



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 05:10 PM UTC

PDB ID : 3O8B / pdb_00003o8b
Title : Visualizing ATP-dependent RNA Translocation by the NS3 Helicase from HCV
Authors : Appleby, T.C.; Somoza, J.R.
Deposited on : 2010-08-02
Resolution : 1.95 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

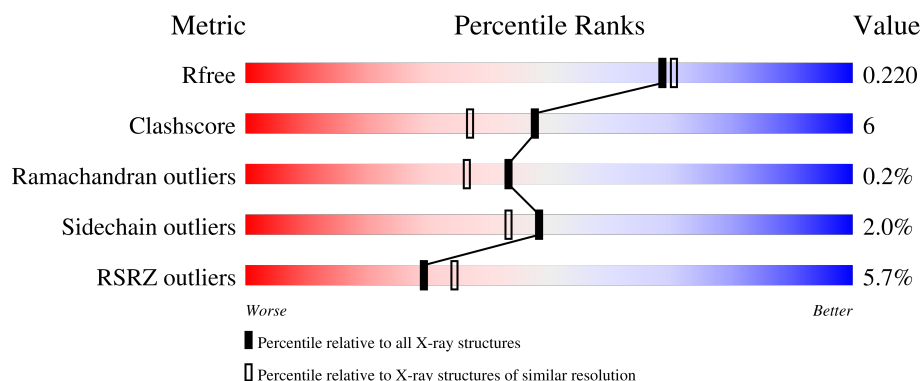
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	666	6% 86% 10% ..
1	B	666	5% 85% 11% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10624 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 HCV NS3 protease/helicase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	645	Total	C	N	O	S	0	0	0
			4807	3026	834	917	30			
1	B	645	Total	C	N	O	S	0	0	0
			4807	3026	834	917	30			

There are 74 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-36	MET	-	expression tag	UNP Q99AU2
A	-35	GLY	-	expression tag	UNP Q99AU2
A	-34	SER	-	expression tag	UNP Q99AU2
A	-33	SER	-	expression tag	UNP Q99AU2
A	-32	HIS	-	expression tag	UNP Q99AU2
A	-31	HIS	-	expression tag	UNP Q99AU2
A	-30	HIS	-	expression tag	UNP Q99AU2
A	-29	HIS	-	expression tag	UNP Q99AU2
A	-28	HIS	-	expression tag	UNP Q99AU2
A	-27	HIS	-	expression tag	UNP Q99AU2
A	-26	SER	-	expression tag	UNP Q99AU2
A	-25	SER	-	expression tag	UNP Q99AU2
A	-24	GLY	-	expression tag	UNP Q99AU2
A	-23	LEU	-	expression tag	UNP Q99AU2
A	-22	VAL	-	expression tag	UNP Q99AU2
A	-21	PRO	-	expression tag	UNP Q99AU2
A	-20	ARG	-	expression tag	UNP Q99AU2
A	-19	GLY	-	expression tag	UNP Q99AU2
A	-18	SER	-	expression tag	UNP Q99AU2
A	-17	HIS	-	expression tag	UNP Q99AU2
A	-16	MET	-	expression tag	UNP Q99AU2
A	-15	GLY	-	expression tag	UNP Q99AU2
A	-14	SER	-	expression tag	UNP Q99AU2
A	-13	VAL	-	expression tag	UNP Q99AU2
A	-12	VAL	-	expression tag	UNP Q99AU2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	ILE	-	expression tag	UNP Q99AU2
A	-10	VAL	-	expression tag	UNP Q99AU2
A	-9	GLY	-	expression tag	UNP Q99AU2
A	-8	ARG	-	expression tag	UNP Q99AU2
A	-7	ILE	-	expression tag	UNP Q99AU2
A	-6	ILE	-	expression tag	UNP Q99AU2
A	-5	LEU	-	expression tag	UNP Q99AU2
A	-4	SER	-	expression tag	UNP Q99AU2
A	-3	GLY	-	expression tag	UNP Q99AU2
A	-2	SER	-	expression tag	UNP Q99AU2
A	-1	GLY	-	expression tag	UNP Q99AU2
A	0	SER	-	expression tag	UNP Q99AU2
B	-36	MET	-	expression tag	UNP Q99AU2
B	-35	GLY	-	expression tag	UNP Q99AU2
B	-34	SER	-	expression tag	UNP Q99AU2
B	-33	SER	-	expression tag	UNP Q99AU2
B	-32	HIS	-	expression tag	UNP Q99AU2
B	-31	HIS	-	expression tag	UNP Q99AU2
B	-30	HIS	-	expression tag	UNP Q99AU2
B	-29	HIS	-	expression tag	UNP Q99AU2
B	-28	HIS	-	expression tag	UNP Q99AU2
B	-27	HIS	-	expression tag	UNP Q99AU2
B	-26	SER	-	expression tag	UNP Q99AU2
B	-25	SER	-	expression tag	UNP Q99AU2
B	-24	GLY	-	expression tag	UNP Q99AU2
B	-23	LEU	-	expression tag	UNP Q99AU2
B	-22	VAL	-	expression tag	UNP Q99AU2
B	-21	PRO	-	expression tag	UNP Q99AU2
B	-20	ARG	-	expression tag	UNP Q99AU2
B	-19	GLY	-	expression tag	UNP Q99AU2
B	-18	SER	-	expression tag	UNP Q99AU2
B	-17	HIS	-	expression tag	UNP Q99AU2
B	-16	MET	-	expression tag	UNP Q99AU2
B	-15	GLY	-	expression tag	UNP Q99AU2
B	-14	SER	-	expression tag	UNP Q99AU2
B	-13	VAL	-	expression tag	UNP Q99AU2
B	-12	VAL	-	expression tag	UNP Q99AU2
B	-11	ILE	-	expression tag	UNP Q99AU2
B	-10	VAL	-	expression tag	UNP Q99AU2
B	-9	GLY	-	expression tag	UNP Q99AU2
B	-8	ARG	-	expression tag	UNP Q99AU2
B	-7	ILE	-	expression tag	UNP Q99AU2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-6	ILE	-	expression tag	UNP Q99AU2
B	-5	LEU	-	expression tag	UNP Q99AU2
B	-4	SER	-	expression tag	UNP Q99AU2
B	-3	GLY	-	expression tag	UNP Q99AU2
B	-2	SER	-	expression tag	UNP Q99AU2
B	-1	GLY	-	expression tag	UNP Q99AU2
B	0	SER	-	expression tag	UNP Q99AU2

