

# Full wwPDB X-ray Structure Validation Report (i)

### Feb 3, 2024 – 03:37 PM EST

PDB ID : 1L61

Title: ANALYSIS OF THE INTERACTION BETWEEN CHARGED SIDE

CHAINS AND THE ALPHA-HELIX DIPOLE USING DESIGNED THER-

MOSTABLE MUTANTS OF PHAGE T4 LYSOZYME

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Deposited on : 1991-05-06

Resolution : 1.80 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
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

 $Mol Probity \quad : \quad 4.02b\text{--}467$ 

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.36

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

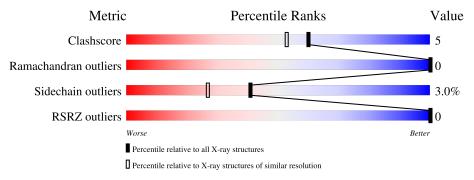
Validation Pipeline (wwPDB-VP) : 2.36

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	Similar resolution		
Wietric	$(\# {\rm Entries})$	$(\# \text{Entries, resolution range}(\text{\AA}))$		
Clashscore	141614	6793 (1.80-1.80)		
Ramachandran outliers	138981	6697 (1.80-1.80)		
Sidechain outliers	138945	6696 (1.80-1.80)		
RSRZ outliers	127900	5850 (1.80-1.80)		

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 >=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 <=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	164	79%	18%	••



# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 1448 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 LYSOZYME.

$\mathbf{Mol}$	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	162	Total 1294	C 815	N 236	O 238	S 5	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

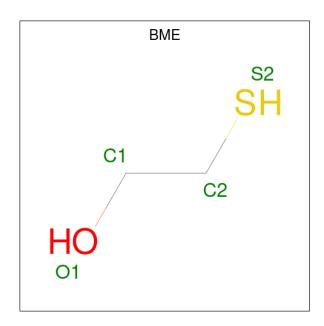
Chain	Residue	Modelled	Actual	Comment	Reference
A	38	ASN	SER	conflict	UNP P00720
A	54	THR	CYS	conflict	UNP P00720
A	97	ALA	CYS	conflict	UNP P00720

• Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Cl 2 2	0	0

 $\bullet$  Molecule 3 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula:  $\mathrm{C_2H_6OS}).$ 





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 4	C 2	O 1	S 1	0	0

• Molecule 4 is water.

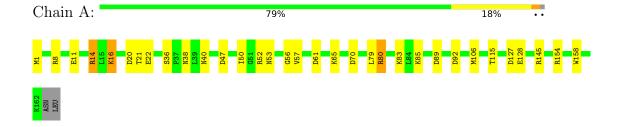
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	148	Total O 148 148	0	0



# 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: LYSOZYME





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants	61.00Å 61.00Å 97.10Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor
Resolution (Å)	6.00 - 1.80	Depositor
Resolution (A)	19.56 - 1.80	EDS
% Data completeness	(Not available) (6.00-1.80)	Depositor
(in resolution range)	71.3 (19.56-1.80)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	5.57 (at 1.80Å)	Xtriage
Refinement program	TNT	Depositor
Ρ. Р.	0.158 , (Not available)	Depositor
$R, R_{free}$	0.157 , (Not available)	DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.8	Xtriage
Anisotropy	0.209	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.38, 93.9	EDS
L-test for twinning <sup>2</sup>	$< L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	0.038 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	1448	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.52% of the height of the origin peak. No significant pseudotranslation is detected.

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



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 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: CL, BME

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	Boı	nd lengths	Во	ond angles
IVIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	A	0.99	2/1314 (0.2%)	1.39	19/1770 (1.1%)

#### All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}( ext{\AA})$
1	A	11	GLU	CD-OE1	-5.69	1.19	1.25
1	A	22	GLU	CD-OE2	5.14	1.31	1.25

