



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 05:06 pm BST

PDB ID : 2XHU
Title : HCV-J4 NS5B Polymerase Orthorhombic Crystal Form
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Deposited on : 2010-06-21
Resolution : 2.29 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 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) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

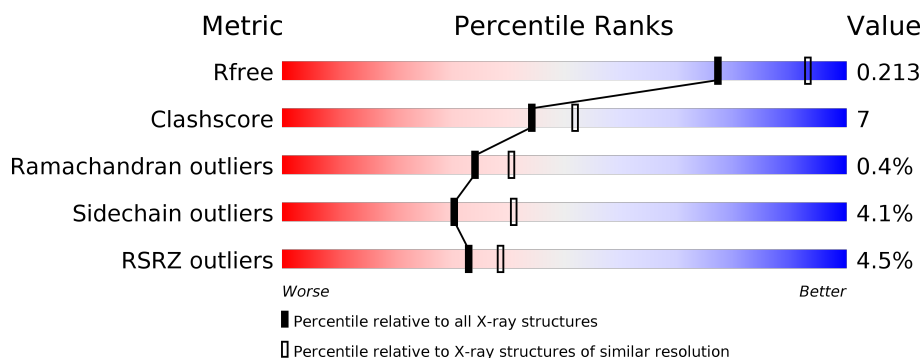
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 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}	130704	6980 (2.30-2.26)
Clashscore	141614	7711 (2.30-2.26)
Ramachandran outliers	138981	7597 (2.30-2.26)
Sidechain outliers	138945	7598 (2.30-2.26)
RSRZ outliers	127900	6849 (2.30-2.26)

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 $\leq 5\%$. 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	579	
1	B	579	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	1571	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9648 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.

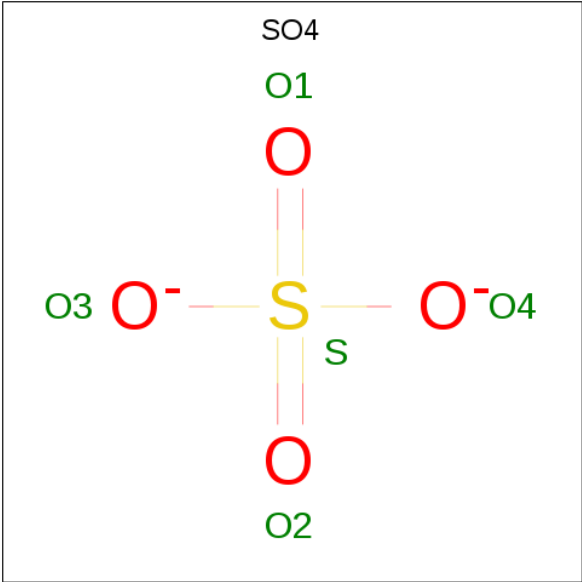
- Molecule 1 is a protein called RNA-DIRECTED RNA POLYMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	562	Total	C	N	O	S	0	3	0
			4390	2763	774	821	32			
1	B	563	Total	C	N	O	S	0	3	0
			4401	2770	779	820	32			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ALA	-	expression tag	UNP O92972
A	571	LEU	-	expression tag	UNP O92972
A	572	GLU	-	expression tag	UNP O92972
A	573	HIS	-	expression tag	UNP O92972
A	574	HIS	-	expression tag	UNP O92972
A	575	HIS	-	expression tag	UNP O92972
A	576	HIS	-	expression tag	UNP O92972
A	577	HIS	-	expression tag	UNP O92972
A	578	HIS	-	expression tag	UNP O92972
B	0	ALA	-	expression tag	UNP O92972
B	571	LEU	-	expression tag	UNP O92972
B	572	GLU	-	expression tag	UNP O92972
B	573	HIS	-	expression tag	UNP O92972
B	574	HIS	-	expression tag	UNP O92972
B	575	HIS	-	expression tag	UNP O92972
B	576	HIS	-	expression tag	UNP O92972
B	577	HIS	-	expression tag	UNP O92972
B	578	HIS	-	expression tag	UNP O92972