- 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 SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

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

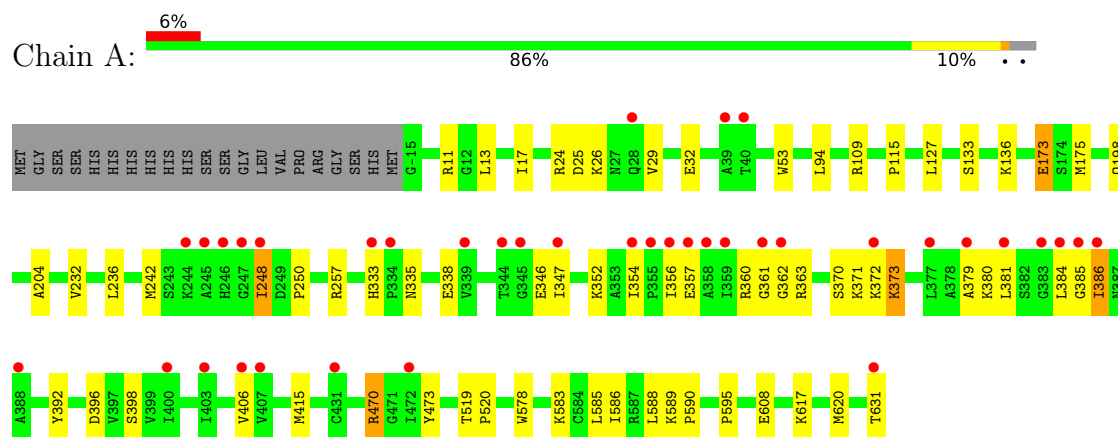
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	558	Total	O	0	0
			558	558		
4	B	430	Total	O	0	0
			430	430		

