



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 05:51 PM UTC

PDB ID : 5VMK / pdb_00005vmk
Title : Crystal structure of a bifunctional GlmU UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase from *Acinetobacter baumannii*
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2017-04-27
Resolution : 2.55 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

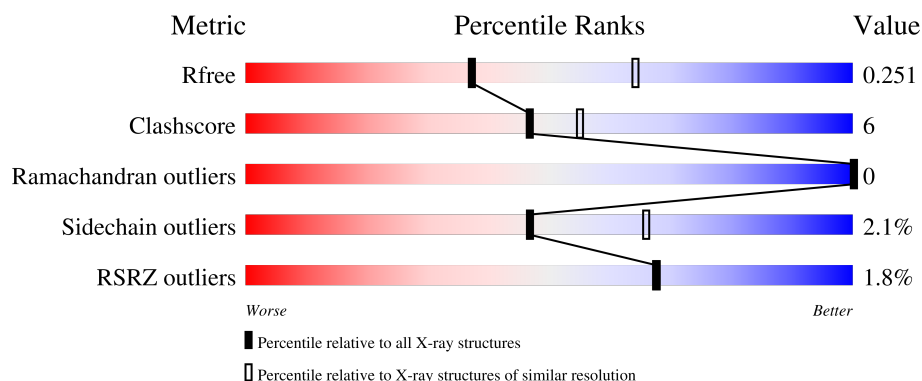
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1091 (2.54-2.54)
Clashscore	190562	1120 (2.54-2.54)
Ramachandran outliers	187476	1106 (2.54-2.54)
Sidechain outliers	187428	1106 (2.54-2.54)
RSRZ outliers	180081	1091 (2.54-2.54)

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	462	0% 86% 11% .
1	B	462	2% 81% 12% 7%
1	C	462	3% 77% 12% . 10%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9670 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 Bifunctional protein GlmU.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	449	Total	C	N	O	S	0	1	0
			3294	2073	580	632	9			
1	B	430	Total	C	N	O	S	0	0	0
			3055	1920	544	583	8			
1	C	415	Total	C	N	O	S	0	0	0
			2930	1833	522	567	8			

There are 24 discrepancies between the modelled and reference sequences:

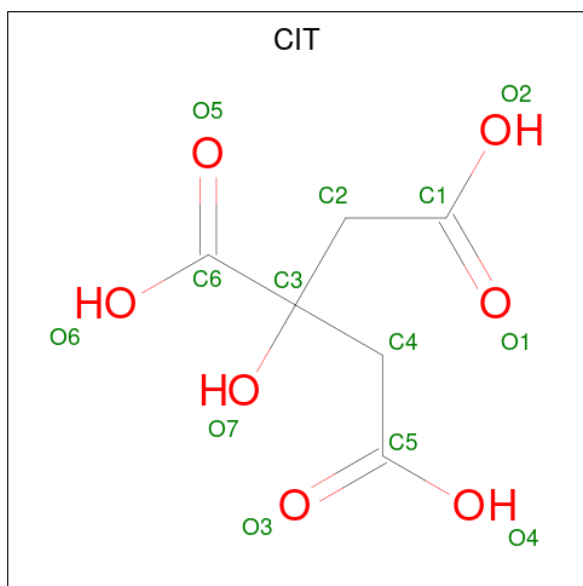
Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	expression tag	UNP A0A0D5YCC7
A	-6	ALA	-	expression tag	UNP A0A0D5YCC7
A	-5	HIS	-	expression tag	UNP A0A0D5YCC7
A	-4	HIS	-	expression tag	UNP A0A0D5YCC7
A	-3	HIS	-	expression tag	UNP A0A0D5YCC7
A	-2	HIS	-	expression tag	UNP A0A0D5YCC7
A	-1	HIS	-	expression tag	UNP A0A0D5YCC7
A	0	HIS	-	expression tag	UNP A0A0D5YCC7
B	-7	MET	-	expression tag	UNP A0A0D5YCC7
B	-6	ALA	-	expression tag	UNP A0A0D5YCC7
B	-5	HIS	-	expression tag	UNP A0A0D5YCC7
B	-4	HIS	-	expression tag	UNP A0A0D5YCC7
B	-3	HIS	-	expression tag	UNP A0A0D5YCC7
B	-2	HIS	-	expression tag	UNP A0A0D5YCC7
B	-1	HIS	-	expression tag	UNP A0A0D5YCC7
B	0	HIS	-	expression tag	UNP A0A0D5YCC7
C	-7	MET	-	expression tag	UNP A0A0D5YCC7
C	-6	ALA	-	expression tag	UNP A0A0D5YCC7
C	-5	HIS	-	expression tag	UNP A0A0D5YCC7
C	-4	HIS	-	expression tag	UNP A0A0D5YCC7
C	-3	HIS	-	expression tag	UNP A0A0D5YCC7
C	-2	HIS	-	expression tag	UNP A0A0D5YCC7
C	-1	HIS	-	expression tag	UNP A0A0D5YCC7

