



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 02:12 PM UTC

PDB ID : 6LHD / pdb_00006lhd
Title : Crystal structure of p53/BCL-xL fusion complex
Authors : Wei, H.; Chen, Y.
Deposited on : 2019-12-07
Resolution : 2.50 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

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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
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)	:	2.49

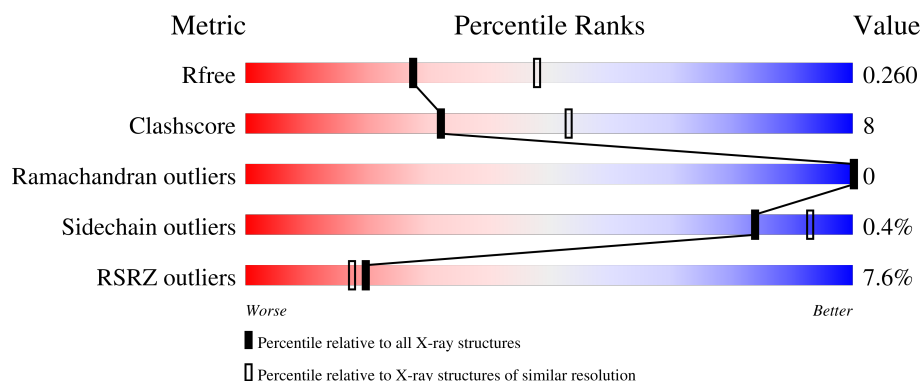
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	375	9% 69% 14% 17%
1	B	375	5% 75% 14% 11%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5114 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 fusion protein of Bcl-2-like protein 1 and Isoform 6 of Cellular tumor antigen p53.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	312	Total	C	N	O	S	0	0	0
			2420	1514	433	454	19			
1	B	332	Total	C	N	O	S	0	0	0
			2587	1626	450	492	19			

There are 116 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP Q07817
A	1	PRO	-	expression tag	UNP Q07817
A	?	-	MET	deletion	UNP Q07817
A	?	-	GLU	deletion	UNP Q07817
A	?	-	THR	deletion	UNP Q07817
A	?	-	PRO	deletion	UNP Q07817
A	?	-	SER	deletion	UNP Q07817
A	?	-	ALA	deletion	UNP Q07817
A	?	-	ILE	deletion	UNP Q07817
A	?	-	ASN	deletion	UNP Q07817
A	?	-	GLY	deletion	UNP Q07817
A	?	-	ASN	deletion	UNP Q07817
A	?	-	PRO	deletion	UNP Q07817
A	?	-	SER	deletion	UNP Q07817
A	?	-	TRP	deletion	UNP Q07817
A	?	-	HIS	deletion	UNP Q07817
A	?	-	LEU	deletion	UNP Q07817
A	?	-	ALA	deletion	UNP Q07817
A	?	-	ASP	deletion	UNP Q07817
A	?	-	SER	deletion	UNP Q07817
A	?	-	PRO	deletion	UNP Q07817
A	?	-	ALA	deletion	UNP Q07817
A	?	-	VAL	deletion	UNP Q07817
A	?	-	ASN	deletion	UNP Q07817

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLY	deletion	UNP Q07817
A	?	-	ALA	deletion	UNP Q07817
A	?	-	THR	deletion	UNP Q07817
A	?	-	GLY	deletion	UNP Q07817
A	?	-	HIS	deletion	UNP Q07817
A	?	-	SER	deletion	UNP Q07817
A	?	-	SER	deletion	UNP Q07817
A	?	-	SER	deletion	UNP Q07817
A	?	-	LEU	deletion	UNP Q07817
A	?	-	ASP	deletion	UNP Q07817
A	?	-	ALA	deletion	UNP Q07817
A	?	-	ARG	deletion	UNP Q07817
A	?	-	GLU	deletion	UNP Q07817
A	?	-	VAL	deletion	UNP Q07817
A	?	-	ILE	deletion	UNP Q07817
A	?	-	PRO	deletion	UNP Q07817
A	?	-	MET	deletion	UNP Q07817
A	?	-	ALA	deletion	UNP Q07817
A	149M	GLY	-	linker	UNP Q07817
A	149N	GLY	-	linker	UNP Q07817
A	149O	GLY	-	linker	UNP Q07817
A	149P	GLY	-	linker	UNP Q07817
A	149Q	SER	-	linker	UNP Q07817
A	149R	LEU	-	linker	UNP Q07817
A	149S	VAL	-	linker	UNP Q07817
A	149T	PRO	-	linker	UNP Q07817
A	149U	ARG	-	linker	UNP Q07817
A	149V	GLY	-	linker	UNP Q07817
A	149W	SER	-	linker	UNP Q07817
A	149X	GLY	-	linker	UNP Q07817
A	149Y	GLY	-	linker	UNP Q07817
A	149Z	GLY	-	linker	UNP Q07817
A	150A	GLY	-	linker	UNP Q07817
A	150B	SER	-	linker	UNP Q07817
B	0	GLY	-	expression tag	UNP Q07817
B	1	PRO	-	expression tag	UNP Q07817
B	?	-	MET	deletion	UNP Q07817
B	?	-	GLU	deletion	UNP Q07817
B	?	-	THR	deletion	UNP Q07817
B	?	-	PRO	deletion	UNP Q07817
B	?	-	SER	deletion	UNP Q07817
B	?	-	ALA	deletion	UNP Q07817

