



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 2, 2021 – 08:54 PM EDT

PDB ID : 2ZGQ  
Title : Crystal structure of AAL mutant L33A in P1 spacegroup  
Authors : Li, D.F.; Yang, N.; Wang, D.C.  
Deposited on : 2008-01-23  
Resolution : 1.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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.

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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  
Xtriage (Phenix) : 1.13  
EDS : 2.23.2  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.23.2

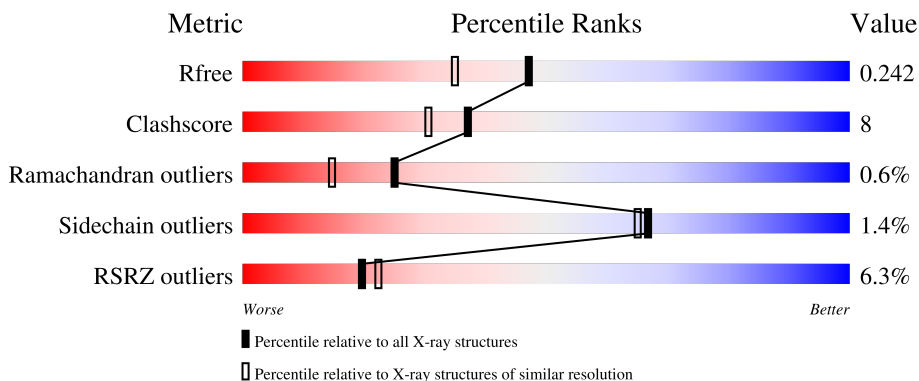
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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))
$R_{free}$	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	167	<div> <div>10%</div> <div>86%</div> <div>13%</div> <div>.</div> </div>
1	B	167	<div> <div>3%</div> <div>78%</div> <div>20%</div> <div>..</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2815 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 Anti-tumor lectin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	167	Total	C	N	O	S	0	0	0
			1281	807	219	253	2			
1	B	166	Total	C	N	O	S	0	0	0
			1270	801	216	251	2			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP Q6WY08
A	33	ALA	LEU	engineered mutation	UNP Q6WY08
A	132	SER	LEU	SEE REMARK 999	UNP Q6WY08
A	159	LEU	-	expression tag	UNP Q6WY08
A	160	GLU	-	expression tag	UNP Q6WY08
A	161	HIS	-	expression tag	UNP Q6WY08
A	162	HIS	-	expression tag	UNP Q6WY08
A	163	HIS	-	expression tag	UNP Q6WY08
A	164	HIS	-	expression tag	UNP Q6WY08
A	165	HIS	-	expression tag	UNP Q6WY08
A	166	HIS	-	expression tag	UNP Q6WY08
B	0	MET	-	initiating methionine	UNP Q6WY08
B	33	ALA	LEU	engineered mutation	UNP Q6WY08
B	132	SER	LEU	SEE REMARK 999	UNP Q6WY08
B	159	LEU	-	expression tag	UNP Q6WY08
B	160	GLU	-	expression tag	UNP Q6WY08
B	161	HIS	-	expression tag	UNP Q6WY08
B	162	HIS	-	expression tag	UNP Q6WY08
B	163	HIS	-	expression tag	UNP Q6WY08
B	164	HIS	-	expression tag	UNP Q6WY08
B	165	HIS	-	expression tag	UNP Q6WY08
B	166	HIS	-	expression tag	UNP Q6WY08

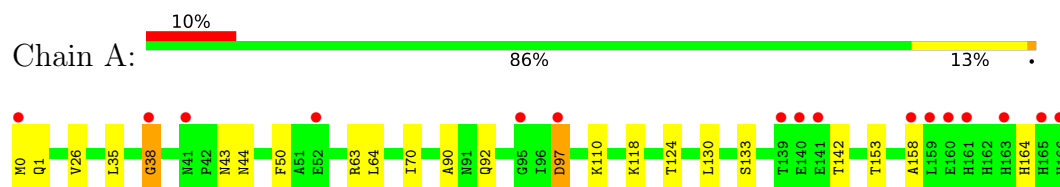
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	132	Total 132	O 132	0	0
2	B	132	Total 132	O 132	0	0

