



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 16, 2022 – 02:14 AM EST

PDB ID : 1L53
Title : STRUCTURAL AND THERMODYNAMIC ANALYSIS OF THE PACKING OF TWO ALPHA-HELICES IN BACTERIOPHAGE T4 LYSOZYME
Authors : Daopin, S.; Matthews, B.W.
Deposited on : 1991-01-28
Resolution : 1.85 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.31.2
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) : 2.31.2

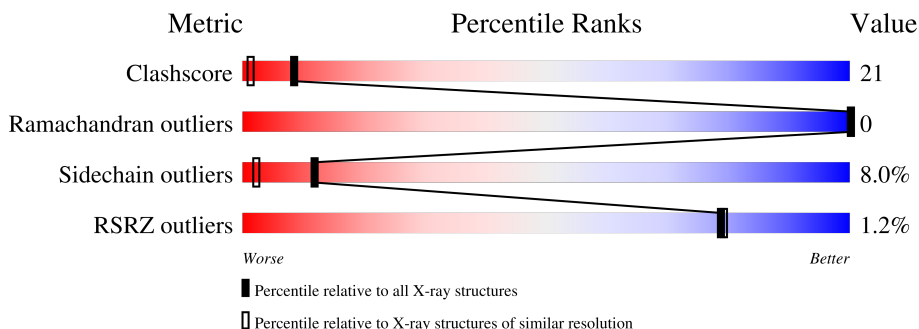
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)
RSRZ outliers	127900	2436 (1.86-1.86)

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 $\leq 5\%$. 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	164	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 1460 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.

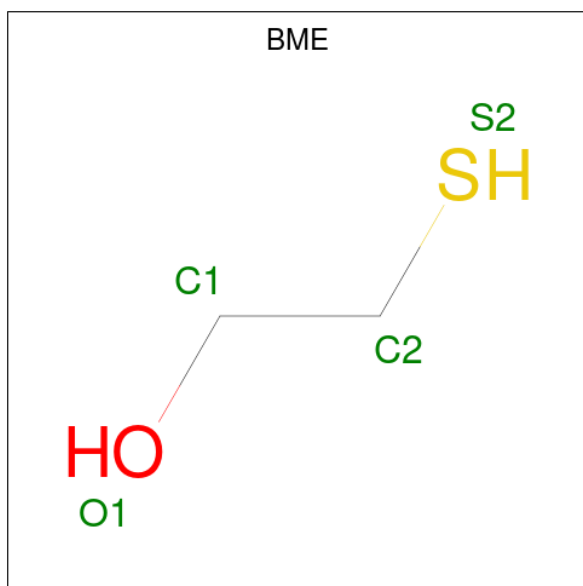
- Molecule 1 is a protein called T4 LYSOZYME.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	164	1308	821	238	241	8	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	149	CYS	VAL	engineered mutation	UNP P00720

- Molecule 2 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C₂H₆OS).



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

- Molecule 3 is water.

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

4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	61.30Å 61.30Å 94.80Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	6.00 – 1.85 19.63 – 1.85	Depositor EDS
% Data completeness (in resolution range)	(Not available) (6.00-1.85) 69.7 (19.63-1.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.11 (at 1.85Å)	Xtrriage
Refinement program	TNT	Depositor
R, R_{free}	0.177 , (Not available) 0.176 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	24.9	Xtrriage
Anisotropy	0.398	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 120.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.045 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	1460	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.20% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	1.04	6/1328 (0.5%)	1.75	33/1786 (1.8%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	22	GLU	CD-OE2	6.46	1.32	1.25
1	A	62	GLU	CD-OE2	6.22	1.32	1.25
1	A	64	GLU	CD-OE2	6.02	1.32	1.25
1	A	45	GLU	CD-OE2	5.37	1.31	1.25
1	A	5	GLU	CD-OE2	5.25	1.31	1.25
1	A	11	GLU	CD-OE1	-5.01	1.20	1.25