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	ILE	deletion	UNP Q07817
B	?	-	ASN	deletion	UNP Q07817
B	?	-	GLY	deletion	UNP Q07817
B	?	-	ASN	deletion	UNP Q07817
B	?	-	PRO	deletion	UNP Q07817
B	?	-	SER	deletion	UNP Q07817
B	?	-	TRP	deletion	UNP Q07817
B	?	-	HIS	deletion	UNP Q07817
B	?	-	LEU	deletion	UNP Q07817
B	?	-	ALA	deletion	UNP Q07817
B	?	-	ASP	deletion	UNP Q07817
B	?	-	SER	deletion	UNP Q07817
B	?	-	PRO	deletion	UNP Q07817
B	?	-	ALA	deletion	UNP Q07817
B	?	-	VAL	deletion	UNP Q07817
B	?	-	ASN	deletion	UNP Q07817
B	?	-	GLY	deletion	UNP Q07817
B	?	-	ALA	deletion	UNP Q07817
B	?	-	THR	deletion	UNP Q07817
B	?	-	GLY	deletion	UNP Q07817
B	?	-	HIS	deletion	UNP Q07817
B	?	-	SER	deletion	UNP Q07817
B	?	-	SER	deletion	UNP Q07817
B	?	-	SER	deletion	UNP Q07817
B	?	-	LEU	deletion	UNP Q07817
B	?	-	ASP	deletion	UNP Q07817
B	?	-	ALA	deletion	UNP Q07817
B	?	-	ARG	deletion	UNP Q07817
B	?	-	GLU	deletion	UNP Q07817
B	?	-	VAL	deletion	UNP Q07817
B	?	-	ILE	deletion	UNP Q07817
B	?	-	PRO	deletion	UNP Q07817
B	?	-	MET	deletion	UNP Q07817
B	?	-	ALA	deletion	UNP Q07817
B	155G	GLY	-	linker	UNP Q07817
B	155H	GLY	-	linker	UNP Q07817
B	155I	GLY	-	linker	UNP Q07817
B	155J	GLY	-	linker	UNP Q07817
B	155K	SER	-	linker	UNP Q07817
B	155L	LEU	-	linker	UNP Q07817
B	155M	VAL	-	linker	UNP Q07817
B	155N	PRO	-	linker	UNP Q07817

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Chain	Residue	Modelled	Actual	Comment	Reference
B	155O	ARG	-	linker	UNP Q07817
B	155P	GLY	-	linker	UNP Q07817
B	155Q	SER	-	linker	UNP Q07817
B	155R	GLY	-	linker	UNP Q07817
B	155S	GLY	-	linker	UNP Q07817
B	155T	GLY	-	linker	UNP Q07817
B	155U	GLY	-	linker	UNP Q07817
B	155V	SER	-	linker	UNP Q07817

