



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:27 PM UTC

PDB ID : 1K0R / pdb_00001k0r
Title : Crystal Structure of Mycobacterium tuberculosis NusA
Authors : Gopal, B.; Haire, L.F.; Gamblin, S.J.; Dodson, E.J.; Lane, A.N.; Papavasasundaram, K.G.; Colston, M.J.; Dodson, G.; TB Structural Genomics Consortium (TBSGC)
Deposited on : 2001-09-20
Resolution : 1.70 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

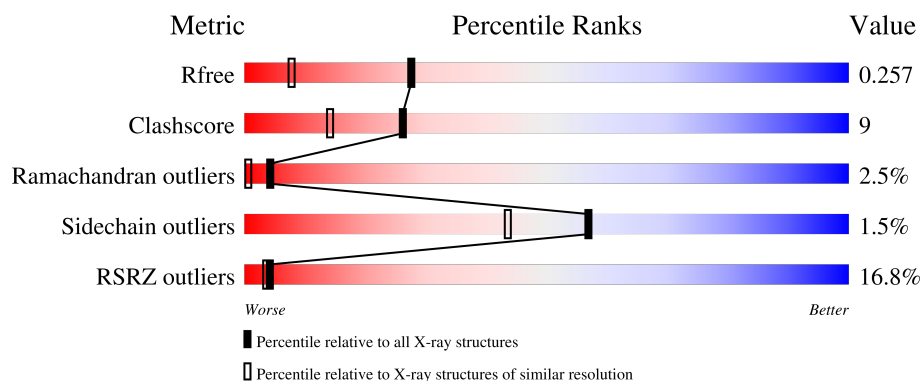
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	366	 6% 79% 10% • 11%
1	B	366	 19% 71% 17% • 11%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5367 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 NusA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	326	Total	C	N	O	S	823	0	0
			2482	1526	476	473	7			
1	B	326	Total	C	N	O	S	6	0	0
			2470	1518	474	471	7			

There are 38 discrepancies between the modelled and reference sequences:

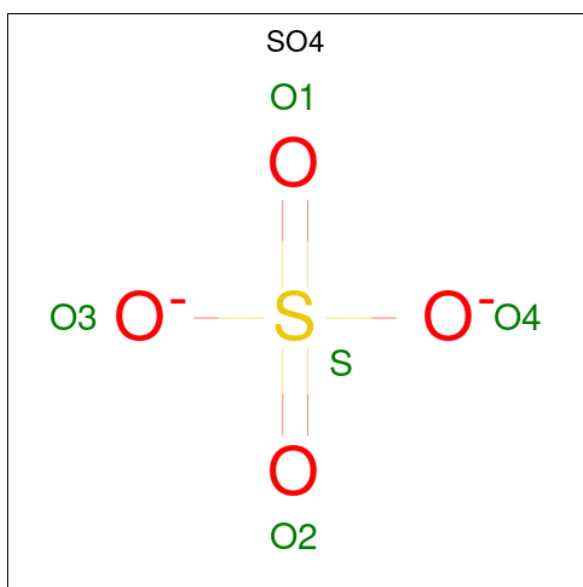
Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MET	-	expression tag	UNP P0A5M2
A	-17	GLY	-	expression tag	UNP P0A5M2
A	-16	SER	-	expression tag	UNP P0A5M2
A	-15	SER	-	expression tag	UNP P0A5M2
A	-14	HIS	-	expression tag	UNP P0A5M2
A	-13	HIS	-	expression tag	UNP P0A5M2
A	-12	HIS	-	expression tag	UNP P0A5M2
A	-11	HIS	-	expression tag	UNP P0A5M2
A	-10	HIS	-	expression tag	UNP P0A5M2
A	-9	HIS	-	expression tag	UNP P0A5M2
A	-8	SER	-	expression tag	UNP P0A5M2
A	-7	SER	-	expression tag	UNP P0A5M2
A	-6	GLY	-	expression tag	UNP P0A5M2
A	-5	LEU	-	expression tag	UNP P0A5M2
A	-4	VAL	-	expression tag	UNP P0A5M2
A	-3	SER	-	expression tag	UNP P0A5M2
A	-2	ARG	-	expression tag	UNP P0A5M2
A	-1	ARG	-	expression tag	UNP P0A5M2
A	0	HIS	-	expression tag	UNP P0A5M2
B	-18	MET	-	expression tag	UNP P0A5M2
B	-17	GLY	-	expression tag	UNP P0A5M2
B	-16	SER	-	expression tag	UNP P0A5M2
B	-15	SER	-	expression tag	UNP P0A5M2
B	-14	HIS	-	expression tag	UNP P0A5M2
B	-13	HIS	-	expression tag	UNP P0A5M2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	HIS	-	expression tag	UNP P0A5M2
B	-11	HIS	-	expression tag	UNP P0A5M2
B	-10	HIS	-	expression tag	UNP P0A5M2
B	-9	HIS	-	expression tag	UNP P0A5M2
B	-8	SER	-	expression tag	UNP P0A5M2
B	-7	SER	-	expression tag	UNP P0A5M2
B	-6	GLY	-	expression tag	UNP P0A5M2
B	-5	LEU	-	expression tag	UNP P0A5M2
B	-4	VAL	-	expression tag	UNP P0A5M2
B	-3	SER	-	expression tag	UNP P0A5M2
B	-2	ARG	-	expression tag	UNP P0A5M2
B	-1	ARG	-	expression tag	UNP P0A5M2
B	0	HIS	-	expression tag	UNP P0A5M2