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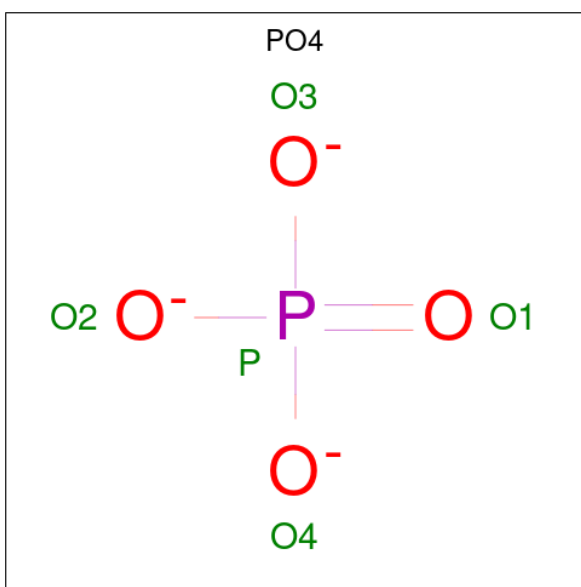
Chain	Residue	Modelled	Actual	Comment	Reference
C	0	HIS	-	expression tag	UNP A0A0D5YCC7

- Molecule 2 is CITRIC ACID (CCD ID: CIT) (formula: $C_6H_8O_7$).



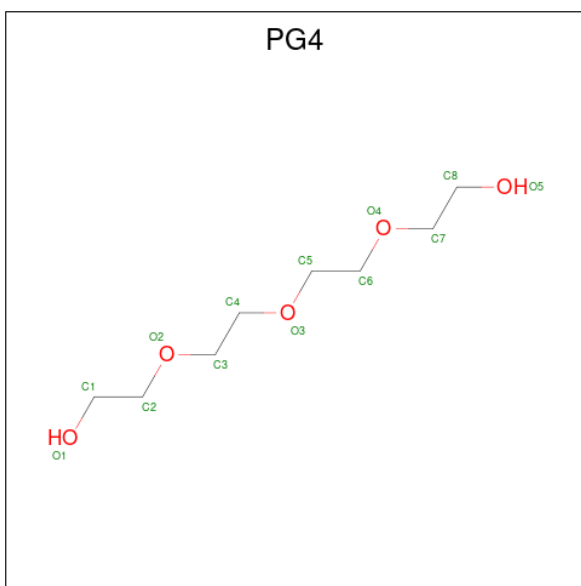
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			13	6	7		
2	B	1	Total	C	O	0	0
			13	6	7		
2	C	1	Total	C	O	0	0
			13	6	7		

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



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

- Molecule 4 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			13	8	5		
4	C	1	Total	C	O	0	0
			13	8	5		
4	C	1	Total	C	O	0	0
			13	8	5		

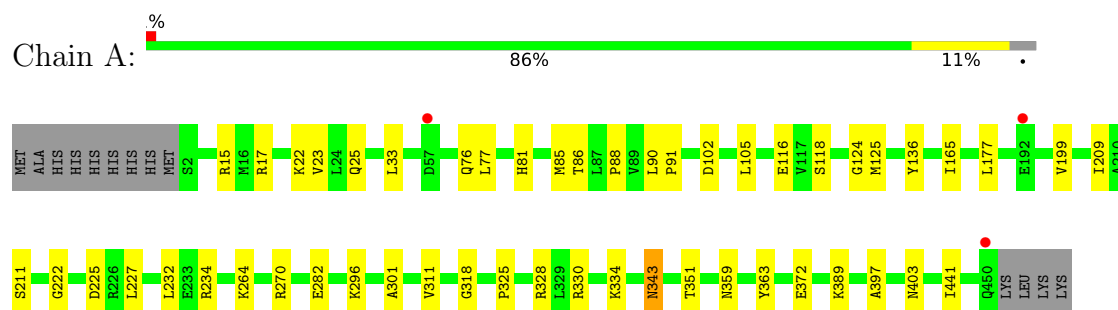
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	108	Total 108	O 108	0	0
5	B	93	Total 93	O 93	0	0
5	C	107	Total 107	O 107	0	0

