

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

#### Jan 27, 2024 – 04:22 PM EST

PDB ID : 188L

Title : SPECIFICITY OF LIGAND BINDING IN A BURIED NON-POLAR CAV-

ITY OF T4 LYSOZYME: LINKAGE OF DYNAMICS AND STRUCTURAL

PLASTICITY

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Deposited on : 1995-04-19

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)

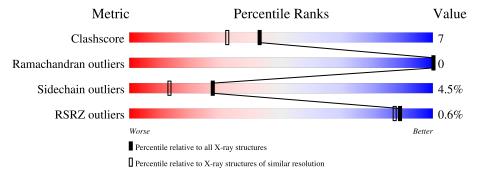
Validation Pipeline (wwPDB-VP) : 2.36

## 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 $(\# \text{Entries})$	Similar resolution $(\#\text{Entries, resolution range}(\mathring{A}))$
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	75%	22%	••			



# 2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 1438 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 T4 LYSOZYME.

$\mathbf{Mol}$	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	162	Total 1289	C 811	N 235	O 238	S 5	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

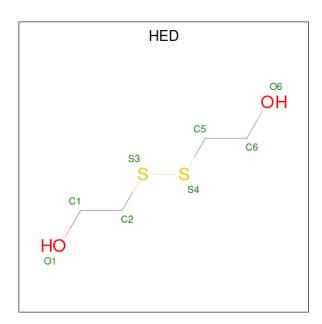
Chain	Residue	Modelled	Actual	Comment	Reference
A	54	THR	CYS	conflict	UNP P00720
A	97	ALA	CYS	conflict	UNP P00720
A	99	ALA	LEU	conflict	UNP P00720

• 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

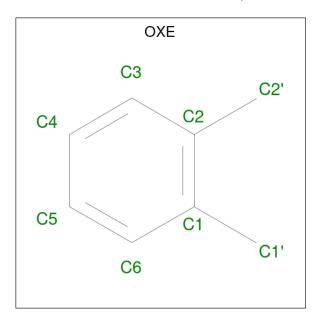
 $\bullet \ \ Molecule\ 3\ is\ 2-HYDROXYETHYL\ DISULFIDE\ (three-letter\ code:\ HED)\ (formula:\ C_4H_{10}O_2S_2).$ 





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 8	C 4	O 2	S 2	0	0

 $\bullet$  Molecule 4 is ORTHO-XYLENE (three-letter code: OXE) (formula:  $\mathrm{C_8H_{10}}).$ 



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C 8 8	0	0

• Molecule 5 is water.

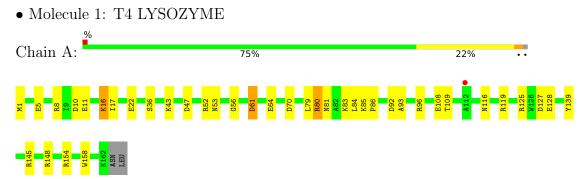


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	131	Total O 131 131	0	0



# 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.





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants	60.80Å 60.80Å 96.70Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $120.00^{\circ}$	Depositor
Resolution (Å)	20.00 - 1.80	Depositor
Resolution (A)	23.12 - 1.79	EDS
% Data completeness	(Not available) (20.00-1.80)	Depositor
(in resolution range)	69.6 (23.12-1.79)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.05 (at 1.79Å)	Xtriage
Refinement program	TNT	Depositor
Ρ. Р.	0.156 , (Not available)	Depositor
$R, R_{free}$	0.146 , (Not available)	DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	15.7	Xtriage
Anisotropy	0.249	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.33, 96.0	EDS
L-test for twinning <sup>2</sup>	$< L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	0.050 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	1438	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.95% 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: HED, OXE, CL

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
MIOI	Chain	RMSZ	# Z  > 5	RMSZ	# Z  > 5
1	A	1.04	6/1309~(0.5%)	1.36	15/1763~(0.9%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	$\operatorname{Ideal}(\text{\AA})$
1	A	22	GLU	CD-OE1	6.78	1.33	1.25
1	A	64	GLU	CD-OE2	6.46	1.32	1.25
1	A	5	GLU	CD-OE2	6.38	1.32	1.25
1	A	108	GLU	CD-OE2	6.38	1.32	1.25
1	A	128	GLU	CD-OE2	5.98	1.32	1.25
1	A	11	GLU	CD-OE1	5.01	1.31	1.25

All (15) bond angle outliers are listed below:

