



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 15, 2026 – 01:12 AM UTC

PDB ID : 5B5R / pdb_00005b5r
Title : Crystal structure of GSDMA3
Authors : Ding, J.; Shao, F.
Deposited on : 2016-05-14
Resolution : 1.90 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
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

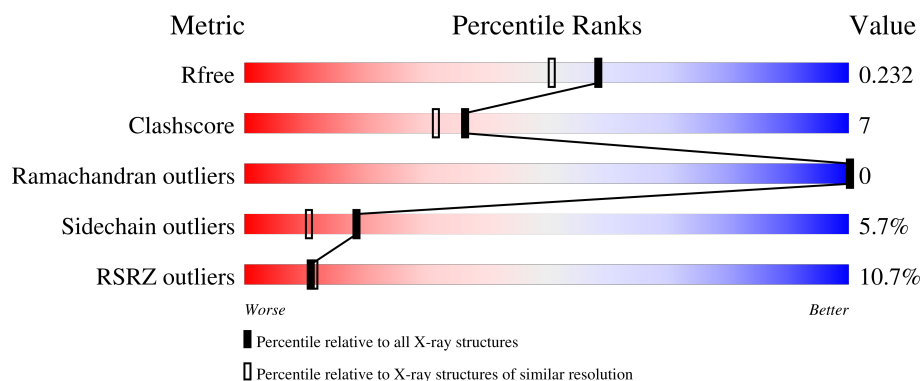
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	468	9% 71% 14% • 13%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3482 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 Gasdermin-A3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	409	Total	C	N	O	S	Se	0	1	0
			3264	2093	551	609	5	6			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	SER	-	expression tag	UNP Q5Y4Y6
A	-2	GLY	-	expression tag	UNP Q5Y4Y6
A	-1	ARG	-	expression tag	UNP Q5Y4Y6
A	0	PRO	-	expression tag	UNP Q5Y4Y6

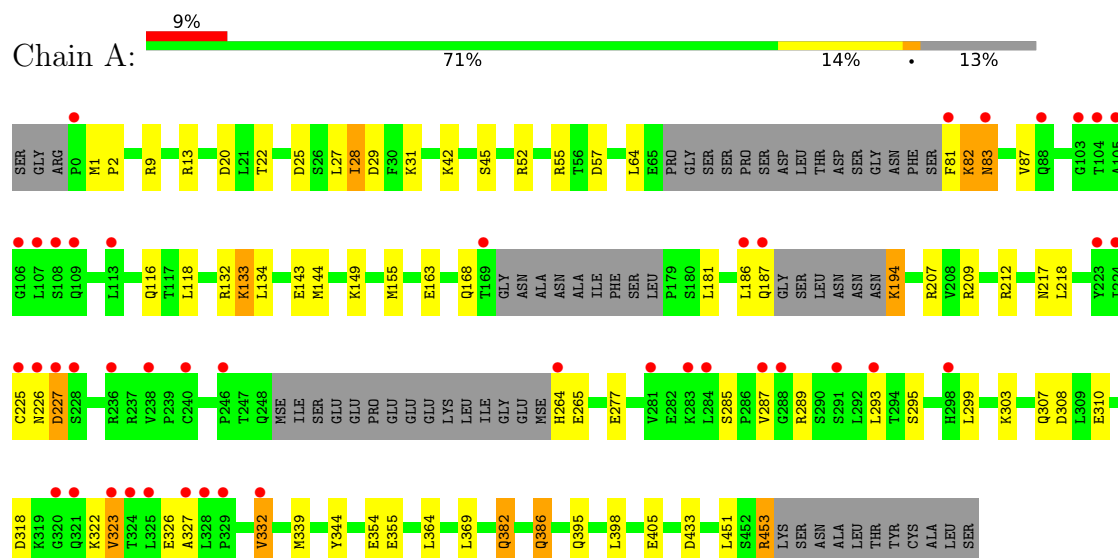
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	218	Total	O	0	0
			218	218		

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: Gasdermin-A3



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	43.45Å 103.41Å 49.62Å 90.00° 110.57° 90.00°	Depositor
Resolution (Å)	37.91 – 1.90 37.91 – 1.90	Depositor EDS
% Data completeness (in resolution range)	69.5 (37.91-1.90) 85.6 (37.91-1.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.72 (at 1.91Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.187 , 0.232 0.191 , 0.232	Depositor DCC
R_{free} test set	1428 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	16.9	Xtriage
Anisotropy	0.059	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 50.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3482	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.52% 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](#)