- 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	A	1	Total	O	S	0	1
			10	8	2		
2	A	1	Total	O	S	0	1
			20	16	4		
2	A	1	Total	O	S	0	1
			10	8	2		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	1
			20	16	4		
2	B	1	Total	O	S	0	1
			10	8	2		
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		
2	B	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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		

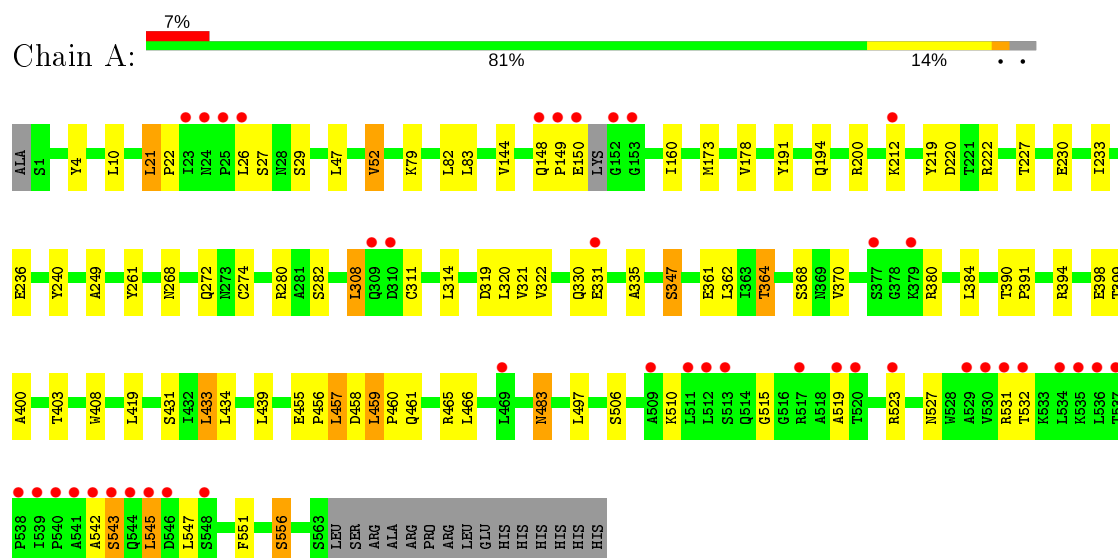
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	312	Total	O	0	0
			312	312		
3	B	415	Total	O	0	0
			415	415		

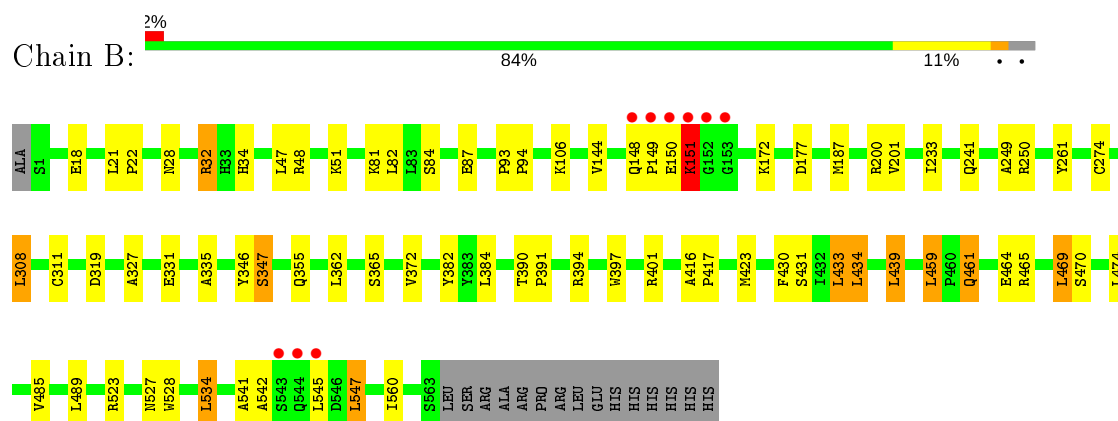
3 Residue-property plots [i](#)