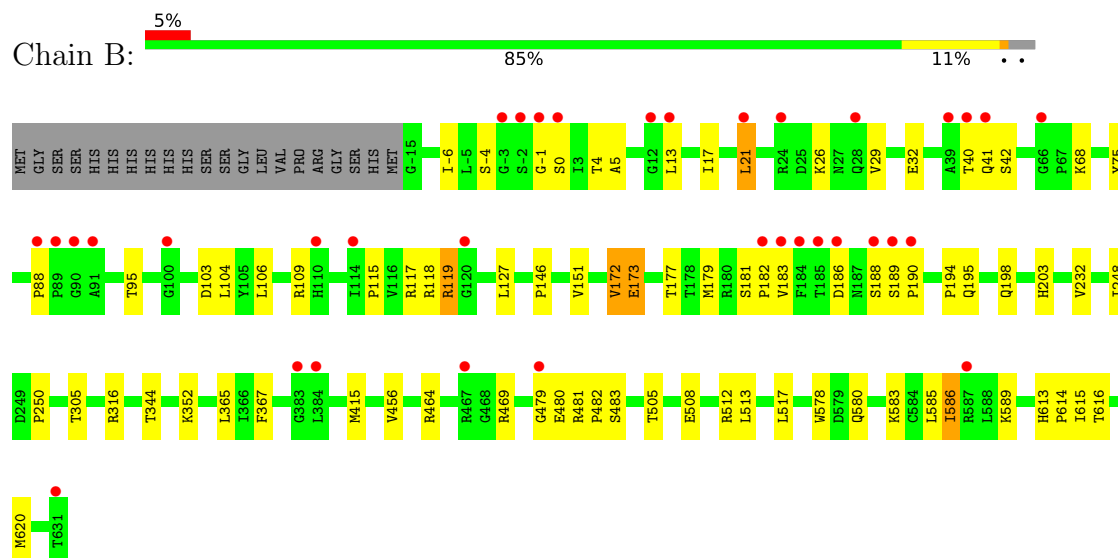
3 Residue-property plots

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: HCV NS3 protease/helicase



- Molecule 1: HCV NS3 protease/helicase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	91.30Å 111.95Å 139.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.95 50.00 – 1.95	Depositor EDS
% Data completeness (in resolution range)	94.0 (50.00-1.95) 93.9 (50.00-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.53 (at 1.95Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.183 , 0.222 0.180 , 0.220	Depositor DCC
R_{free} test set	2000 reflections (1.95%)	wwPDB-VP
Wilson B-factor (Å ²)	20.6	Xtriage
Anisotropy	0.107	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 43.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10624	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.10% 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, 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	0.48	0/4916	0.78	2/6714 (0.0%)
1	B	0.44	0/4916	0.76	0/6714
All	All	0.46	0/9832	0.77	2/13428 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	204	ALA	CA-C-N	5.13	125.06	119.78
1	A	204	ALA	C-N-CA	5.13	125.06	119.78

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	4807	0	4784	63	0
1	B	4807	0	4784	51	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	10	0	0	0	0
3	B	10	0	0	0	0
4	A	558	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	430	0	0	2	0
All	All	10624	0	9568	108	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 6.