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	0.35	0/3313	0.73	0/4464

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	3264	0	3395	48	0
2	A	218	0	0	19	1
All	All	3482	0	3395	48	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 (48) 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:168:GLN:O	2:A:501:HOH:O	1.88	0.90
1:A:289:ARG:NH1	2:A:507:HOH:O	2.17	0.78
1:A:116:GLN:OE1	2:A:502:HOH:O	2.11	0.69
1:A:163:GLU:OE2	2:A:503:HOH:O	2.11	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:ASP:OD1	1:A:207:ARG:NH1	2.27	0.67
1:A:25:ASP:OD1	2:A:504:HOH:O	2.13	0.67
1:A:386:GLN:NE2	2:A:514:HOH:O	2.27	0.67
1:A:310:GLU:OE2	2:A:505:HOH:O	2.13	0.66
1:A:285:SER:N	2:A:516:HOH:O	2.31	0.62
1:A:87:VAL:HG22	1:A:118:LEU:HD22	1.82	0.61
1:A:186:LEU:O	2:A:506:HOH:O	2.16	0.60
1:A:155:MSE:HG3	1:A:209:ARG:HD3	1.85	0.58
1:A:226:ASN:OD1	1:A:227:ASP:N	2.37	0.57
1:A:13:ARG:NH1	1:A:433:ASP:OD2	2.37	0.57
1:A:181:LEU:HD13	1:A:187:GLN:HB3	1.86	0.56
1:A:382:GLN:OE1	2:A:508:HOH:O	2.17	0.56
1:A:22:THR:HG23	1:A:52[B]:ARG:HD2	1.87	0.56
1:A:354:GLU:OE1	2:A:509:HOH:O	2.18	0.56
1:A:2:PRO:HG2	1:A:194:LYS:HE2	1.89	0.55
1:A:395:GLN:HB2	1:A:398:LEU:HG	1.89	0.54
1:A:323:VAL:HG21	1:A:339:MSE:SE	2.59	0.52
1:A:303:LYS:O	1:A:307:GLN:HG3	2.13	0.49
1:A:332:VAL:HA	2:A:551:HOH:O	2.13	0.49
1:A:453:ARG:NH2	2:A:531:HOH:O	2.46	0.49
1:A:293:LEU:HB2	1:A:451:LEU:HB3	1.95	0.49
1:A:133:LYS:HD2	1:A:218:LEU:HD23	1.93	0.48
1:A:405:GLU:OE1	2:A:510:HOH:O	2.20	0.47
1:A:364:LEU:HG	1:A:369:LEU:HD11	1.97	0.47
1:A:82:LYS:HD3	1:A:82:LYS:H	1.79	0.46
1:A:212:ARG:NH1	2:A:513:HOH:O	2.25	0.46
1:A:42:LYS:HB3	1:A:45:SER:HB3	1.98	0.46
1:A:64:LEU:HD23	1:A:134:LEU:HD23	1.98	0.46
1:A:354:GLU:HG3	2:A:695:HOH:O	2.16	0.45
1:A:83:ASN:OD1	1:A:83:ASN:N	2.38	0.45
1:A:9:ARG:NH2	2:A:512:HOH:O	2.23	0.45
1:A:144:MSE:SE	1:A:149:LYS:HD3	2.68	0.44
1:A:55:ARG:NH2	1:A:57:ASP:OD1	2.51	0.44
1:A:264:HIS:N	2:A:539:HOH:O	2.51	0.43
1:A:133:LYS:HG3	1:A:217:ASN:O	2.19	0.43
1:A:295:SER:HB3	1:A:327:ALA:O	2.18	0.43
1:A:355:GLU:H	1:A:355:GLU:CD	2.27	0.42
1:A:1:MSE:HE3	1:A:28:ILE:HG23	2.01	0.42
1:A:225:CYS:HB3	2:A:624:HOH:O	2.18	0.42
1:A:82:LYS:HB2	1:A:82:LYS:NZ	2.34	0.42
1:A:1:MSE:HE1	1:A:27:LEU:HD12	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:GLU:HG3	1:A:344:TYR:CD2	2.55	0.41
1:A:322:LYS:HD2	1:A:323:VAL:H	1.86	0.41
1:A:299:LEU:HD23	1:A:299:LEU:HA	1.88	0.40

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	Interatomic distance (Å)	Clash overlap (Å)
2:A:551:HOH:O	2:A:655:HOH:O[1_556]	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	400/468 (86%)	389 (97%)	11 (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	371/411 (90%)	350 (94%)	21 (6%)	18	11

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	ILE
1	A	29	ASP
1	A	31	LYS
1	A	81	PHE
1	A	82	LYS
1	A	83	ASN
1	A	132	ARG
1	A	133	LYS
1	A	143	GLU
1	A	194	LYS
1	A	227	ASP
1	A	265	GLU
1	A	287	VAL
1	A	308	ASP
1	A	318	ASP
1	A	323	VAL
1	A	326	GLU
1	A	332	VAL
1	A	382	GLN
1	A	386	GLN
1	A	453	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	88	GLN
1	A	109	GLN
1	A	230	GLN
1	A	383	ASN
1	A	386	GLN
1	A	437	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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](#)

There are no ligands in this entry.

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

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	403/468 (86%)	0.53	43 (10%)	11 11	6, 25, 58, 91	1 (0%)

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	81	PHE	5.6
1	A	187	GLN	5.1
1	A	323	VAL	4.8
1	A	225	CYS	4.2
1	A	105	ALA	4.0
1	A	238	VAL	4.0
1	A	107	LEU	3.5
1	A	103	GLY	3.4
1	A	104	THR	3.4
1	A	240	CYS	3.2
1	A	108	SER	3.1
1	A	169	THR	3.1
1	A	298	HIS	3.1
1	A	287	VAL	3.0
1	A	284	LEU	2.9
1	A	113	LEU	2.9
1	A	226	ASN	2.8
1	A	283	LYS	2.8
1	A	329	PRO	2.8
1	A	320	GLY	2.8
1	A	325	LEU	2.8
1	A	332	VAL	2.7
1	A	223	TYR	2.7
1	A	328	LEU	2.6
1	A	327	ALA	2.6
1	A	83	ASN	2.6
1	A	293	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	324	THR	2.3
1	A	321	GLN	2.3
1	A	246	PRO	2.3
1	A	186	LEU	2.3
1	A	224	ILE	2.2
1	A	281	VAL	2.2
1	A	228	SER	2.2
1	A	227	ASP	2.2
1	A	106	GLY	2.2
1	A	288	GLY	2.2
1	A	264	HIS	2.1
1	A	109	GLN	2.1
1	A	0	PRO	2.1
1	A	236	ARG	2.1
1	A	88	GLN	2.1
1	A	291	SER	2.1

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.