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	8	ARG	NE-CZ-NH1	17.28	128.94	120.30
1	A	14	ARG	NE-CZ-NH1	16.00	128.30	120.30
1	A	8	ARG	NE-CZ-NH2	-12.06	114.27	120.30
1	A	14	ARG	NE-CZ-NH2	-11.01	114.80	120.30
1	A	47	ASP	CB-CG-OD1	9.43	126.78	118.30
1	A	70	ASP	CB-CG-OD1	8.81	126.23	118.30
1	A	47	ASP	CB-CG-OD2	-8.71	110.46	118.30
1	A	70	ASP	CB-CG-OD2	-8.00	111.10	118.30
1	A	61	ASP	CB-CG-OD2	-7.91	111.18	118.30
1	A	14	ARG	CD-NE-CZ	7.77	134.47	123.60
1	A	72	ASP	CB-CG-OD1	7.59	125.13	118.30
1	A	80	ARG	CB-CA-C	-7.56	95.29	110.40
1	A	106	MET	CA-CB-CG	7.26	125.64	113.30
1	A	80	ARG	NE-CZ-NH2	-6.82	116.89	120.30
1	A	119	ARG	NE-CZ-NH1	6.45	123.53	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	92	ASP	CB-CG-OD2	-6.28	112.65	118.30
1	A	92	ASP	CB-CG-OD1	6.16	123.85	118.30
1	A	154	ARG	NE-CZ-NH1	6.14	123.37	120.30
1	A	19	LYS	N-CA-CB	5.99	121.38	110.60
1	A	10	ASP	CB-CG-OD2	-5.92	112.97	118.30
1	A	20	ASP	CB-CA-C	5.88	122.16	110.40
1	A	80	ARG	NE-CZ-NH1	5.66	123.13	120.30
1	A	61	ASP	CB-CG-OD1	5.60	123.34	118.30
1	A	137	ARG	NE-CZ-NH2	-5.56	117.52	120.30
1	A	57	VAL	CB-CA-C	-5.55	100.85	111.40
1	A	106	MET	N-CA-CB	-5.54	100.63	110.60
1	A	72	ASP	CB-CG-OD2	-5.52	113.33	118.30
1	A	61	ASP	CA-CB-CG	-5.47	101.37	113.40
1	A	162	LYS	CB-CA-C	5.43	121.25	110.40
1	A	145	ARG	NE-CZ-NH1	5.38	122.99	120.30
1	A	57	VAL	CG1-CB-CG2	-5.20	102.58	110.90
1	A	119	ARG	NE-CZ-NH2	-5.09	117.75	120.30
1	A	37	PRO	N-CA-CB	5.01	109.31	103.30

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	1308	0	1329	55	2
2	A	4	0	5	0	0
3	A	148	0	0	10	2
All	All	1460	0	1334	55	2

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 21.