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 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: RNA-DIRECTED RNA POLYMERASE



• Molecule 1: RNA-DIRECTED RNA POLYMERASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	106.52Å 107.82Å 133.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.10 – 2.29 48.10 – 2.29	Depositor EDS
% Data completeness (in resolution range)	98.2 (48.10-2.29) 98.2 (48.10-2.29)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.51 (at 2.29Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.165 , 0.218 0.161 , 0.213	Depositor DCC
R_{free} test set	3447 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	25.6	Xtriage
Anisotropy	0.481	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 55.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.024 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9648	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.16% 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	0/4491	0.50	0/6094
1	B	0.39	1/4503 (0.0%)	0.53	0/6110
All	All	0.37	1/8994 (0.0%)	0.52	0/12204

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	274	CYS	CB-SG	-5.96	1.72	1.81

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	4390	0	4398	66	0
1	B	4401	0	4419	51	0
2	A	65	0	0	2	0
2	B	65	0	0	0	0
3	A	312	0	0	6	0
3	B	415	0	0	4	0
All	All	9648	0	8817	117	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 7.

All (117) 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:230:GLU:HG2	3:A:2183:HOH:O	1.72	0.88
1:A:398:GLU:HG2	1:A:403:THR:HG21	1.55	0.85
1:A:144:VAL:HG22	1:A:394:ARG:HG2	1.58	0.84
1:B:18:GLU:HG3	1:B:401:ARG:NH1	1.96	0.81
1:B:187:MET:SD	3:B:2174:HOH:O	2.38	0.81
1:B:84:SER:OG	1:B:87:GLU:HG3	1.86	0.75
1:A:268:ASN:HD21	1:A:272:GLN:HE21	1.34	0.75
1:B:28:ASN:O	1:B:32:ARG:HD2	1.91	0.71
1:B:523:ARG:HD3	1:B:534:LEU:HD22	1.72	0.70
1:A:308:LEU:HB3	1:A:311:CYS:SG	2.35	0.66
1:B:327:ALA:O	1:B:331:GLU:HG3	1.96	0.66
1:B:545:LEU:HG	1:B:547:LEU:HD13	1.78	0.65
1:B:200:ARG:HD3	1:B:384:LEU:HD11	1.78	0.65
1:A:461:GLN:HB3	1:A:545:LEU:HD21	1.78	0.64
1:A:22:PRO:HG2	1:A:400:ALA:HB1	1.79	0.64
1:B:172:LYS:HE3	1:B:560:ILE:HD13	1.80	0.64
1:B:148:GLN:HG3	1:B:149:PRO:HD2	1.80	0.62
1:B:201:VAL:CG2	1:B:384:LEU:HG	2.31	0.61