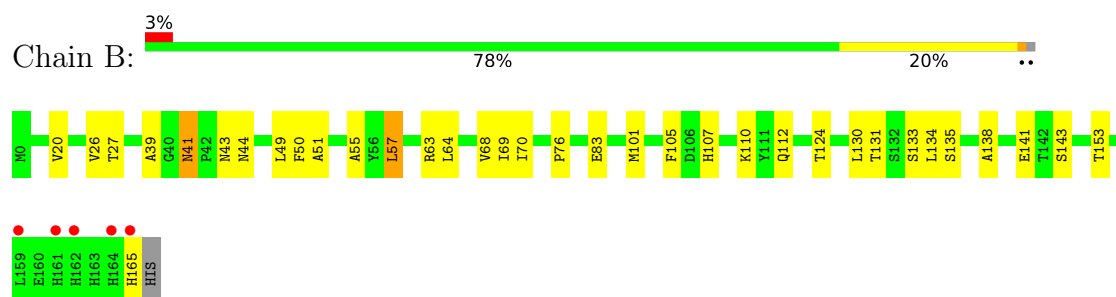
### 3 Residue-property plots [i](#)

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 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: Anti-tumor lectin



#### • Molecule 1: Anti-tumor lectin



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	41.35Å 43.43Å 56.42Å 69.83° 82.44° 61.80°	Depositor
Resolution (Å)	20.37 – 1.90 20.36 – 1.90	Depositor EDS
% Data completeness (in resolution range)	90.1 (20.37-1.90) 90.3 (20.36-1.90)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	0.04	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	8.76 (at 1.90Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.210 , 0.242 0.211 , 0.242	Depositor DCC
$R_{free}$ test set	2279 reflections (9.88%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	14.9	Xtriage
Anisotropy	0.788	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 38.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	2815	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.07% 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

### 5.1 Standard geometry

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	0/1308	0.67	0/1784
1	B	0.35	0/1296	0.65	0/1769
All	All	0.35	0/2604	0.66	0/3553

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

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	1281	0	1233	15	0
1	B	1270	0	1226	26	0
2	A	132	0	0	1	0
2	B	132	0	0	2	0
All	All	2815	0	2459	39	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 8.