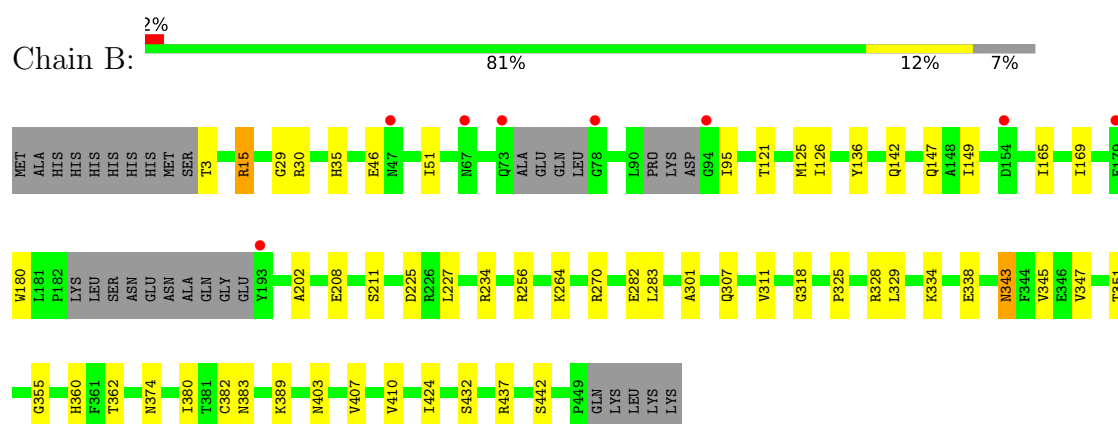
3 Residue-property plots [i](#)

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.

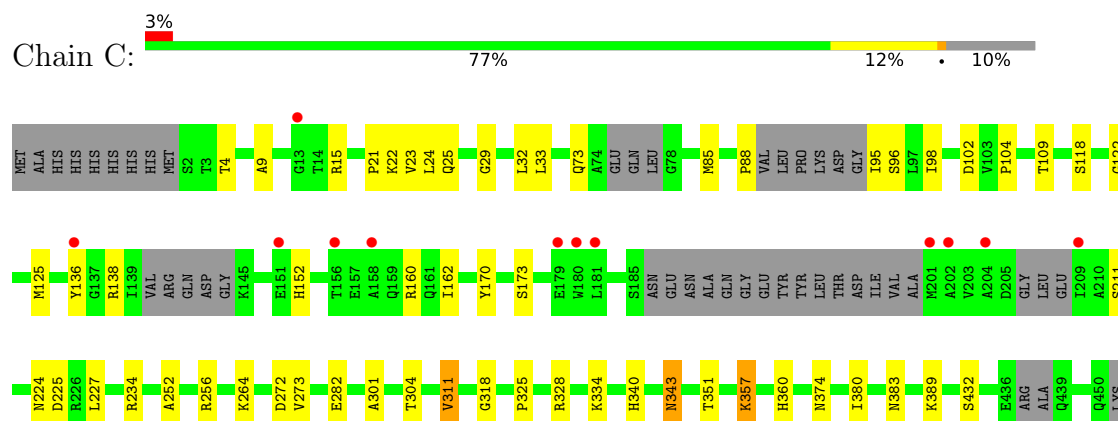
• Molecule 1: Bifunctional protein GlmU



• Molecule 1: Bifunctional protein GlmU



• Molecule 1: Bifunctional protein GlmU



LEU
LYS
LYS

4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	96.62Å 96.62Å 262.42Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.51 – 2.55 47.51 – 2.55	Depositor EDS
% Data completeness (in resolution range)	99.6 (47.51-2.55) 99.8 (47.51-2.55)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.51 (at 2.54Å)	Xtriage
Refinement program	PHENIX (dev_2744: ???)	Depositor
R, R_{free}	0.185 , 0.248 0.189 , 0.251	Depositor DCC
R_{free} test set	1948 reflections (4.12%)	wwPDB-VP
Wilson B-factor (Å ²)	44.7	Xtriage
Anisotropy	0.343	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 70.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.017 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9670	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 21.67 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.6796e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: PG4, CIT, PO4