#### All (19) bond angle outliers are listed below:

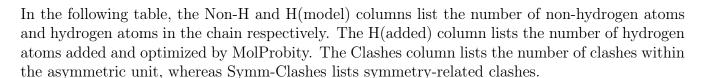
Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$\operatorname{Ideal}({}^{o})$
1	A	80	ARG	NE-CZ-NH1	10.95	125.78	120.30
1	A	80	ARG	NE-CZ-NH2	-9.51	115.55	120.30
1	A	47	ASP	CB-CG-OD2	-9.18	110.03	118.30
1	A	47	ASP	CB-CG-OD1	8.25	125.72	118.30
1	A	127	ASP	CB-CG-OD1	7.88	125.39	118.30
1	A	127	ASP	CB-CG-OD2	-7.71	111.36	118.30
1	A	70	ASP	CB-CG-OD1	6.84	124.46	118.30
1	A	14	ARG	NE-CZ-NH1	6.60	123.60	120.30
1	A	61	ASP	CB-CG-OD2	-6.38	112.56	118.30
1	A	106	MET	CA-CB-CG	6.38	124.14	113.30
1	A	8	ARG	NE-CZ-NH1	5.96	123.28	120.30
1	A	92	ASP	CB-CG-OD2	-5.89	113.00	118.30
1	A	20	ASP	CB-CG-OD1	5.73	123.46	118.30
1	A	70	ASP	CB-CG-OD2	-5.73	113.14	118.30
1	A	115	THR	CA-CB-CG2	-5.61	104.55	112.40
1	A	145	ARG	CD-NE-CZ	-5.35	116.12	123.60
1	A	89	ASP	CB-CG-OD1	5.26	123.03	118.30
1	A	14	ARG	NE-CZ-NH2	-5.15	117.73	120.30
1	A	89	ASP	CB-CG-OD2	-5.10	113.71	118.30



There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts (i)



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1294	0	1320	12	0
2	A	2	0	0	0	0
3	A	4	0	6	0	0
4	A	148	0	0	6	0
All	All	1448	0	1326	12	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 5.

All (12) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{aligned} &  ext{Interatomic} \ &  ext{distance} \ &  ext{(Å)} \end{aligned}$	Clash overlap (Å)
1:A:65:LYS:HG3	4:A:320:HOH:O	1.84	0.78
1:A:128:GLU:HG3	4:A:311:HOH:O	2.04	0.58
1:A:21:THR:HG23	4:A:509:HOH:O	2.04	0.57
1:A:16:LYS:HE3	1:A:57:VAL:HG23	1.92	0.52
1:A:79:LEU:O	1:A:85:LYS:HD2	2.11	0.51
1:A:14:ARG:HG3	4:A:298:HOH:O	2.12	0.49
1:A:16:LYS:HE2	1:A:56:GLY:O	2.14	0.48
1:A:38:ASN:OD1	1:A:40:ASN:HB2	2.13	0.47
1:A:1:MET:HG2	1:A:158:TRP:CE3	2.50	0.47
1:A:80:ARG:NH2	4:A:242:HOH:O	2.49	0.43
1:A:50:ILE:HG22	1:A:52:ARG:HG2	1.99	0.43
1:A:83:LYS:HG2	4:A:276:HOH:O	2.21	0.41

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.

Mo	l Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	160/164 (98%)	158 (99%)	2 (1%)	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	135/137 (98%)	131 (97%)	4 (3%)	41 27	

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

Mol	Chain	Res	Type
1	A	16	LYS
1	A	36	SER
1	A	53	ASN
1	A	154	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

#### 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)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type Chain		Chain Pos	Res Link		Bond lengths			Bond angles		
MIOI	Туре	Chain	Res Lill	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2	
3	BME	A	900	3	3,3,3	0.38	0	1,2,2	0.35	0	

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	BME	A	900	3	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	900	BME	O1-C1-C2-S2

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)

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,  $95^{th}$  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>	RSRZ> $#RSRZ>2$		Q<0.9
1	A	162/164 (98%)	-0.72	0 100 100	13, 22, 50, 66	0

There are no RSRZ outliers to report.

### 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)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median,  $95^{th}$  percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
3	BME	A	900	4/4	0.95	0.07	20,44,52,56	0
2	CL	A	178	1/1	0.98	0.13	30,30,30,30	1
2	CL	A	173	1/1	0.98	0.03	28,28,28,28	0

## 6.5 Other polymers (i)

There are no such residues in this entry.