All (39) 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:B:43:ASN:ND2	1:B:63:ARG:HE	1.75	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:27:THR:HG21	1:B:101:MET:HE3	1.66	0.78
1:A:43:ASN:ND2	1:A:63:ARG:HE	1.84	0.74
1:B:44:ASN:ND2	1:B:64:LEU:H	1.87	0.71
1:A:43:ASN:HD21	1:A:63:ARG:HE	1.38	0.70
1:B:64:LEU:HB2	2:B:359:HOH:O	1.91	0.70
1:A:0:MET:HG2	1:A:1:GLN:N	2.09	0.67
1:A:44:ASN:ND2	1:A:64:LEU:H	1.95	0.63
1:B:39:ALA:HA	2:B:359:HOH:O	1.99	0.62
1:A:0:MET:HG2	1:A:1:GLN:H	1.66	0.61
1:A:38:GLY:HA3	1:A:142:THR:HG22	1.83	0.59
1:B:51:ALA:HB2	1:B:57:LEU:HD11	1.87	0.57
1:B:51:ALA:HB2	1:B:57:LEU:CD1	2.37	0.55
1:B:50:PHE:HE1	1:B:135:SER:HG	1.55	0.54
1:B:43:ASN:HD22	1:B:63:ARG:HE	1.54	0.54
1:B:27:THR:HG21	1:B:101:MET:CE	2.38	0.50
1:B:130:LEU:HD12	1:B:130:LEU:N	2.27	0.50
1:B:110:LYS:HG2	1:B:124:THR:HA	1.93	0.49
1:B:70:ILE:HG23	1:B:83:GLU:HG3	1.93	0.49
1:A:26:VAL:HG23	1:A:153:THR:HG22	1.95	0.49
1:B:55:ALA:HA	1:B:76:PRO:HD3	1.96	0.48
1:B:43:ASN:HD21	1:B:63:ARG:HE	1.56	0.47
1:B:49:LEU:HD22	1:B:134:LEU:HD22	1.96	0.47
1:B:50:PHE:HB2	1:B:133:SER:OG	2.15	0.47
1:A:97:ASP:HB3	2:A:232:HOH:O	2.15	0.46
1:B:105:PHE:HB2	1:B:112:GLN:HB3	1.97	0.46
1:B:138:ALA:HB1	1:B:143:SER:HB2	1.98	0.45
1:B:68:VAL:HG22	1:B:69:ILE:N	2.31	0.44
1:A:164:HIS:ND1	1:B:165:HIS:HE1	2.16	0.43
1:A:35:LEU:HD13	1:A:90:ALA:HA	2.01	0.42
1:B:26:VAL:HG23	1:B:153:THR:HG22	2.00	0.42
1:A:50:PHE:HB2	1:A:133:SER:OG	2.20	0.42
1:A:1:GLN:HG2	1:B:107:HIS:HE1	1.83	0.42
1:A:63:ARG:CZ	1:A:70:ILE:HD12	2.49	0.42
1:A:92:GLN:HA	1:A:118:LYS:CE	2.51	0.41
1:B:20:VAL:HB	1:B:131:THR:HB	2.01	0.41
1:A:110:LYS:HG2	1:A:124:THR:HA	2.03	0.41
1:B:41:ASN:H	1:B:41:ASN:HD22	1.69	0.41
1:B:141:GLU:H	1:B:141:GLU:CD	2.25	0.40

There are no symmetry-related clashes.



## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	165/167 (99%)	156 (94%)	7 (4%)	2 (1%)	13	4
1	B	164/167 (98%)	155 (94%)	9 (6%)	0	100	100
All	All	329/334 (98%)	311 (94%)	16 (5%)	2 (1%)	25	15

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	158	ALA
1	A	38	GLY

### 5.3.2 Protein sidechains

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	139/139 (100%)	137 (99%)	2 (1%)	67	65
1	B	138/139 (99%)	136 (99%)	2 (1%)	67	65
All	All	277/278 (100%)	273 (99%)	4 (1%)	67	65

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	97	ASP
1	A	130	LEU
1	B	41	ASN
1	B	57	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	ASN
1	A	44	ASN
1	A	92	GLN
1	A	165	HIS
1	B	4	ASN
1	B	41	ASN
1	B	43	ASN
1	B	44	ASN
1	B	92	GLN
1	B	165	HIS

### 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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

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	167/167 (100%)	0.35	16 (9%) <b>8</b> <b>9</b>	8, 15, 36, 60	0
1	B	166/167 (99%)	0.18	5 (3%) 50 53	9, 16, 33, 59	0
All	All	333/334 (99%)	0.27	21 (6%) <b>20</b> <b>22</b>	8, 16, 34, 60	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	166	HIS	5.0
1	A	163	HIS	4.1
1	A	140	GLU	3.8
1	B	165	HIS	3.7
1	A	161	HIS	3.7
1	A	41	ASN	3.5
1	B	162	HIS	3.5
1	A	0	MET	3.5
1	A	159	LEU	3.4
1	A	141	GLU	2.9
1	B	161	HIS	2.7
1	A	97	ASP	2.5
1	B	159	LEU	2.4
1	A	38	GLY	2.3
1	A	52	GLU	2.3
1	A	165	HIS	2.3
1	A	95	GLY	2.2
1	A	160	GLU	2.2
1	A	158	ALA	2.1
1	A	139	THR	2.1
1	B	164	HIS	2.0

## 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 monosaccharides 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.