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	0.33	0/3346	0.53	0/4555
1	B	0.31	0/3097	0.51	0/4215
1	C	0.32	0/2966	0.52	0/4033
All	All	0.32	0/9409	0.52	0/12803

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	3294	0	3249	38	0
1	B	3055	0	2918	36	0
1	C	2930	0	2771	35	0
2	A	13	0	5	0	0
2	B	13	0	5	3	0
2	C	13	0	5	1	0
3	A	5	0	0	1	0
4	B	13	0	18	3	0
4	C	26	0	36	4	0
5	A	108	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	93	0	0	3	0
5	C	107	0	0	2	0
All	All	9670	0	9007	105	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 (105) 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:B:29:GLY:H	4:B:502:PG4:H72	1.50	0.75
1:B:234:ARG:NH1	5:B:602:HOH:O	2.16	0.75
1:A:15[B]:ARG:NH1	3:A:502:PO4:O3	2.23	0.71
1:B:282:GLU:OE2	5:B:601:HOH:O	2.10	0.69
1:A:234:ARG:NH1	5:A:601:HOH:O	2.22	0.68
1:C:234:ARG:NH1	5:C:601:HOH:O	2.27	0.64
1:C:138:ARG:NH2	1:C:160:ARG:O	2.32	0.62
1:B:270:ARG:HB3	4:C:503:PG4:H42	1.82	0.61
1:B:15:ARG:HB3	1:B:225:ASP:HB3	1.83	0.61
1:A:15[B]:ARG:HB2	1:A:225:ASP:HB3	1.84	0.60
1:B:29:GLY:N	4:B:502:PG4:H72	2.19	0.57
1:A:270:ARG:HB3	4:B:502:PG4:H31	1.86	0.57
1:C:264:LYS:HB3	1:C:282:GLU:HG2	1.88	0.55
1:A:15[A]:ARG:HB3	1:A:225:ASP:HB3	1.89	0.54
1:A:264:LYS:HB3	1:A:282:GLU:HG2	1.88	0.54
1:C:23:VAL:HB	1:C:33:LEU:HB2	1.88	0.54
1:C:85:MET:O	1:C:88:PRO:HD2	2.08	0.54
1:B:30:ARG:NH1	5:B:608:HOH:O	2.41	0.53
1:B:360:HIS:NE2	2:C:502:CIT:O7	2.41	0.53
1:A:325:PRO:O	1:A:343:ASN:HA	2.09	0.52
1:B:227:LEU:HD12	1:B:227:LEU:H	1.75	0.52
1:C:311:VAL:HG22	1:C:328:ARG:HG2	1.92	0.52
1:C:340:HIS:HD2	5:C:686:HOH:O	1.93	0.51
1:A:334:LYS:HD2	1:A:351:THR:HG22	1.92	0.51
1:B:125:MET:HE1	1:B:149:ILE:HD11	1.92	0.50
1:C:9:ALA:HB1	1:C:23:VAL:HG21	1.92	0.50
1:C:15:ARG:HB3	1:C:225:ASP:HB3	1.93	0.50
1:A:296:LYS:NZ	5:A:607:HOH:O	2.43	0.49
1:A:389:LYS:NZ	5:A:603:HOH:O	2.30	0.49
1:C:98:ILE:HD12	1:C:170:TYR:HB2	1.96	0.48
1:A:359:ASN:HD22	2:B:501:CIT:H42	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:359:ASN:ND2	2:B:501:CIT:H42	2.28	0.48
1:A:85:MET:O	1:A:88:PRO:HD2	2.15	0.47
1:C:227:LEU:H	1:C:227:LEU:HD12	1.79	0.47
1:A:311:VAL:CG2	1:A:328:ARG:HG2	2.44	0.47
1:A:199:VAL:HG13	1:A:209:ILE:CD1	2.44	0.47
1:B:125:MET:O	1:B:211:SER:HA	2.14	0.47
1:B:121:THR:HG21	1:B:208:GLU:O	2.14	0.47
1:C:118:SER:O	1:C:122:GLY:N	2.37	0.47
1:B:136:TYR:CD1	1:B:165:ILE:HD13	2.50	0.47
1:C:4:THR:O	1:C:96:SER:HA	2.14	0.47
1:C:29:GLY:H	4:C:503:PG4:H11	1.79	0.46
1:C:383:ASN:O	1:C:389:LYS:HA	2.16	0.46
1:A:136:TYR:CD1	1:A:165:ILE:HD13	2.50	0.46
1:A:403:ASN:CG	1:B:380:ILE:HD12	2.40	0.46
1:C:21:PRO:HD2	1:C:24:LEU:HD12	1.97	0.46
1:A:227:LEU:HD12	1:A:227:LEU:H	1.79	0.46
1:B:180:TRP:CZ2	1:B:202:ALA:HA	2.51	0.46
1:B:403:ASN:CG	1:C:380:ILE:HD12	2.42	0.45
1:A:118:SER:OG	1:A:124:GLY:HA3	2.16	0.45
1:C:138:ARG:NE	1:C:162:ILE:O	2.45	0.45