All (55) 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:A:163:ASN:HB2	1:A:164:LEU:HD13	1.17	1.15
1:A:52:ARG:HH11	1:A:52:ARG:HG3	1.24	1.01
1:A:16:LYS:HE3	1:A:57:VAL:HG23	1.39	0.99
1:A:163:ASN:HB2	1:A:164:LEU:CD1	1.98	0.92
1:A:16:LYS:HE3	1:A:57:VAL:CG2	2.04	0.88
1:A:52:ARG:HG3	1:A:52:ARG:NH1	1.93	0.81
1:A:164:LEU:HD13	1:A:164:LEU:N	1.96	0.80
1:A:14:ARG:HG3	3:A:532:HOH:O	1.82	0.79
1:A:163:ASN:CB	1:A:164:LEU:HD13	2.10	0.74
1:A:16:LYS:CE	1:A:57:VAL:HG23	2.18	0.73
1:A:16:LYS:HE2	1:A:56:GLY:O	1.90	0.71
1:A:145:ARG:HD2	3:A:269:HOH:O	1.90	0.70
1:A:108:GLU:HB2	3:A:316:HOH:O	1.93	0.69
1:A:164:LEU:CD1	1:A:164:LEU:N	2.56	0.68
1:A:21:THR:HG23	3:A:544:HOH:O	1.92	0.68
1:A:53:ASN:ND2	3:A:407:HOH:O	2.26	0.67
1:A:105:GLN:HG3	1:A:145:ARG:NH2	2.09	0.67
1:A:161:TYR:HA	1:A:164:LEU:HD22	1.77	0.66
1:A:11:GLU:CD	1:A:145:ARG:HH12	1.99	0.66
1:A:105:GLN:HG3	1:A:145:ARG:CZ	2.25	0.65
1:A:52:ARG:HH11	1:A:52:ARG:CG	2.04	0.65
1:A:52:ARG:HH12	1:A:54:CYS:HA	1.62	0.64
1:A:16:LYS:CE	1:A:57:VAL:CG2	2.76	0.63
1:A:137:ARG:NH2	3:A:549:HOH:O	2.31	0.63
1:A:148:ARG:HD3	1:A:164:LEU:HD21	1.84	0.60
1:A:92:ASP:O	1:A:96:ARG:HG3	2.04	0.57
1:A:20:ASP:OD2	1:A:22:GLU:HB2	2.04	0.57
1:A:8:ARG:O	1:A:8:ARG:HG3	2.04	0.56
1:A:3:ILE:HG23	1:A:4:PHE:N	2.21	0.55
1:A:105:GLN:OE1	1:A:145:ARG:NE	2.40	0.55
1:A:27:ILE:HD13	1:A:58:ILE:HD13	1.89	0.54
1:A:22:GLU:OE1	1:A:137:ARG:NH1	2.43	0.51
1:A:1:MET:HG2	1:A:158:TRP:CD2	2.46	0.51
1:A:151:THR:HG22	3:A:543:HOH:O	2.10	0.51
1:A:11:GLU:OE1	1:A:145:ARG:NH1	2.42	0.50
1:A:50:ILE:HD12	3:A:206:HOH:O	2.11	0.49
1:A:50:ILE:HG22	1:A:52:ARG:HG2	1.94	0.49
1:A:44:SER:OG	3:A:204:HOH:O	2.20	0.48
1:A:16:LYS:HD2	1:A:57:VAL:HG22	1.95	0.48
1:A:148:ARG:HD3	1:A:164:LEU:CD2	2.44	0.47
1:A:1:MET:HG2	1:A:158:TRP:CE3	2.51	0.45
1:A:52:ARG:NH1	1:A:54:CYS:SG	2.89	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:VAL:O	1:A:97:CYS:HB2	2.17	0.45
1:A:87:VAL:O	1:A:91:LEU:HG	2.17	0.44
1:A:20:ASP:OD2	1:A:22:GLU:N	2.42	0.44
1:A:163:ASN:ND2	3:A:260:HOH:O	2.50	0.44
1:A:61:ASP:N	1:A:61:ASP:OD2	2.51	0.43
1:A:54:CYS:O	1:A:55:ASN:HB3	2.19	0.43
1:A:106:MET:HB3	1:A:106:MET:HE3	1.07	0.41
1:A:16:LYS:HE2	1:A:56:GLY:C	2.41	0.41
1:A:38:SER:CB	1:A:41:ALA:H	2.34	0.41
1:A:160:ALA:O	1:A:164:LEU:HD22	2.21	0.40
1:A:36:SER:HA	1:A:37:PRO:HD3	1.88	0.40
1:A:39:LEU:HD12	1:A:39:LEU:HA	1.91	0.40
1:A:106:MET:HE1	1:A:138:TRP:CD1	2.56	0.40

All (2) 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	Interatomic distance (Å)	Clash overlap (Å)
1:A:147:LYS:NZ	3:A:524:HOH:O[4_655]	1.98	0.22
1:A:14:ARG:NH1	3:A:268:HOH:O[4_655]	2.15	0.05

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	162/164 (99%)	158 (98%)	4 (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 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	138/138 (100%)	127 (92%)	11 (8%)	12 2

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	LYS
1	A	20	ASP
1	A	36	SER
1	A	52	ARG
1	A	53	ASN
1	A	61	ASP
1	A	65	LYS
1	A	83	LYS
1	A	105	GLN
1	A	106	MET
1	A	164	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	68	ASN

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](#)

1 ligand is modelled in this entry.

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	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	BME	A	165	1	3,3,3	1.10	0	1,2,2	1.00	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
2	BME	A	165	1	-	0/1/1/1	-

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

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, 95th 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 ²)	Q<0.9
1	A	164/164 (100%)	-0.45	2 (1%) 79 79	17, 32, 56, 83	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	164	LEU	7.9
1	A	163	ASN	3.0

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](#)

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, 95th 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	B-factors(Å ²)	Q<0.9
2	BME	A	165	4/4	0.98	0.09	24,27,32,43	2

6.5 Other polymers [i](#)

There are no such residues in this entry.