



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 1J7N
Title : Anthrax Toxin Lethal factor
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Deposited on : 2001-05-17
Resolution : 2.30 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 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

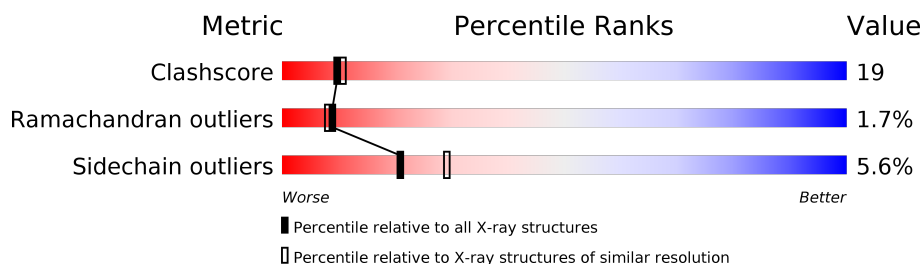
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)

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 on 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	776	
1	B	776	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 12924 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 Lethal Factor precursor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	725	Total	C	N	O	S	0	0	0
			5947	3785	1003	1152	7			
1	B	736	Total	C	N	O	S	0	0	0
			6031	3832	1017	1175	7			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 4 is water.

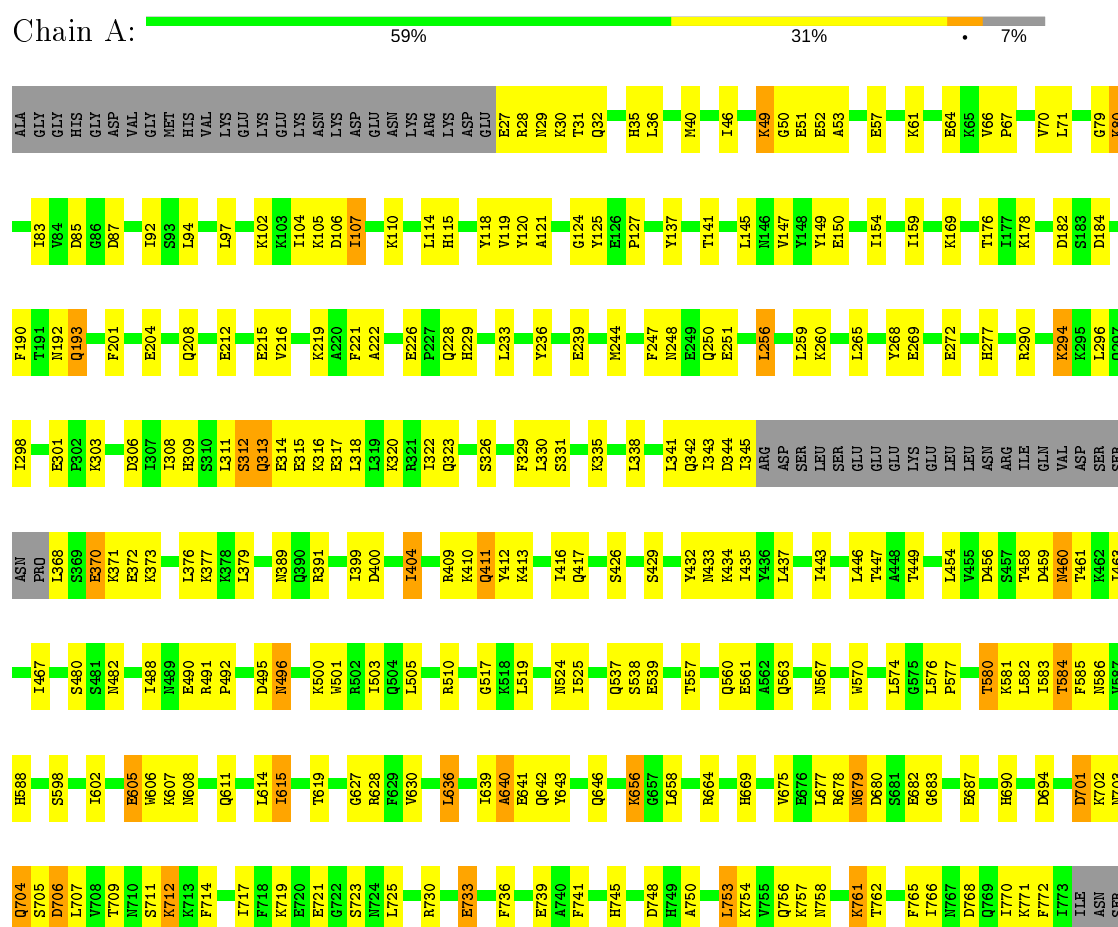
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	436	Total 436	O 436	0	0
4	B	498	Total 498	O 498	0	0

3 Residue-property plots

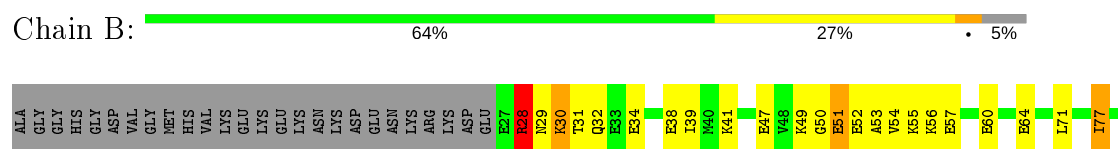
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according 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. 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.