1:B:325:PRO:O	1:B:343:ASN:HA	2.16	0.45
1:C:325:PRO:O	1:C:343:ASN:HA	2.16	0.44
1:A:372:GLU:O	1:A:397:ALA:HA	2.16	0.44
1:B:3:THR:O	1:B:46:GLU:N	2.46	0.44
1:B:30:ARG:HG3	1:B:35:HIS:NE2	2.32	0.44
4:C:503:PG4:H32	4:C:503:PG4:H51	1.85	0.44
1:B:383:ASN:O	1:B:389:LYS:HA	2.18	0.44
1:B:142:GLN:H	1:B:147:GLN:HE21	1.65	0.44
1:C:95:ILE:HA	1:C:173:SER:HA	2.00	0.43
1:C:252:ALA:HB2	4:C:501:PG4:H41	2.00	0.43
1:A:125:MET:O	1:A:211:SER:HA	2.17	0.43
1:B:345:VAL:HG13	1:B:362:THR:HG23	1.99	0.43
1:A:311:VAL:HG22	1:A:328:ARG:HG2	2.01	0.43
1:B:382:CYS:HB2	1:B:407:VAL:HA	2.00	0.43
1:B:227:LEU:HD12	1:B:227:LEU:N	2.33	0.43
1:B:264:LYS:HB3	1:B:282:GLU:HG2	2.00	0.43
1:C:125:MET:O	1:C:211:SER:HA	2.19	0.43
1:A:105:LEU:HD12	1:A:232:LEU:HD11	2.01	0.42
1:B:311:VAL:HG22	1:B:328:ARG:HG2	2.01	0.42
1:C:22:LYS:O	1:C:25:GLN:HG2	2.19	0.42
1:A:77:LEU:HB2	1:A:81:HIS:ND1	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:126:ILE:HD12	1:B:169:ILE:HG21	2.01	0.42
1:C:32:LEU:HD22	1:C:104:PRO:HG3	1.99	0.42
1:B:410:VAL:HG21	1:B:424:ILE:HG22	2.01	0.42
1:A:301:ALA:HB3	1:A:318:GLY:C	2.44	0.42
1:B:329:LEU:HD22	1:B:347:VAL:HB	2.01	0.42
1:A:264:LYS:NZ	5:A:616:HOH:O	2.53	0.42
1:A:102:ASP:O	1:A:222:GLY:HA2	2.20	0.42
1:A:441:ILE:HD11	1:B:437:ARG:HB2	2.02	0.42
1:B:301:ALA:HB3	1:B:318:GLY:C	2.45	0.42
1:C:340:HIS:HB2	1:C:357:LYS:HB3	2.02	0.42
1:B:256:ARG:HD3	1:C:256:ARG:HG2	2.01	0.41
1:C:22:LYS:HD3	1:C:102:ASP:CB	2.50	0.41
1:A:77:LEU:HD12	1:A:81:HIS:CE1	2.55	0.41
1:A:177:LEU:HD23	1:A:177:LEU:HA	1.90	0.41
1:B:282:GLU:O	1:B:283:LEU:HD23	2.19	0.41
1:B:334:LYS:HB2	1:B:351:THR:HG22	2.01	0.41
1:C:301:ALA:HB3	1:C:318:GLY:C	2.45	0.41
1:A:22:LYS:O	1:A:25:GLN:HG2	2.20	0.41
1:A:90:LEU:HA	1:A:91:PRO:HD3	1.94	0.41
1:A:76:GLN:O	1:A:77:LEU:HD23	2.21	0.41
1:A:227:LEU:HD12	1:A:227:LEU:N	2.36	0.41
1:A:328:ARG:NH1	1:A:330:ARG:HD2	2.35	0.41
1:B:389:LYS:HE3	2:B:501:CIT:O6	2.20	0.41
1:C:272:ASP:OD1	1:C:273:VAL:N	2.51	0.41
1:A:363:TYR:CZ	1:C:360:HIS:CE1	3.09	0.40
1:A:86:THR:O	1:A:90:LEU:HB2	2.22	0.40
1:C:15:ARG:HE	1:C:224:ASN:HB3	1.86	0.40
1:B:338:GLU:HB2	1:B:355:GLY:HA2	2.04	0.40
1:C:334:LYS:HB2	1:C:351:THR:HG22	2.02	0.40
1:A:23:VAL:HB	1:A:33:LEU:HB2	2.04	0.40
1:C:22:LYS:HD3	1:C:102:ASP:HB3	2.03	0.40
1:C:136:TYR:O	1:C:152:HIS:HB2	2.21	0.40
1:C:311:VAL:CG2	1:C:328:ARG:HG2	2.51	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	448/462 (97%)	437 (98%)	11 (2%)	0	100	100
1	B	422/462 (91%)	413 (98%)	9 (2%)	0	100	100
1	C	401/462 (87%)	393 (98%)	8 (2%)	0	100	100
All	All	1271/1386 (92%)	1243 (98%)	28 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	334/372 (90%)	331 (99%)	3 (1%)	70	82
1	B	289/372 (78%)	281 (97%)	8 (3%)	38	57
1	C	278/372 (75%)	270 (97%)	8 (3%)	37	55
All	All	901/1116 (81%)	882 (98%)	19 (2%)	47	66