1:A:22:PRO:CG	1:A:400:ALA:HB1	2.29	0.61
1:A:439:LEU:HG	1:A:457:LEU:HD13	1.82	0.61
1:B:308:LEU:HB3	1:B:311:CYS:SG	2.39	0.61
1:B:434:LEU:HD13	1:B:439:LEU:HD21	1.82	0.61
1:A:545:LEU:HD13	1:A:547:LEU:HD13	1.84	0.60
1:A:268:ASN:HB3	1:A:274:CYS:SG	2.42	0.60
1:B:48[A]:ARG:NH1	1:B:51:LYS:HD2	2.17	0.59
1:A:200:ARG:HD3	1:A:384:LEU:HD11	1.85	0.59
1:A:545:LEU:HD12	1:A:545:LEU:H	1.68	0.58
1:A:27:SER:OG	1:A:29:SER:HB3	2.04	0.58
1:A:532:THR:O	1:A:532:THR:HG23	2.04	0.57
1:A:236[A]:GLU:OE2	1:A:280:ARG:NH2	2.26	0.57
1:B:523:ARG:HD3	1:B:534:LEU:CD2	2.34	0.56
1:B:201:VAL:HG22	1:B:384:LEU:HG	1.86	0.56
1:A:222:ARG:HG2	1:A:222:ARG:HH11	1.70	0.56
1:A:433:LEU:HB3	1:A:439:LEU:HD13	1.87	0.56
1:A:465:ARG:HH11	1:A:545:LEU:CD1	2.19	0.56
1:A:268:ASN:HD21	1:A:272:GLN:NE2	2.02	0.56
1:B:433:LEU:HB3	1:B:439:LEU:HD13	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:465:ARG:NH1	1:B:545:LEU:HD23	2.20	0.56
1:B:82:LEU:HD13	1:B:249:ALA:HB2	1.87	0.56
1:B:397:TRP:CE2	1:B:401:ARG:HD2	2.41	0.55
1:A:27:SER:CB	1:A:399:THR:HG21	2.36	0.55
1:A:4:TYR:CE1	1:A:52:VAL:HG13	2.42	0.55
1:A:26:LEU:O	1:A:26:LEU:HD23	2.07	0.54
1:A:191:TYR:O	1:A:194:GLN:HG2	2.06	0.54
1:A:542:ALA:O	1:A:543:SER:HB2	2.07	0.54
1:B:34:HIS:HD2	3:B:2018:HOH:O	1.91	0.54
1:B:423:MET:HA	1:B:528:TRP:CZ2	2.42	0.53
1:A:27:SER:HB2	1:A:399:THR:HG21	1.89	0.53
1:B:331:GLU:CD	1:B:331:GLU:H	2.11	0.53
1:A:515:GLY:HA2	1:A:519:ALA:HB2	1.91	0.53
1:A:219:TYR:HB3	1:A:320:LEU:HD23	1.91	0.52
1:A:542:ALA:O	1:A:543:SER:CB	2.58	0.52
1:B:433:LEU:HB3	1:B:439:LEU:CD1	2.40	0.52
1:B:485:VAL:O	1:B:489:LEU:HG	2.10	0.51
1:A:236[B]:GLU:HG2	1:A:240:TYR:CZ	2.46	0.51
1:B:144:VAL:HB	1:B:394:ARG:HG2	1.93	0.50
1:B:461:GLN:HG2	1:B:541:ALA:HB3	1.93	0.50
1:A:361:GLU:HG3	1:A:370:VAL:O	2.12	0.49
1:A:433:LEU:HB3	1:A:439:LEU:CD1	2.42	0.49
1:B:527:ASN:HB3	3:B:2379:HOH:O	2.11	0.49
1:A:148:GLN:CG	1:A:149:PRO:HD2	2.43	0.49
1:B:308:LEU:HD13	1:B:335:ALA:HB1	1.95	0.49
1:A:144:VAL:HG22	1:A:394:ARG:CG	2.37	0.48
1:A:227:THR:HB	1:A:347[B]:SER:O	2.13	0.48
1:B:150:GLU:O	1:B:150:GLU:HG2	2.14	0.48
1:A:506:SER:O	1:A:510:LYS:HG3	2.13	0.48
1:A:483:ASN:N	1:A:483:ASN:HD22	2.11	0.48
1:A:556:SER:HB2	3:A:2296:HOH:O	2.14	0.48
1:B:241:GLN:OE1	1:B:250:ARG:HG3	2.13	0.48
1:B:416:ALA:N	1:B:417:PRO:CD	2.77	0.47
