



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 27, 2025 – 04:05 PM EDT

PDB ID : 9PUK / pdb\_00009puk  
Title : Neutralizing monoclonal antibody Fab fragment for human leptin  
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Deposited on : 2025-07-31  
Resolution : 3.30 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 : 4-5-2 with Phenix2.0  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.46

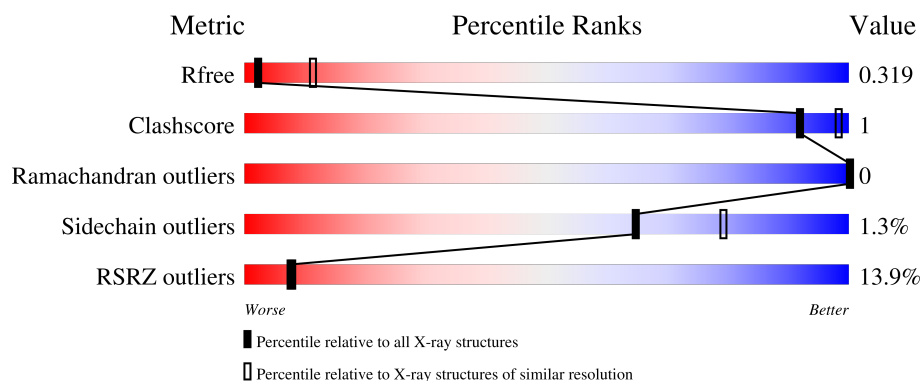
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.30 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))
$R_{free}$	164625	1085 (3.32-3.28)
Clashscore	180529	1128 (3.32-3.28)
Ramachandran outliers	177936	1125 (3.32-3.28)
Sidechain outliers	177891	1124 (3.32-3.28)
RSRZ outliers	164620	1085 (3.32-3.28)

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  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	225	<div> <div>9%</div> <div>85% 7% 8%</div> </div>
1	C	225	<div> <div>18%</div> <div>92% 5% .</div> </div>
2	B	217	<div> <div>15%</div> <div>92% . 5%</div> </div>
2	D	217	<div> <div>10%</div> <div>93% . .</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12336 atoms, of which 6086 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 Neutralizing monoclonal antibody Fab fragment for human leptin, heavy chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	208	Total	C	H	N	O	S	0	0	0
			3042	967	1510	254	303	8			
1	C	217	Total	C	H	N	O	S	0	0	0
			3178	1010	1576	265	319	8			

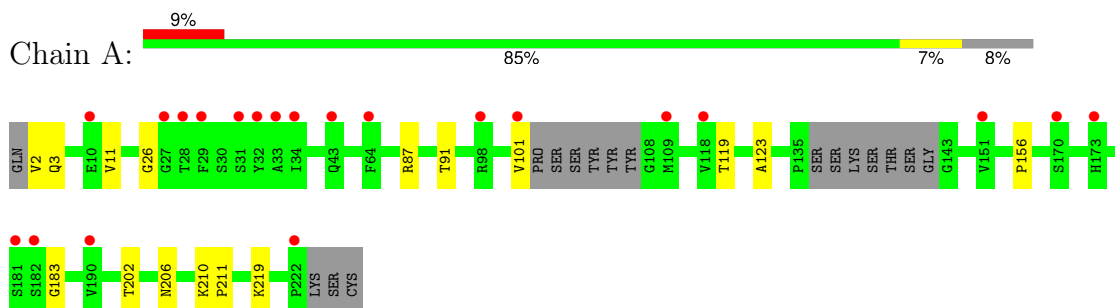
- Molecule 2 is a protein called Neutralizing monoclonal antibody Fab fragment for human leptin, light chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	207	Total	C	H	N	O	S	0	0	0
			3043	973	1493	267	306	4			
2	D	210	Total	C	H	N	O	S	0	0	0
			3073	981	1507	270	311	4			

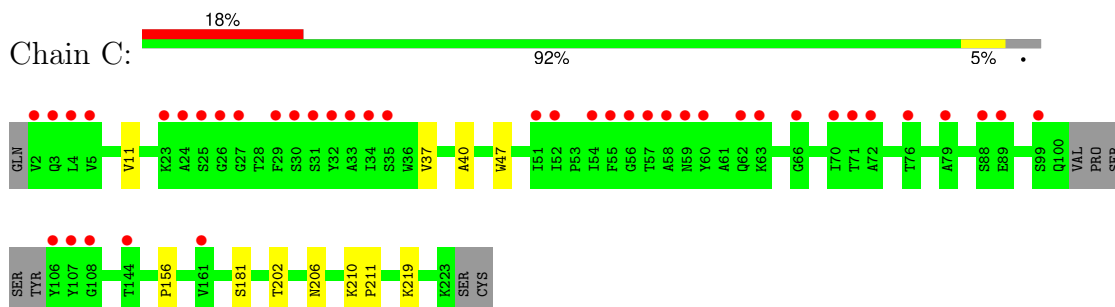
### 3 Residue-property plots [i](#)

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 and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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.