Note EDS was not executed.

- Molecule 1: Lethal Factor precursor



- Molecule 1: Lethal Factor precursor



S776	I666	T509	R391	E317	T176	V84
	K673	R510	L392	L318	I176	D85
	G674	Y513	L398	L319	K178	I88
	V675	L514				
	E676	E515	P402	I322	Q186	T89
	L677	N516	V408	I324	K195	R90
	R678	G517		D325	F201	H91
		R518		S326		I92
	H690	L519	Q411	S327		S93
		I520			L206	L94
	D693	L521	K413	S331	E207	E95
		Q522	R414	T332		A96
	L700	R523	D415	E333	E212	
	D701		I416	E334	V213	K102
	K702	K530	D420	K335	V216	K103
	N703	I635		E336	F217	I104
	G704	K336	H424	K339		K105
	S705	Q537	Q425	K340	F221	D106
	D706	R544	S426	L341		I107
	L707		I427	Q342	E226	
	K712		G428	I343	P227	L113
	K713	A547	L431	D244	Q228	L114
	I717	P651	Y432	I345		H115
	G722	K554	M441	K346	D231	
	R730	Q563		D347	V232	V119
	E733	L564		S348	L233	Y120
	F741	Q568	N444	LEU	Q234	A121
	M744	R579	N445	SER	L235	K122
	H745	F585	N446	GLU	Y236	E123
	S746		L446	GLU	A237	G124
	T747		T447	GLU	P238	Y125
	H748	Q578	A448	LYS	E239	E126
	H749	K378	D456	GLU	A240	P127
	A750	Y579	S457	LEU	F241	V128
	E751	F585	N464	LEU		L129
	R752	Q611	N482	ASN	M244	V130
	L753	D613	I488	ARG	D245	I131
	A759	L614		ILE		S132
	P760	I615	R491	GLN	N248	Q133
	K761	F629	P492	VAL	E249	S134
			D495		Q250	E135
	F765	T632	M496		E251	D136
	I766	D633	L499	K373		
	N767	I634				M140
	D768	I639	K500	K377	L286	
	Q769	I639	W501	K378	L265	K143
	I770	I649	R502	E370	Y278	A144
			I503	D372		L145
	I773		Q504	E372	Q297	H146
	I774	Y659	L505	K373		V147
	N775				K304	E150
					L265	K153
					E370	L154
					K371	L155
					E372	S156
					Q297	

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	96.20 Å 137.46 Å 98.55 Å 90.00° 98.35° 90.00°	Depositor
Resolution (Å)	15.00 – 2.30	Depositor
% Data completeness (in resolution range)	5.0 (15.00-2.30)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.229 , 0.261	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	12924	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

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, SO4

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	0.34	0/6053	0.57	1/8153 (0.0%)
1	B	0.36	1/6139 (0.0%)	0.59	2/8272 (0.0%)
All	All	0.35	1/12192 (0.0%)	0.58	3/16425 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	615	ILE	CG1-CD1	-5.50	1.12	1.50

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	615	ILE	CB-CG1-CD1	8.66	138.14	113.90
1	A	615	ILE	CB-CG1-CD1	-7.22	93.67	113.90
1	B	629	PHE	N-CA-C	-5.57	95.95	111.00

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	5947	0	5938	247	0
1	B	6031	0	5992	221	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	436	0	0	16	0
4	B	498	0	0	17	0
All	All	12924	0	11930	461	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 19.

The worst 5 of 461 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:615:ILE:CD1	1:A:615:ILE:CG1	1.74	1.58
1:A:268:TYR:HB3	1:B:125:TYR:CE2	1.87	1.09
1:B:704:GLN:NE2	1:B:706:ASP:H	1.52	1.07
1:A:92:ILE:HD12	1:A:92:ILE:H	1.25	1.01
1:A:677:LEU:HD13	1:A:683:GLY:HA2	1.43	1.01

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	721/776 (93%)	670 (93%)	38 (5%)	13 (2%)	8	7
1	B	732/776 (94%)	685 (94%)	35 (5%)	12 (2%)	9	9
All	All	1453/1552 (94%)	1355 (93%)	73 (5%)	25 (2%)	9	8

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	49	LYS
1	A	313	GLN
1	A	640	ALA
1	B	28	ARG
1	B	96	ALA

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	660/710 (93%)	623 (94%)	37 (6%)	21	29
1	B	669/710 (94%)	631 (94%)	38 (6%)	20	28
All	All	1329/1420 (94%)	1254 (94%)	75 (6%)	21	29

5 of 75 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	712	LYS
1	B	102	LYS
1	B	615	ILE
1	A	733	GLU
1	B	51	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 73 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	767	ASN
1	B	193	GLN
1	B	638	ASN
1	B	164	ASN
1	B	214	GLN

5.3.3 RNA ⓘ

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 carbohydrates 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	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SO4	B	777	-	4,4,4	0.25	0	6,6,6	0.05	0
2	SO4	A	777	-	4,4,4	0.21	0	6,6,6	0.17	0

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 [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.