1:A:233:ILE:HD13	1:A:261:TYR:O	2.14	0.47
1:A:419:LEU:HD11	1:A:497:LEU:HD13	1.95	0.47
1:A:178:VAL:HG23	3:A:2150:HOH:O	2.14	0.47
1:A:456:PRO:C	1:A:458:ASP:H	2.18	0.47
1:A:465:ARG:HH11	1:A:545:LEU:HD12	1.81	0.46
1:A:556:SER:HB3	3:A:2295:HOH:O	2.15	0.46
1:A:532:THR:HG22	2:A:1571:SO4:S	2.54	0.46
1:A:398:GLU:OE2	1:A:408:TRP:HD1	1.99	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:233:ILE:HD13	1:B:261:TYR:O	2.15	0.46
1:B:32:ARG:NH2	3:B:2032:HOH:O	2.49	0.45
1:A:236[B]:GLU:OE2	1:A:240:TYR:OH	2.24	0.45
1:A:390:THR:HB	1:A:391:PRO:HD3	1.98	0.45
1:B:150:GLU:O	1:B:151:LYS:C	2.55	0.45
1:B:346:TYR:O	1:B:347[A]:SER:HB3	2.17	0.45
1:B:542:ALA:O	1:B:545:LEU:HD22	2.18	0.43
1:A:79:LYS:NZ	3:A:2082:HOH:O	2.50	0.43
1:B:48[A]:ARG:HH11	1:B:51:LYS:HD2	1.80	0.43
1:A:83:LEU:HB2	1:A:173:MET:HA	1.99	0.43
1:A:531:ARG:N	2:A:1571:SO4:O4	2.50	0.43
1:A:455:GLU:O	1:A:458:ASP:HB2	2.18	0.43
1:A:21:LEU:HD12	1:A:21:LEU:HA	1.87	0.43
1:A:27:SER:HB3	1:A:399:THR:HG21	2.02	0.42
1:B:465:ARG:HG3	1:B:545:LEU:HD21	2.01	0.42
1:A:160:ILE:HA	1:A:282:SER:OG	2.20	0.42
1:B:18:GLU:HG3	1:B:401:ARG:HH12	1.77	0.42
1:B:430:PHE:O	1:B:434:LEU:HB2	2.19	0.42
1:B:200:ARG:HD3	1:B:384:LEU:CD1	2.49	0.42
1:A:82:LEU:HD13	1:A:249:ALA:HB2	2.00	0.42
1:A:466:LEU:HD21	1:A:551:PHE:HE1	1.84	0.42
1:B:51:LYS:HB2	1:B:51:LYS:HE3	1.89	0.42
1:A:314:LEU:HB3	1:A:321:VAL:HG13	2.01	0.41
1:A:461:GLN:HB3	1:A:545:LEU:CD2	2.46	0.41
1:B:93:PRO:HA	1:B:94:PRO:HD3	1.87	0.41
1:A:364:THR:HA	1:A:368:SER:O	2.20	0.41
1:A:523:ARG:O	1:A:527:ASN:HB2	2.20	0.41
1:B:372:VAL:HG22	1:B:382:TYR:CD2	2.56	0.41
1:A:148:GLN:C	1:A:150:GLU:H	2.24	0.41
1:A:308:LEU:HD13	1:A:335:ALA:HB1	2.02	0.41
1:B:21:LEU:HD12	1:B:22:PRO:HD2	2.02	0.41
1:B:464:GLU:HG3	1:B:469:LEU:HD13	2.01	0.41
1:B:470:SER:O	1:B:474:LEU:HG	2.21	0.41
1:B:81:LYS:HG2	1:B:177:ASP:OD1	2.21	0.41
1:A:220:ASP:HB2	3:A:2174:HOH:O	2.19	0.40
1:A:27:SER:C	1:A:29:SER:N	2.73	0.40
1:A:459:LEU:N	1:A:460:PRO:CD	2.84	0.40
1:B:390:THR:HB	1:B:391:PRO:HD3	2.03	0.40
1:B:459:LEU:HD12	1:B:459:LEU:HA	1.99	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	561/579 (97%)	543 (97%)	15 (3%)	3 (0%)	29	34
1	B	564/579 (97%)	550 (98%)	11 (2%)	3 (0%)	29	34
All	All	1125/1158 (97%)	1093 (97%)	26 (2%)	6 (0%)	34	34