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0

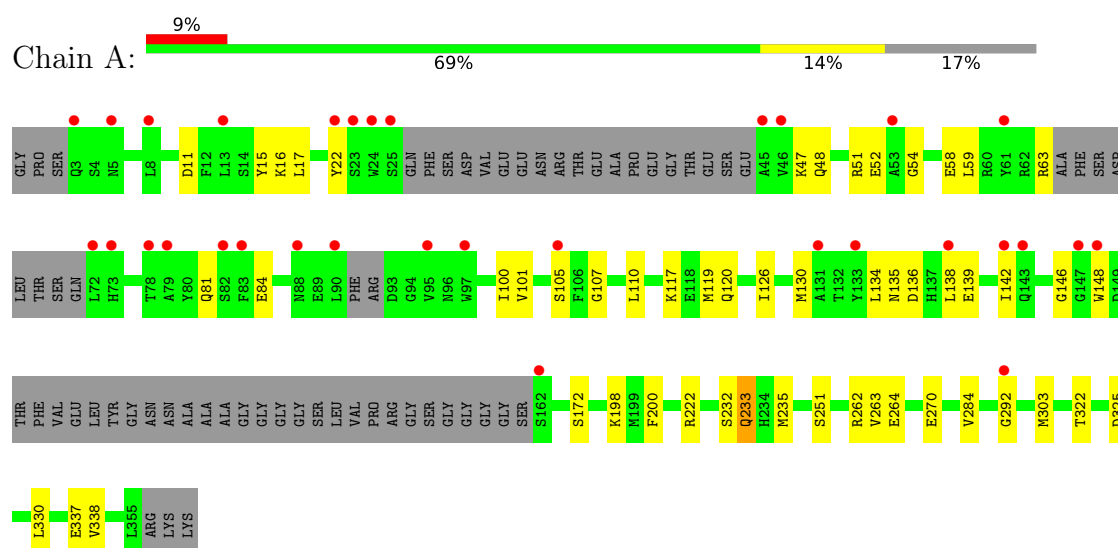
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	48	Total O 48 48	0	0
3	B	57	Total O 57 57	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: fusion protein of Bcl-2-like protein 1 and Isoform 6 of Cellular tumor antigen p53



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	72.22Å 68.85Å 75.03Å 90.00° 110.27° 90.00°	Depositor
Resolution (Å)	49.22 – 2.50 49.22 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.3 (49.22-2.50) 97.3 (49.22-2.50)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.75 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.202 , 0.260 0.203 , 0.260	Depositor DCC
R_{free} test set	1213 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	38.1	Xtriage
Anisotropy	0.450	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 61.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.025 for l,-k,h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5114	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.22% 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: ZN

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	0.19	0/2474	0.37	0/3356
1	B	0.17	0/2649	0.34	0/3598
All	All	0.18	0/5123	0.35	0/6954

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	2420	0	2297	45	0
1	B	2587	0	2430	38	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	48	0	0	5	0
3	B	57	0	0	8	0
All	All	5114	0	4727	78	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.

The worst 5 of 78 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:270:GLU:OE2	3:B:501:HOH:O	1.93	0.85
1:B:68:LEU:HD11	1:B:113:GLU:HB2	1.57	0.85
1:A:325:ASP:OD2	3:A:502:HOH:O	1.98	0.82
1:B:44:GLU:N	3:B:504:HOH:O	2.13	0.81
1:A:251:SER:OG	3:A:501:HOH:O	1.98	0.79

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	302/375 (80%)	292 (97%)	10 (3%)	0	100	100
1	B	326/375 (87%)	316 (97%)	10 (3%)	0	100	100
All	All	628/750 (84%)	608 (97%)	20 (3%)	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	260/320 (81%)	259 (100%)	1 (0%)	84	93
1	B	278/320 (87%)	277 (100%)	1 (0%)	84	93

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	538/640 (84%)	536 (100%)	2 (0%)	84	93

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	233	GLN
1	B	120	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	135	ASN
1	B	137	HIS
1	B	231	GLN
1	A	137	HIS
1	A	19	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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

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	312/375 (83%)	0.62	32 (10%)	12 10	27, 51, 112, 123	0
1	B	332/375 (88%)	0.47	17 (5%)	33 29	22, 53, 96, 131	0
All	All	644/750 (85%)	0.54	49 (7%)	20 17	22, 53, 108, 131	0

The worst 5 of 49 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	71	GLN	4.8
1	A	79	ALA	4.5
1	A	82	SER	4.1
1	B	80	TYR	4.0
1	A	46	VAL	4.0

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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
2	ZN	A	401	1/1	0.99	0.02	41,41,41,41	0
2	ZN	B	401	1/1	0.99	0.03	39,39,39,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.