- Molecule 2 is SULFATE ION (CCD ID: 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		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

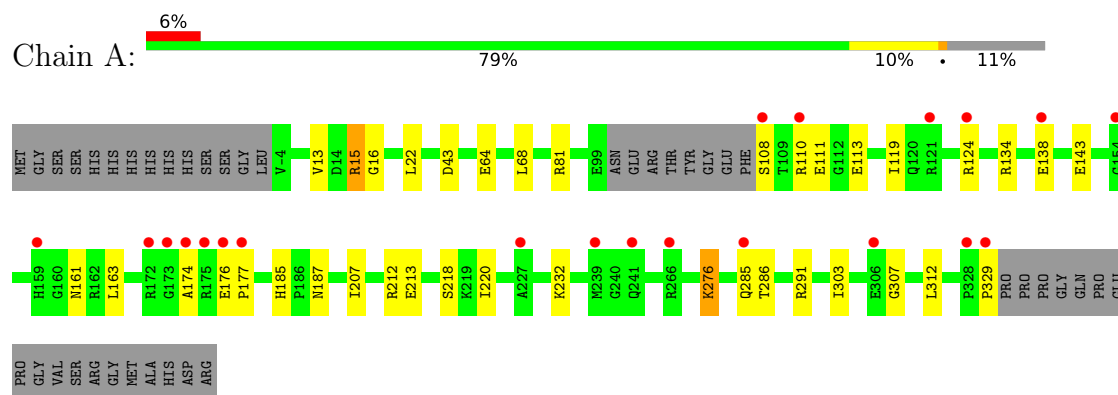
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	165	Total 165	O 165	0	0
3	B	230	Total 230	O 230	0	0

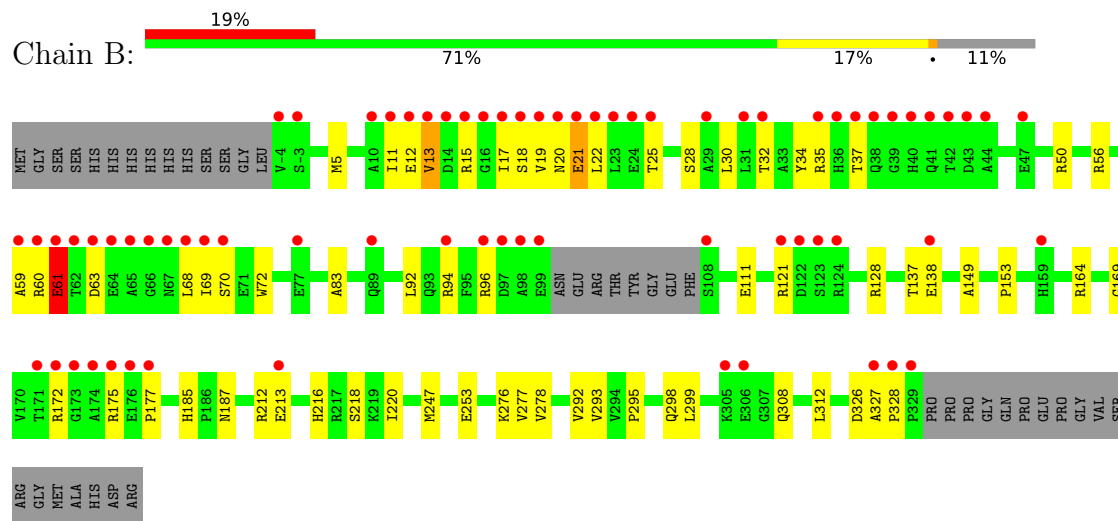
3 Residue-property plots [i](#)