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	ARG
1	A	116	GLU
1	A	343	ASN
1	B	15	ARG
1	B	51	ILE

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Mol	Chain	Res	Type
1	B	95	ILE
1	B	307	GLN
1	B	343	ASN
1	B	374	ASN
1	B	432	SER
1	B	442	SER
1	C	73	GLN
1	C	109	THR
1	C	304	THR
1	C	311	VAL
1	C	343	ASN
1	C	357	LYS
1	C	374	ASN
1	C	432	SER

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	19	GLN
1	A	47	ASN
1	A	188	ASN
1	A	359	ASN
1	A	440	GLN
1	B	280	ASN
1	B	307	GLN
1	B	343	ASN
1	B	374	ASN
1	C	19	GLN
1	C	129	HIS
1	C	163	GLN
1	C	239	GLN
1	C	320	ASN
1	C	440	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

7 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	CIT	A	501	-	12,12,12	1.21	1 (8%)	17,17,17	1.60	4 (23%)
3	PO4	A	502	-	4,4,4	0.82	0	6,6,6	0.65	0
4	PG4	B	502	-	12,12,12	0.54	0	11,11,11	0.31	0
2	CIT	C	502	-	12,12,12	1.17	0	17,17,17	1.44	3 (17%)
2	CIT	B	501	-	12,12,12	1.24	1 (8%)	17,17,17	1.59	4 (23%)
4	PG4	C	501	-	12,12,12	0.55	0	11,11,11	0.40	0
4	PG4	C	503	-	12,12,12	0.54	0	11,11,11	0.46	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CIT	A	501	-	-	0/16/16/16	-
4	PG4	B	502	-	-	4/10/10/10	-
2	CIT	C	502	-	-	3/16/16/16	-
2	CIT	B	501	-	-	3/16/16/16	-
4	PG4	C	501	-	-	5/10/10/10	-
4	PG4	C	503	-	-	5/10/10/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	CIT	C3-C6	-2.30	1.51	1.53
2	A	501	CIT	C3-C6	-2.09	1.51	1.53