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	543	SER
1	A	347[A]	SER
1	A	347[B]	SER
1	B	151	LYS
1	B	347[A]	SER
1	B	347[B]	SER

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	481/493 (98%)	460 (96%)	21 (4%)	28	37
1	B	482/493 (98%)	464 (96%)	18 (4%)	34	45
All	All	963/986 (98%)	924 (96%)	39 (4%)	30	42

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	LEU
1	A	21	LEU
1	A	47	LEU
1	A	52	VAL
1	A	212	LYS
1	A	308	LEU
1	A	319	ASP
1	A	322	VAL
1	A	330	GLN
1	A	331	GLU
1	A	362	LEU
1	A	364	THR
1	A	380	ARG
1	A	431	SER
1	A	433	LEU
1	A	434	LEU
1	A	457	LEU
1	A	459	LEU
1	A	483	ASN
1	A	545	LEU
1	A	556	SER
1	B	32	ARG
1	B	47	LEU
1	B	106	LYS
1	B	151	LYS
1	B	308	LEU
1	B	319	ASP
1	B	355	GLN
1	B	362	LEU
1	B	365	SER
1	B	431	SER
1	B	433	LEU
1	B	434	LEU
1	B	439	LEU
1	B	459	LEU
1	B	461	GLN
1	B	469	LEU
1	B	534	LEU
1	B	547	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	ASN
1	A	272	GLN
1	A	483	ASN
1	A	514	GLN
1	B	34	HIS
1	B	35	ASN
1	B	206	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

26 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	A	1567[B]	-	4,4,4	0.13	0	6,6,6	0.11	0
2	SO4	A	1567[A]	-	4,4,4	0.15	0	6,6,6	0.20	0
2	SO4	A	1002[A]	-	4,4,4	0.14	0	6,6,6	0.06	0
2	SO4	B	1001[A]	-	4,4,4	0.14	0	6,6,6	0.15	0
2	SO4	A	1002[B]	-	4,4,4	0.14	0	6,6,6	0.07	0
2	SO4	A	1571	-	4,4,4	0.16	0	6,6,6	0.10	0
2	SO4	B	1568	-	4,4,4	0.14	0	6,6,6	0.09	0
2	SO4	B	1567	-	4,4,4	0.15	0	6,6,6	0.09	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	A	1003[A]	-	4,4,4	0.14	0	6,6,6	0.13	0
2	SO4	A	1003[B]	-	4,4,4	0.14	0	6,6,6	0.07	0
2	SO4	A	1570	-	4,4,4	0.13	0	6,6,6	0.12	0
2	SO4	A	1003[C]	-	4,4,4	0.14	0	6,6,6	0.12	0
2	SO4	A	1003[D]	-	4,4,4	0.12	0	6,6,6	0.11	0
2	SO4	B	1001[B]	-	4,4,4	0.12	0	6,6,6	0.08	0
2	SO4	A	1568	-	4,4,4	0.13	0	6,6,6	0.15	0
2	SO4	A	1001	-	4,4,4	0.14	0	6,6,6	0.10	0
2	SO4	B	1571	-	4,4,4	0.14	0	6,6,6	0.12	0
2	SO4	B	1002[D]	-	4,4,4	0.15	0	6,6,6	0.10	0
2	SO4	B	1002[B]	-	4,4,4	0.16	0	6,6,6	0.08	0
2	SO4	B	1002[C]	-	4,4,4	0.15	0	6,6,6	0.08	0
2	SO4	B	1570	-	4,4,4	0.14	0	6,6,6	0.17	0
2	SO4	B	1002[A]	-	4,4,4	0.15	0	6,6,6	0.06	0
2	SO4	A	1569	-	4,4,4	0.15	0	6,6,6	0.07	0
2	SO4	B	1572	-	4,4,4	0.14	0	6,6,6	0.09	0
2	SO4	B	1566	-	4,4,4	0.11	0	6,6,6	0.34	0
2	SO4	B	1569	-	4,4,4	0.13	0	6,6,6	0.07	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.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1571	SO4	2	0