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: NusA



• Molecule 1: NusA



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	88.99Å 88.99Å 180.21Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	15.00 – 1.70 15.00 – 1.70	Depositor EDS
% Data completeness (in resolution range)	86.2 (15.00-1.70) 90.8 (15.00-1.70)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 1.70Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.248 , 0.271 0.249 , 0.257	Depositor DCC
R_{free} test set	4160 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	29.2	Xtriage
Anisotropy	0.045	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 46.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.021 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5367	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.11% 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: 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	0/2512	0.80	0/3399
1	B	0.35	0/2500	0.83	1/3381 (0.0%)
All	All	0.34	0/5012	0.81	1/6780 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	299	LEU	N-CA-C	5.08	116.51	111.07

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	2482	0	2512	25	1
1	B	2470	0	2496	57	0
2	A	5	0	0	0	0
2	B	15	0	0	0	0
3	A	165	0	0	6	0
3	B	230	0	0	12	0
All	All	5367	0	5008	78	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 9.

All (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:A:185:HIS:HD2	1:A:187:ASN:H	1.22	0.86
1:B:185:HIS:HD2	1:B:187:ASN:H	1.23	0.83
1:A:124:ARG:NH2	1:B:128:ARG:HE	1.81	0.79
1:B:12:GLU:HG3	1:B:13:VAL:HG23	1.64	0.79
1:A:124:ARG:HH22	1:B:128:ARG:HE	1.31	0.76
1:B:278:VAL:HG23	1:B:295:PRO:HD3	1.77	0.67
1:A:207:ILE:HD13	1:A:220:ILE:HD11	1.79	0.64
1:A:185:HIS:CD2	1:A:187:ASN:H	2.12	0.63
1:B:277:VAL:HG13	1:B:293:VAL:O	1.98	0.63
1:B:277:VAL:HG11	1:B:292:VAL:HG13	1.81	0.62
1:A:213:GLU:HG3	1:A:312:LEU:HD21	1.80	0.62
1:B:213:GLU:OE1	1:B:308:GLN:HG3	2.00	0.61
1:B:18:SER:HB2	1:B:21:GLU:HB3	1.82	0.61
1:A:212:ARG:HG3	1:A:218:SER:OG	2.04	0.58
1:B:328:PRO:HB2	3:B:710:HOH:O	2.03	0.58
1:B:327:ALA:HA	3:B:668:HOH:O	2.06	0.55
1:B:185:HIS:CD2	1:B:187:ASN:H	2.14	0.55
1:B:61:GLU:HB2	1:B:69:ILE:HG21	1.89	0.55
1:B:17:ILE:HA	3:B:698:HOH:O	2.06	0.54
1:B:18:SER:CB	1:B:21:GLU:HB3	2.37	0.54
1:B:213:GLU:HG3	1:B:312:LEU:HD21	1.90	0.53
1:B:34:TYR:O	1:B:37:THR:HG22	2.09	0.52
1:B:69:ILE:HD12	1:B:69:ILE:N	2.25	0.51