All (108) 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:470:ARG:HH11	1:A:470:ARG:HG3	1.27	0.96
1:A:17:ILE:HD12	1:B:17:ILE:HD12	1.47	0.95
1:A:384:LEU:HD22	1:A:386:ILE:HD11	1.67	0.75
1:A:470:ARG:HG3	1:A:470:ARG:NH1	2.01	0.72
1:A:360:ARG:HD2	1:A:361:GLY:N	2.10	0.67
1:A:360:ARG:HH11	1:A:361:GLY:H	1.43	0.67
1:B:181:SER:O	1:B:183:VAL:N	2.28	0.66
1:A:384:LEU:HD23	1:A:384:LEU:O	1.96	0.66
1:A:384:LEU:CD2	1:A:386:ILE:HD11	2.25	0.65
1:A:133:SER:HA	1:A:136:LYS:HG2	1.81	0.62
1:A:346:GLU:CD	1:A:356:ILE:HG22	2.26	0.61
1:B:481:ARG:HB3	1:B:482:PRO:HD2	1.82	0.60
1:A:136:LYS:HD3	1:A:631:THR:HG22	1.83	0.60
1:B:17:ILE:O	1:B:21:LEU:HD13	2.02	0.60
1:A:17:ILE:CD1	1:B:17:ILE:HD12	2.29	0.60
1:A:360:ARG:HD2	1:A:361:GLY:H	1.67	0.59
1:A:24:ARG:HH11	1:A:26:LYS:NZ	2.01	0.59
1:A:379:ALA:C	1:A:381:LEU:H	2.12	0.58
1:A:13:LEU:HG	1:B:17:ILE:HD13	1.84	0.58
1:B:40:THR:OG1	1:B:41:GLN:HG2	2.04	0.57
1:A:370:SER:OG	1:A:372:LYS:HG2	2.05	0.56
1:A:381:LEU:HD22	1:A:386:ILE:HD13	1.87	0.56
1:B:189:SER:OG	1:B:190:PRO:HD2	2.06	0.55
1:A:32:GLU:HG3	1:A:94:LEU:CD2	2.36	0.54
1:A:333:HIS:HE1	1:A:335:ASN:HB2	1.73	0.54
1:A:236:LEU:HD22	1:A:257:ARG:HE	1.73	0.54
1:B:305:THR:OG1	1:B:512:ARG:HD3	2.07	0.54
1:B:173:GLU:H	1:B:173:GLU:CD	2.15	0.53
1:B:505:THR:OG1	1:B:508:GLU:HG3	2.08	0.53
1:A:380:LYS:O	1:A:380:LYS:HG3	2.09	0.53
1:A:32:GLU:HG3	1:A:94:LEU:HG	1.90	0.53
1:B:-4:SER:HB3	1:B:4:THR:OG1	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:333:HIS:CE1	1:A:335:ASN:HB2	2.44	0.52
1:B:186:ASP:OD2	1:B:188:SER:HB3	2.10	0.52
1:B:195:GLN:HA	1:B:316:ARG:HH21	1.75	0.51
1:A:371:LYS:HG3	1:A:392:TYR:CE2	2.45	0.51
1:A:242:MET:CG	1:A:248:ILE:HG12	2.40	0.51
1:A:470:ARG:NH1	1:A:470:ARG:CG	2.73	0.51
1:B:456:VAL:HG23	1:B:483:SER:HB2	1.92	0.51
1:A:115:PRO:HB2	1:A:127:LEU:HD22	1.92	0.51
1:B:29:VAL:HG21	1:B:88:PRO:CG	2.41	0.50
1:B:415:MET:HA	1:B:464:ARG:HH21	1.75	0.50
1:B:194:PRO:HG3	1:B:198:GLN:HB2	1.93	0.50
1:A:242:MET:HG2	1:A:248:ILE:O	2.12	0.49
1:B:29:VAL:HG21	1:B:88:PRO:HG2	1.95	0.49
1:A:17:ILE:HD13	1:B:13:LEU:HG	1.94	0.49
1:A:595:PRO:HB3	1:A:608:GLU:HG3	1.95	0.49
1:A:381:LEU:CD2	1:A:386:ILE:HD13	2.42	0.49
1:B:613:HIS:CE1	1:B:615:ILE:HG12	2.48	0.49
1:B:583:LYS:O	1:B:586:ILE:HG13	2.14	0.48
1:A:24:ARG:HH11	1:A:26:LYS:HZ1	1.59	0.48
1:A:242:MET:HG2	1:A:248:ILE:HG12	1.95	0.48
1:A:173:GLU:H	1:A:173:GLU:CD	2.22	0.48