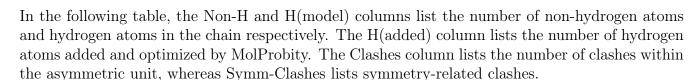
Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	47	ASP	CB-CG-OD2	-9.81	109.47	118.30
1	A	47	ASP	CB-CG-OD1	9.26	126.64	118.30
1	A	92	ASP	CB-CG-OD1	-7.53	111.53	118.30
1	A	80	ARG	NE-CZ-NH1	7.30	123.95	120.30
1	A	70	ASP	CB-CG-OD2	-7.25	111.78	118.30
1	A	154	ARG	NE-CZ-NH1	6.66	123.63	120.30
1	A	70	ASP	CB-CG-OD1	6.62	124.25	118.30
1	A	96	ARG	NE-CZ-NH1	-6.61	116.99	120.30
1	A	10	ASP	CB-CG-OD2	-6.38	112.56	118.30
1	A	61	ASP	CB-CG-OD2	6.08	123.77	118.30
1	A	125	ARG	NE-CZ-NH1	5.96	123.28	120.30
1	A	139	TYR	CB-CG-CD1	-5.85	117.49	121.00
1	A	127	ASP	CB-CG-OD2	-5.66	113.21	118.30
1	A	148	ARG	NE-CZ-NH1	5.32	122.96	120.30
1	A	128	GLU	CG-CD-OE2	-5.10	108.11	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	1289	0	1313	18	0
2	A	2	0	0	0	0
3	A	8	0	10	1	1
4	A	8	0	10	0	0
5	A	131	0	0	2	0
All	All	1438	0	1333	18	1

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 7.

All (18) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:A:8:ARG:HH11	1:A:8:ARG:HG3	1.52	0.75
1:A:16:LYS:HE3	1:A:56:GLY:O	1.90	0.71
1:A:80:ARG:NH2	5:A:242:HOH:O	2.30	0.63
1:A:93:ALA:HB1	3:A:170:HED:H61	1.85	0.59
1:A:43:LYS:HB3	5:A:176:HOH:O	2.06	0.55
1:A:8:ARG:HG3	1:A:8:ARG:NH1	2.19	0.55
1:A:1:MET:HG2	1:A:158:TRP:CE3	2.44	0.53
1:A:16:LYS:HE3	1:A:17:ILE:H	1.74	0.53
1:A:8:ARG:HG3	1:A:8:ARG:O	2.09	0.52
1:A:1:MET:HG2	1:A:158:TRP:CD2	2.50	0.46
1:A:85:LYS:N	1:A:86:PRO:CD	2.79	0.45
1:A:79:LEU:O	1:A:85:LYS:HD2	2.17	0.45
1:A:8:ARG:NH1	1:A:8:ARG:CG	2.81	0.43
1:A:85:LYS:HB3	1:A:86:PRO:HD3	2.01	0.43
1:A:81:ASN:HB3	1:A:84:LEU:HB2	1.99	0.42
1:A:116:ASN:HA	1:A:119:ARG:NH1	2.35	0.41
1:A:52:ARG:HH11	1:A:52:ARG:HG3	1.86	0.41
1:A:145:ARG:HH11	1:A:145:ARG:HD2	1.59	0.41



All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$egin{aligned}  ext{Clash} \  ext{overlap } ( ext{Å}) \end{aligned}$	
3:A:170:HED:O1	3:A:170:HED:O1[5_555]	1.86	0.34	

#### 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	Perce	$\mathbf{ntiles}$
1	A	160/164 (98%)	157 (98%)	3 (2%)	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 side chain 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	134/136 (98%)	128 (96%)	6 (4%)	27 13		

All (6) 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	61	ASP
1	A	83	LYS
1	A	109	THR



Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	53	ASN
1	A	69	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 monosaccharides in this entry.

### 5.6 Ligand geometry (i)

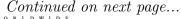
Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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	Res	Link	$\mathbf{B}$	ond leng	${ m gths}$	Bond angles		
L	IVIOI	туре	Chain	nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
	3	$_{ m HED}$	A	170	-	7,7,7	0.56	0	6,6,6	1.02	0
	4	OXE	A	400	-	8,8,8	1.02	1 (12%)	10,10,10	0.80	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.

$\mathbf{Mol}$	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	HED	A	170	-	-	1/5/5/5	-





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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	OXE	A	400	-	=	-	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	$\mathbf{Z}$	Observed(A)	$\operatorname{Ideal}( ext{\AA})$
4	A	400	OXE	C6-C1	2.30	1.44	1.39

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	170	HED	C1-C2-S3-S4

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	170	HED	1	1

### 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>	$\# \mathrm{RSRZ}{>}2$		$OWAB(Å^2)$	Q<0.9
1	A	162/164 (98%)	-0.93	1 (0%)	89 87	8, 16, 53, 91	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	112	ALA	2.5

#### 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 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	HED	A	170	8/8	0.91	0.17	29,36,69,88	0
4	OXE	A	400	8/8	0.97	0.09	16,28,42,45	0
2	CL	A	178	1/1	0.98	0.17	32,32,32,32	1
2	CL	A	173	1/1	0.99	0.02	24,24,24,24	0



## 6.5 Other polymers (i)

There are no such residues in this entry.