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	CIT	O6-C6-C3	3.94	120.69	113.14
2	A	501	CIT	O6-C6-C3	3.53	119.92	113.14
2	C	502	CIT	O6-C6-C3	3.34	119.54	113.14
2	B	501	CIT	O7-C3-C6	-2.20	105.84	108.96
2	B	501	CIT	O2-C1-C2	2.17	121.23	114.35
2	A	501	CIT	O4-C5-O3	-2.14	117.82	123.33
2	C	502	CIT	O2-C1-C2	2.13	121.09	114.35
2	C	502	CIT	O4-C5-O3	-2.10	117.94	123.33
2	A	501	CIT	C3-C2-C1	-2.04	108.34	113.92
2	B	501	CIT	O4-C5-O3	-2.02	118.13	123.33
2	A	501	CIT	O2-C1-C2	2.01	120.72	114.35

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	501	CIT	C1-C2-C3-C4
2	B	501	CIT	C1-C2-C3-C6
2	C	502	CIT	C1-C2-C3-C4
2	C	502	CIT	C1-C2-C3-C6
4	C	501	PG4	O2-C3-C4-O3
2	B	501	CIT	C1-C2-C3-O7
2	C	502	CIT	C1-C2-C3-O7
4	C	503	PG4	O3-C5-C6-O4
4	C	503	PG4	O4-C7-C8-O5
4	C	501	PG4	C5-C6-O4-C7
4	B	502	PG4	O4-C7-C8-O5
4	B	502	PG4	C8-C7-O4-C6
4	C	501	PG4	C1-C2-O2-C3
4	C	503	PG4	C5-C6-O4-C7
4	C	501	PG4	C4-C3-O2-C2
4	C	503	PG4	C8-C7-O4-C6
4	C	501	PG4	O4-C7-C8-O5
4	B	502	PG4	O3-C5-C6-O4
4	B	502	PG4	C5-C6-O4-C7

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Mol	Chain	Res	Type	Atoms
4	C	503	PG4	C3-C4-O3-C5

There are no ring outliers.

6 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	502	PO4	1	0
4	B	502	PG4	3	0
2	C	502	CIT	1	0
2	B	501	CIT	3	0
4	C	501	PG4	1	0
4	C	503	PG4	3	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	449/462 (97%)	-0.38	3 (0%) 84 86	24, 51, 89, 114	1 (0%)
1	B	430/462 (93%)	-0.08	8 (1%) 66 66	25, 60, 108, 134	0
1	C	415/462 (89%)	-0.09	12 (2%) 53 55	25, 53, 124, 165	0
All	All	1294/1386 (93%)	-0.19	23 (1%) 67 68	24, 54, 110, 165	1 (0%)

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	193	TYR	4.2
1	B	78	GLY	3.9
1	C	180	TRP	3.8
1	C	201	MET	3.8
1	C	202	ALA	2.9
1	A	450	GLN	2.8
1	B	154	ASP	2.8
1	B	94	GLY	2.6
1	C	156	THR	2.6
1	B	47	ASN	2.4
1	C	204	ALA	2.4
1	A	57	ASP	2.4
1	C	151	GLU	2.4
1	A	192	GLU	2.3
1	B	179	GLU	2.3
1	B	67	ASN	2.2
1	C	13	GLY	2.2
1	B	73	GLN	2.1
1	C	181	LEU	2.1
1	C	158	ALA	2.1
1	C	179	GLU	2.1
1	C	136	TYR	2.0
1	C	209	ILE	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
3	PO4	A	502	5/5	0.65	0.12	115,117,119,120	0
2	CIT	A	501	13/13	0.90	0.10	61,66,83,83	0
2	CIT	B	501	13/13	0.93	0.08	58,66,70,74	0
4	PG4	C	503	13/13	0.93	0.12	52,57,76,79	0
4	PG4	C	501	13/13	0.94	0.10	45,55,62,64	0
2	CIT	C	502	13/13	0.94	0.07	55,60,64,65	0
4	PG4	B	502	13/13	0.95	0.09	47,53,71,75	0

6.5 Other polymers [i](#)

There are no such residues in this entry.