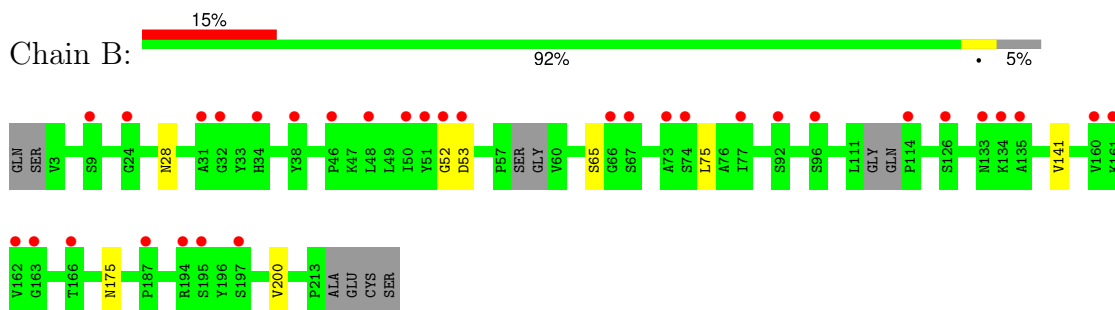
- Molecule 1: Neutralizing monoclonal antibody Fab fragment for human leptin, heavy chain



- Molecule 1: Neutralizing monoclonal antibody Fab fragment for human leptin, heavy chain

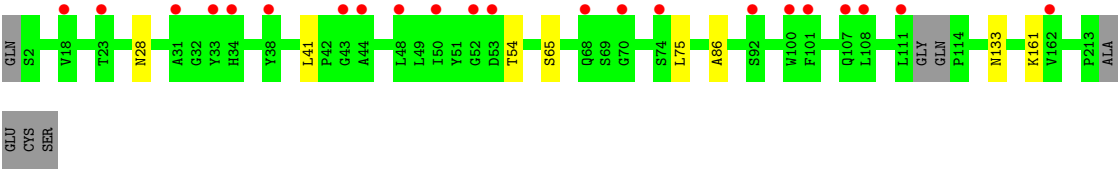


- Molecule 2: Neutralizing monoclonal antibody Fab fragment for human leptin, light chain



- Molecule 2: Neutralizing monoclonal antibody Fab fragment for human leptin, light chain





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.22Å 207.94Å 72.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.33 – 3.30 49.33 – 3.30	Depositor EDS
% Data completeness (in resolution range)	93.9 (49.33-3.30) 93.9 (49.33-3.30)	Depositor EDS
$R_{merge}$	0.16	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.22 (at 3.33Å)	Xtriage
Refinement program	PHENIX 1.21.2_5419	Depositor
R, $R_{free}$	0.267 , 0.320 0.267 , 0.319	Depositor DCC
$R_{free}$ test set	1576 reflections (9.43%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	47.8	Xtriage
Anisotropy	0.074	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 34.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.033 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.82	EDS
Total number of atoms	12336	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.19% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

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

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	0.11	0/1565	0.29	0/2130
1	C	0.10	0/1638	0.29	0/2228
2	B	0.11	0/1590	0.30	0/2168
2	D	0.11	0/1607	0.31	0/2192
All	All	0.11	0/6400	0.30	0/8718

There are no bond length outliers.

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	1532	1510	1510	8	0
1	C	1602	1576	1576	7	0
2	B	1550	1493	1493	3	0
2	D	1566	1507	1507	3	0
All	All	6250	6086	6086	18	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 1.

The worst 5 of 18 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)
1:C:11:VAL:HG22	1:C:156:PRO:HG3	1.82	0.62
1:A:2:VAL:HG22	1:A:26:GLY:O	2.05	0.56
2:B:65:SER:O	2:B:75:LEU:HD12	2.07	0.54
2:D:54:THR:O	2:D:54:THR:HG22	2.08	0.54
1:A:202:THR:HG23	1:A:219:LYS:HE3	1.91	0.53

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	202/225 (90%)	193 (96%)	9 (4%)	0	100	100
1	C	213/225 (95%)	205 (96%)	8 (4%)	0	100	100
2	B	201/217 (93%)	189 (94%)	12 (6%)	0	100	100
2	D	206/217 (95%)	195 (95%)	11 (5%)	0	100	100
All	All	822/884 (93%)	782 (95%)	40 (5%)	0	100	100

There are no Ramachandran outliers to report.

### 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	172/188 (92%)	169 (98%)	3 (2%)	56	74
1	C	180/188 (96%)	179 (99%)	1 (1%)	84	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	169/176 (96%)	167 (99%)	2 (1%)	67	80
2	D	171/176 (97%)	168 (98%)	3 (2%)	54	74
All	All	692/728 (95%)	683 (99%)	9 (1%)	65	79

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	133	ASN
2	D	161	LYS
2	B	28	ASN
2	B	175	ASN
1	C	206	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	208	ASN
1	C	59	ASN
1	C	65	GLN
2	D	36	HIS
2	D	55	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 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](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å <sup>2</sup> )	Q<0.9
1	A	208/225 (92%)	0.88	21 (10%)	14 13	29, 61, 96, 129	0
1	C	217/225 (96%)	1.08	41 (18%)	4 3	14, 66, 149, 173	0
2	B	207/217 (95%)	1.24	33 (15%)	6 5	26, 74, 112, 155	0
2	D	210/217 (96%)	0.74	22 (10%)	13 13	11, 63, 99, 121	0
All	All	842/884 (95%)	0.98	117 (13%)	7 8	11, 66, 117, 173	0

The worst 5 of 117 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	32	GLY	6.6
2	B	162	VAL	6.1
1	C	55	PHE	6.1
1	C	52	ILE	5.8
2	B	34	HIS	5.5

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

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

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.