1:A:346:GLU:OE1	1:A:356:ILE:HG22	2.13	0.48
1:B:115:PRO:HB2	1:B:127:LEU:HD22	1.96	0.47
1:A:589:LYS:N	1:A:590:PRO:HD2	2.29	0.47
1:B:232:VAL:HG23	4:B:950:HOH:O	2.15	0.47
1:A:362:GLY:HA3	4:A:828:HOH:O	2.14	0.46
1:B:479:GLY:O	1:B:480:GLU:HB3	2.15	0.46
1:A:357:GLU:HA	1:A:360:ARG:HG2	1.98	0.46
1:A:371:LYS:HG3	1:A:392:TYR:CZ	2.50	0.46
1:B:620:MET:HE3	4:B:869:HOH:O	2.14	0.46
1:B:578:TRP:CZ2	1:B:589:LYS:HG3	2.51	0.46
1:A:198:GLN:NE2	4:A:923:HOH:O	2.47	0.46
1:A:363:ARG:HA	1:A:406:VAL:O	2.16	0.46
1:A:519:THR:HA	1:A:520:PRO:HD3	1.83	0.46
1:A:24:ARG:NH1	1:A:26:LYS:HZ1	2.14	0.45
1:B:68:LYS:HA	1:B:68:LYS:HD3	1.71	0.45
1:A:373:LYS:HB2	1:A:373:LYS:NZ	2.31	0.45
1:B:104:LEU:HD22	1:B:151:VAL:HG21	1.98	0.45
1:B:195:GLN:HA	1:B:316:ARG:NH2	2.31	0.45
1:A:385:GLY:O	1:A:386:ILE:HG13	2.17	0.45
1:B:103:ASP:O	1:B:146:PRO:HD3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:117:ARG:HG2	1:B:119:ARG:NH2	2.33	0.44
1:A:379:ALA:C	1:A:381:LEU:N	2.75	0.44
1:A:381:LEU:O	1:A:386:ILE:HD12	2.18	0.44
1:B:151:VAL:O	1:B:172:VAL:HG22	2.17	0.44
1:A:53:TRP:CD1	1:A:175:MET:HE3	2.53	0.44
1:A:583:LYS:HA	1:A:586:ILE:HG13	1.98	0.44
1:B:173:GLU:O	1:B:177:THR:HG23	2.18	0.44
1:A:385:GLY:C	1:A:386:ILE:HG13	2.43	0.43
1:B:188:SER:HA	1:B:203:HIS:O	2.19	0.43
1:B:616:THR:O	1:B:620:MET:HG3	2.18	0.43
1:A:232:VAL:HG12	4:A:961:HOH:O	2.18	0.42
1:A:396:ASP:OD2	1:A:398:SER:OG	2.35	0.42
1:B:365:LEU:HD21	1:B:367:PHE:CZ	2.54	0.42
1:A:338:GLU:HA	1:A:473:TYR:O	2.20	0.42
1:B:106:LEU:C	1:B:106:LEU:HD23	2.44	0.42
1:A:617:LYS:HA	1:A:620:MET:HE3	2.02	0.42
1:B:248:ILE:O	1:B:250:PRO:HD3	2.20	0.42
1:A:248:ILE:O	1:A:250:PRO:HD3	2.20	0.41
1:A:347:ILE:HG13	1:A:354:ILE:O	2.21	0.41
1:A:578:TRP:CZ2	1:A:589:LYS:HG3	2.55	0.41
1:B:42:SER:OG	1:B:109:ARG:NH2	2.49	0.41
1:B:352:LYS:HD3	1:B:352:LYS:HA	1.78	0.41
1:A:17:ILE:HD12	1:B:17:ILE:CD1	2.34	0.41
1:B:75:TYR:CE1	1:B:179:MET:HA	2.56	0.41
1:B:583:LYS:HA	1:B:586:ILE:HG13	2.03	0.41
1:B:580:GLN:O	1:B:583:LYS:HE3	2.21	0.41
1:B:613:HIS:CG	1:B:614:PRO:HD2	2.56	0.41
1:B:-6:ILE:O	1:B:5:ALA:HA	2.20	0.41
1:B:104:LEU:HD11	1:B:118:ARG:HB2	2.03	0.41
1:A:11:ARG:HH12	1:A:25:ASP:CG	2.28	0.40
1:A:32:GLU:HG3	1:A:94:LEU:CG	2.51	0.40
1:A:588:LEU:C	1:A:590:PRO:HD2	2.46	0.40
1:B:513:LEU:O	1:B:517:LEU:HD13	2.21	0.40
1:A:17:ILE:CD1	1:B:13:LEU:HG	2.51	0.40
1:B:117:ARG:HE	1:B:119:ARG:HH21	1.70	0.40