1:A:143:GLU:OE2	1:B:128:ARG:NH1	2.39	0.51
1:B:277:VAL:HG12	1:B:278:VAL:N	2.27	0.50
1:B:69:ILE:O	1:B:70:SER:C	2.53	0.50
1:B:177:PRO:HD3	3:B:694:HOH:O	2.12	0.49
1:B:137:THR:HB	3:B:607:HOH:O	2.13	0.49
1:A:213:GLU:CG	1:A:312:LEU:HD21	2.43	0.49
1:B:60:ARG:HD2	3:B:729:HOH:O	2.11	0.48
1:A:111:GLU:HG3	3:A:561:HOH:O	2.12	0.48
1:B:61:GLU:CD	1:B:69:ILE:HG21	2.38	0.48
1:A:285:GLN:HG2	3:A:559:HOH:O	2.14	0.47
1:B:216:HIS:HB3	1:B:308:GLN:NE2	2.28	0.47
1:A:119:ILE:HD12	1:A:161:ASN:HB2	1.96	0.47
1:A:110:ARG:HB2	1:A:113:GLU:OE2	2.15	0.47
1:B:326:ASP:C	1:B:328:PRO:HD3	2.40	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:35:ARG:HG2	3:B:663:HOH:O	2.14	0.47
1:B:22:LEU:O	1:B:25:THR:HG22	2.14	0.47
1:A:285:GLN:HG3	1:A:286:THR:N	2.30	0.46
1:B:17:ILE:HB	3:B:734:HOH:O	2.15	0.46
1:B:111:GLU:HG2	1:B:169:GLY:HA2	1.96	0.46
1:B:220:ILE:HG13	1:B:220:ILE:O	2.15	0.46
1:B:172:ARG:HG3	1:B:172:ARG:O	2.15	0.46
1:B:295:PRO:HG2	1:B:298:GLN:CG	2.46	0.45
1:B:277:VAL:CG1	1:B:278:VAL:N	2.79	0.45
1:A:276:LYS:HA	1:A:276:LYS:HE2	1.97	0.45
1:B:276:LYS:H	1:B:298:GLN:HE21	1.64	0.45
1:B:277:VAL:HG11	1:B:292:VAL:CG1	2.46	0.45
1:A:207:ILE:CD1	1:A:220:ILE:HD11	2.45	0.45
1:B:30:LEU:HD21	1:B:83:ALA:HA	1.98	0.45
1:B:94:ARG:HG2	1:B:94:ARG:HH11	1.83	0.44
1:A:303:ILE:HG22	1:A:307:GLY:HA2	2.00	0.44
1:B:59:ALA:HB3	1:B:72:TRP:CE2	2.53	0.43
1:B:92:LEU:O	1:B:96:ARG:HG3	2.17	0.43
1:A:108:SER:N	1:A:138:GLU:HB2	2.33	0.43
1:A:124:ARG:HH22	1:B:128:ARG:NE	2.09	0.43
1:B:164:ARG:NE	3:B:728:HOH:O	2.47	0.43
1:B:5:MET:HE2	1:B:50:ARG:O	2.19	0.43
1:B:276:LYS:H	1:B:298:GLN:NE2	2.17	0.43
1:B:327:ALA:N	1:B:328:PRO:HD3	2.35	0.42
1:B:28:SER:O	1:B:32:THR:HG23	2.20	0.42
1:A:176:GLU:HA	1:A:177:PRO:HD3	1.91	0.42
1:B:68:LEU:C	1:B:69:ILE:HD12	2.45	0.42
1:B:212:ARG:HG3	1:B:218:SER:OG	2.20	0.42
1:B:247:MET:HG2	1:B:253:GLU:O	2.20	0.42
1:A:276:LYS:HE2	1:A:276:LYS:CA	2.50	0.42
1:B:153:PRO:HG2	3:B:636:HOH:O	2.20	0.42
1:A:187:ASN:ND2	3:A:588:HOH:O	2.53	0.41
1:A:285:GLN:HB2	3:A:659:HOH:O	2.20	0.41
1:B:61:GLU:HB2	1:B:69:ILE:CG2	2.50	0.41
1:B:19:VAL:HG12	1:B:19:VAL:O	2.21	0.41
1:B:61:GLU:HB2	1:B:69:ILE:CB	2.51	0.41
1:B:175:ARG:HA	1:B:175:ARG:HD3	1.95	0.40
1:A:329:PRO:HD2	3:A:643:HOH:O	2.21	0.40
1:A:161:ASN:ND2	3:A:614:HOH:O	2.54	0.40
1:B:149:ALA:HB3	3:B:611:HOH:O	2.22	0.40
1:B:56:ARG:HD2	3:B:696:HOH:O	2.21	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)
1:A:291:ARG:NH2	1:A:291:ARG:NH2[4_555]	1.95	0.25

