	22
2	E	221/239 (92%)	206 (93%)	15 (7%)	13	15
2	F	199/239 (83%)	191 (96%)	8 (4%)	27	35
All	All	1236/1436 (86%)	1168 (94%)	68 (6%)	18	22

5 of 68 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	568	GLN
2	E	596	LEU
2	F	556	LEU
2	C	466	ASN
2	C	444	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 65 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	376	ASN
2	F	471	HIS
2	C	466	ASN
2	C	402	HIS
2	F	474	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 28 ligands modelled in this entry, 28 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section is therefore empty.

### 6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

### 6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

### 6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.