There are no symmetry-related clashes.

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	643/666 (96%)	632 (98%)	11 (2%)	0	100	100
1	B	643/666 (96%)	624 (97%)	16 (2%)	3 (0%)	24	16
All	All	1286/1332 (96%)	1256 (98%)	27 (2%)	3 (0%)	43	36

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	-1	GLY
1	B	0	SER
1	B	182	PRO

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	526/544 (97%)	516 (98%)	10 (2%)	50	45
1	B	526/544 (97%)	515 (98%)	11 (2%)	47	41
All	All	1052/1088 (97%)	1031 (98%)	21 (2%)	48	43

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

Mol	Chain	Res	Type
1	A	29	VAL
1	A	109	ARG
1	A	173	GLU

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Mol	Chain	Res	Type
1	A	248	ILE
1	A	352	LYS
1	A	373	LYS
1	A	386	ILE
1	A	415	MET
1	A	470	ARG
1	A	585	LEU
1	B	21	LEU
1	B	26	LYS
1	B	32	GLU
1	B	95	THR
1	B	119	ARG
1	B	172	VAL
1	B	173	GLU
1	B	344	THR
1	B	469	ARG
1	B	585	LEU
1	B	586	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	GLN
1	A	41	GLN
1	A	221	GLN
1	A	246	HIS
1	A	549	GLN
1	B	28	GLN
1	B	34	GLN
1	B	80	GLN
1	B	198	GLN
1	B	246	HIS
1	B	387	ASN
1	B	434	GLN
1	B	549	GLN
1	B	556	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	$\# Z > 2$
3	SO4	B	2	-	4,4,4	0.23	0	6,6,6	0.14	0
3	SO4	A	825	-	4,4,4	0.20	0	6,6,6	0.26	0
3	SO4	A	1	-	4,4,4	0.27	0	6,6,6	0.08	0
3	SO4	B	825	-	4,4,4	0.26	0	6,6,6	0.35	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 ⓘ

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	645/666 (96%)	0.02	38 (5%) 28 32	10, 21, 46, 65	0
1	B	645/666 (96%)	0.15	35 (5%) 31 37	13, 24, 45, 82	0
All	All	1290/1332 (96%)	0.08	73 (5%) 29 34	10, 23, 46, 82	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	183	VAL	6.5
1	B	184	PHE	5.6
1	A	245	ALA	5.5
1	B	189	SER	5.0
1	A	386	ILE	4.7
1	A	356	ILE	4.5
1	B	89	PRO	4.3
1	A	384	LEU	4.0
1	B	185	THR	3.7
1	A	347	ILE	3.7
1	B	40	THR	3.6
1	B	186	ASP	3.5
1	A	383	GLY	3.4
1	B	91	ALA	3.3
1	A	244	LYS	3.3
1	B	39	ALA	3.3
1	A	631	THR	3.2
1	B	631	THR	3.2
1	A	379	ALA	3.1
1	A	247	GLY	3.1
1	A	406	VAL	3.0
1	B	12	GLY	3.0
1	B	88	PRO	3.0
1	A	248	ILE	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	381	LEU	3.0
1	A	372	LYS	3.0
1	B	21	LEU	2.9
1	A	28	GLN	2.9
1	B	-1	GLY	2.8
1	A	361	GLY	2.8
1	B	188	SER	2.7
1	A	359	ILE	2.7
1	A	355	PRO	2.6
1	B	0	SER	2.6
1	A	377	LEU	2.6
1	A	40	THR	2.6
1	B	90	GLY	2.5
1	A	358	ALA	2.5
1	A	388	ALA	2.5
1	A	357	GLU	2.5
1	A	246	HIS	2.4
1	B	28	GLN	2.4
1	A	403	ILE	2.4
1	A	472	ILE	2.4
1	A	407	VAL	2.4
1	A	400	ILE	2.3
1	B	587	ARG	2.3
1	A	344	THR	2.3
1	A	385	GLY	2.3
1	B	120	GLY	2.3
1	A	362	GLY	2.3
1	B	-3	GLY	2.3
1	B	383	GLY	2.3
1	B	66	GLY	2.2
1	B	-2	SER	2.2
1	B	41	GLN	2.2
1	A	334	PRO	2.2
1	B	110	HIS	2.2
1	B	384	LEU	2.2
1	B	479	GLY	2.2
1	A	431	CYS	2.1
1	B	13	LEU	2.1
1	B	467	ARG	2.1
1	A	354	ILE	2.1
1	B	100	GLY	2.1
1	A	39	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	339	VAL	2.0
1	B	182	PRO	2.0
1	B	190	PRO	2.0
1	A	333	HIS	2.0
1	B	114	ILE	2.0
1	A	345	GLY	2.0
1	B	24	ARG	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(Å ²)	Q<0.9
3	SO4	A	1	5/5	0.97	0.10	23,25,35,37	0
3	SO4	B	2	5/5	0.97	0.11	26,32,39,41	0
2	ZN	B	800	1/1	0.98	0.04	45,45,45,45	0
3	SO4	B	825	5/5	0.98	0.05	22,22,25,26	0
3	SO4	A	825	5/5	0.98	0.05	20,22,24,24	0
2	ZN	A	800	1/1	1.00	0.01	19,19,19,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.