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	562/579 (97%)	0.05	42 (7%) 14 18	13, 37, 89, 134	0
1	B	563/579 (97%)	-0.43	9 (1%) 72 77	13, 26, 58, 128	0
All	All	1125/1158 (97%)	-0.19	51 (4%) 33 39	13, 30, 78, 134	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	152	GLY	8.9
1	B	151	LYS	6.1
1	A	542	ALA	5.8
1	A	23	ILE	5.8
1	B	152	GLY	5.0
1	B	153	GLY	4.5
1	A	523	ARG	4.5
1	A	544	GLN	4.3
1	A	534	LEU	4.2
1	A	149	PRO	4.0
1	A	535	LYS	3.9
1	A	532	THR	3.9
1	A	25	PRO	3.9
1	A	26	LEU	3.8
1	A	469	LEU	3.8
1	A	546	ASP	3.7
1	A	545	LEU	3.6
1	A	543	SER	3.6
1	A	24	ASN	3.6
1	A	519	ALA	3.6
1	A	536	LEU	3.6
1	A	537	THR	3.4
1	A	511	LEU	3.4
1	A	539	ILE	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	545	LEU	3.4
1	A	548	SER	3.1
1	A	379	LYS	3.0
1	B	150	GLU	3.0
1	B	149	PRO	3.0
1	A	538	PRO	3.0
1	A	212	LYS	3.0
1	A	513	SER	2.9
1	A	531	ARG	2.9
1	A	148	GLN	2.7
1	A	153	GLY	2.7
1	B	543	SER	2.7
1	A	509	ALA	2.6
1	A	540	PRO	2.6
1	A	150	GLU	2.5
1	A	541	ALA	2.4
1	B	544	GLN	2.3
1	A	520	THR	2.3
1	A	331	GLU	2.2
1	A	512	LEU	2.2
1	A	309	GLN	2.2
1	A	529	ALA	2.1
1	B	148	GLN	2.1
1	A	530	VAL	2.1
1	A	517	ARG	2.1
1	A	377	SER	2.1
1	A	310	ASP	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 carbohydrates 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
2	SO4	A	1570	5/5	0.74	0.28	91,95,96,99	5
2	SO4	A	1571	5/5	0.81	0.20	118,124,125,128	0
2	SO4	B	1570	5/5	0.83	0.16	93,93,96,96	0
2	SO4	A	1569	5/5	0.87	0.23	114,116,120,120	0
2	SO4	B	1572	5/5	0.88	0.23	82,83,89,89	5
2	SO4	B	1571	5/5	0.89	0.19	101,102,105,113	0
2	SO4	B	1002[D]	5/5	0.91	0.40	20,22,26,30	5
2	SO4	B	1002[A]	5/5	0.91	0.40	21,21,22,28	5
2	SO4	B	1002[B]	5/5	0.91	0.40	4,30,33,34	5
2	SO4	B	1002[C]	5/5	0.91	0.40	12,15,20,24	5
2	SO4	A	1003[C]	5/5	0.92	0.58	12,23,25,29	5
2	SO4	A	1003[D]	5/5	0.92	0.58	12,25,32,35	5
2	SO4	A	1568	5/5	0.92	0.25	38,49,61,67	5
2	SO4	A	1001	5/5	0.92	0.26	110,111,113,115	0
2	SO4	A	1003[B]	5/5	0.92	0.58	12,15,18,29	5
2	SO4	A	1003[A]	5/5	0.92	0.58	27,30,39,42	5
2	SO4	B	1569	5/5	0.92	0.19	87,88,91,97	0
2	SO4	A	1567[A]	5/5	0.93	0.17	24,35,48,49	5
2	SO4	A	1567[B]	5/5	0.93	0.17	25,36,40,46	5
2	SO4	B	1001[B]	5/5	0.94	0.22	49,50,55,56	5
2	SO4	A	1002[A]	5/5	0.94	0.34	56,60,62,63	5
2	SO4	B	1001[A]	5/5	0.94	0.22	28,36,43,48	5
2	SO4	A	1002[B]	5/5	0.94	0.34	34,45,48,49	5
2	SO4	B	1568	5/5	0.95	0.12	71,73,76,79	5
2	SO4	B	1567	5/5	0.97	0.09	64,69,73,75	0
2	SO4	B	1566	5/5	0.98	0.11	40,41,47,51	0

6.5 Other polymers

There are no such residues in this entry.