5.3 Torsion angles

5.3.1 Protein backbone

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	322/366 (88%)	285 (88%)	28 (9%)	9 (3%)	4	0
1	B	322/366 (88%)	296 (92%)	19 (6%)	7 (2%)	5	1
All	All	644/732 (88%)	581 (90%)	47 (7%)	16 (2%)	4	0

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	15	ARG
1	A	22	LEU
1	A	68	LEU
1	B	20	ASN
1	B	21	GLU
1	A	64	GLU
1	A	81	ARG
1	B	61	GLU
1	B	63	ASP
1	A	15	ARG
1	A	16	GLY
1	A	43	ASP
1	A	174	ALA
1	B	13	VAL
1	B	11	ILE
1	A	13	VAL

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	260/294 (88%)	255 (98%)	5 (2%)	50	34
1	B	258/294 (88%)	255 (99%)	3 (1%)	63	51
All	All	518/588 (88%)	510 (98%)	8 (2%)	57	43

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	ARG
1	A	134	ARG
1	A	163	LEU
1	A	232	LYS
1	A	276	LYS
1	B	61	GLU
1	B	121	ARG
1	B	138	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	120	GLN
1	A	126	ASN
1	A	161	ASN
1	A	185	HIS
1	A	187	ASN
1	A	241	GLN
1	A	298	GLN
1	B	126	ASN
1	B	159	HIS
1	B	161	ASN
1	B	185	HIS
1	B	187	ASN
1	B	285	GLN
1	B	298	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	308	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](#)

4 ligands are 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	SO4	B	508	-	4,4,4	0.37	0	6,6,6	0.07	0
2	SO4	A	506	-	4,4,4	0.38	0	6,6,6	0.10	0
2	SO4	B	509	-	4,4,4	0.36	0	6,6,6	0.07	0
2	SO4	B	505	-	4,4,4	0.32	0	6,6,6	0.10	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

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	222/366 (60%)	0.57	21 (9%) 14 14	19, 28, 46, 73	1 (0%)
1	B	326/366 (89%)	1.41	71 (21%) 2 2	14, 31, 79, 97	2 (0%)
All	All	548/732 (74%)	1.07	92 (16%) 4 3	14, 29, 73, 97	3 (0%)

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	69	ILE	15.0
1	B	328	PRO	13.6
1	B	-4	VAL	13.5
1	B	329	PRO	10.7
1	B	174	ALA	10.1
1	B	19	VAL	9.7
1	B	14	ASP	9.4
1	B	62	THR	8.9
1	B	17	ILE	8.6
1	B	65	ALA	8.0
1	B	327	ALA	7.8
1	A	329	PRO	7.7
1	B	13	VAL	7.5
1	B	98	ALA	7.4
1	B	68	LEU	6.9
1	B	43	ASP	6.8
1	B	61	GLU	6.7
1	B	22	LEU	6.5
1	B	20	ASN	6.5
1	B	60	ARG	6.4
1	B	97	ASP	6.1
1	B	39	GLY	6.0
1	B	173	GLY	6.0
1	B	99	GLU	5.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	66	GLY	5.6
1	B	37	THR	5.5
1	B	11	ILE	5.5
1	A	173	GLY	5.4
1	A	174	ALA	5.2
1	B	176	GLU	5.1
1	B	42	THR	5.1
1	B	16	GLY	5.1
1	B	67	ASN	5.0
1	B	41	GLN	4.8
1	B	64	GLU	4.8
1	B	21	GLU	4.7
1	B	63	ASP	4.7
1	B	12	GLU	4.5
1	A	175	ARG	4.5
1	B	40	HIS	4.4
1	B	175	ARG	4.2
1	B	108	SER	4.1
1	A	177	PRO	4.1
1	B	18	SER	4.0
1	B	15	ARG	3.9
1	B	89	GLN	3.8
1	B	306	GLU	3.8
1	B	70	SER	3.8
1	A	172	ARG	3.8
1	B	171	THR	3.8
1	B	172	ARG	3.7
1	A	285	GLN	3.7
1	B	36	HIS	3.5
1	A	110	ARG	3.5
1	B	159	HIS	3.5
1	A	176	GLU	3.4
1	B	44	ALA	3.4
1	B	-3	SER	3.4
1	B	32	THR	3.3
1	B	38	GLN	3.2
1	A	124	ARG	3.2
1	A	266	ARG	3.2
1	A	108	SER	3.2
1	A	121	ARG	3.2
1	B	96	ARG	3.0
1	B	177	PRO	3.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	138	GLU	2.9
1	B	10	ALA	2.7
1	B	31	LEU	2.7
1	B	94	ARG	2.6
1	A	306	GLU	2.6
1	B	123	SER	2.6
1	B	138	GLU	2.6
1	A	241	GLN	2.5
1	B	24	GLU	2.5
1	B	124	ARG	2.5
1	B	25	THR	2.5
1	A	227	ALA	2.5
1	A	159	HIS	2.5
1	B	213	GLU	2.5
1	B	29	ALA	2.4
1	B	121	ARG	2.4
1	B	23	LEU	2.3
1	B	305	LYS	2.3
1	A	154	GLY	2.3
1	B	47	GLU	2.2
1	B	35	ARG	2.2
1	B	122	ASP	2.1
1	A	328	PRO	2.1
1	B	77	GLU	2.0
1	A	239	MET	2.0
1	B	59	ALA	2.0

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	SO4	B	508	5/5	0.44	0.22	87,87,88,88	0
2	SO4	B	509	5/5	0.51	0.19	95,95,95,96	0
2	SO4	B	505	5/5	0.92	0.14	54,55,56,56	0
2	SO4	A	506	5/5	0.95	0.09	45,45,45,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.