



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 08:31 PM EDT

PDB ID : 4CE7 / pdb_00004ce7
Title : Crystal structure of a novel unsaturated beta-glucuronyl hydrolase enzyme, belonging to family GH105, involved in ulvan degradation
Authors : Nyvall Collen, P.; Jeudy, A.; Groisillier, A.; Coutinho, P.M.; Helbert, W.; Czjzek, M.
Deposited on : 2013-11-09
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

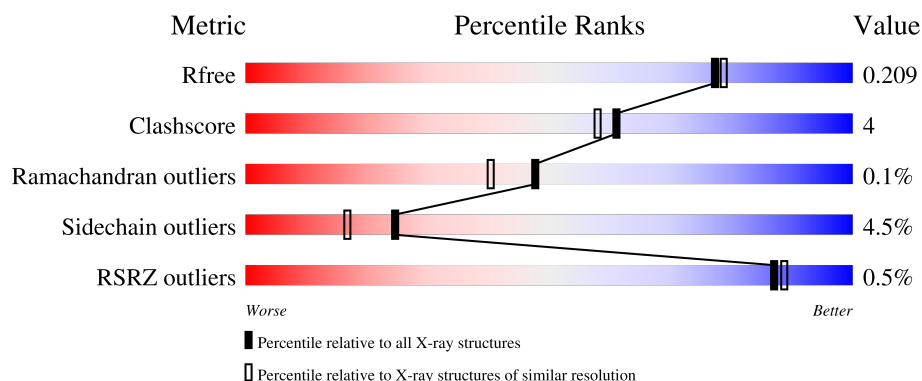
1 Overall quality at a glance

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	370	% 78% 14% • 7%
1	B	370	82% 10% • 6%
1	C	370	% 80% 11% • 8%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9354 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 UNSATURATED 3S-RHAMNOGLYCURONYL HYDROLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	345	Total	C	N	O	S	0	3	0
			2868	1841	479	535	13			
1	B	348	Total	C	N	O	S	0	2	0
			2873	1843	480	537	13			
1	C	342	Total	C	N	O	S	0	5	0
			2855	1832	477	533	13			

There are 24 discrepancies between the modelled and reference sequences:

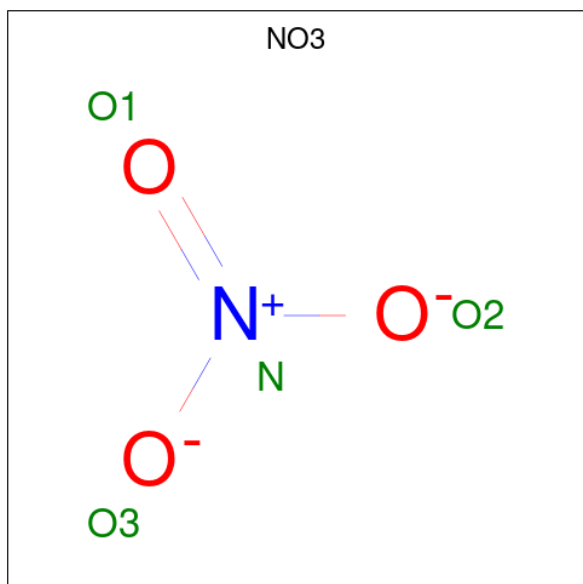
Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	HIS	-	expression tag	UNP L7P9J4
A	-6	HIS	-	expression tag	UNP L7P9J4
A	-5	HIS	-	expression tag	UNP L7P9J4
A	-4	HIS	-	expression tag	UNP L7P9J4
A	-3	HIS	-	expression tag	UNP L7P9J4
A	-2	HIS	-	expression tag	UNP L7P9J4
A	-1	GLY	-	expression tag	UNP L7P9J4
A	0	SER	-	expression tag	UNP L7P9J4
B	-7	HIS	-	expression tag	UNP L7P9J4
B	-6	HIS	-	expression tag	UNP L7P9J4
B	-5	HIS	-	expression tag	UNP L7P9J4
B	-4	HIS	-	expression tag	UNP L7P9J4
B	-3	HIS	-	expression tag	UNP L7P9J4
B	-2	HIS	-	expression tag	UNP L7P9J4
B	-1	GLY	-	expression tag	UNP L7P9J4
B	0	SER	-	expression tag	UNP L7P9J4
C	-7	HIS	-	expression tag	UNP L7P9J4
C	-6	HIS	-	expression tag	UNP L7P9J4
C	-5	HIS	-	expression tag	UNP L7P9J4
C	-4	HIS	-	expression tag	UNP L7P9J4
C	-3	HIS	-	expression tag	UNP L7P9J4
C	-2	HIS	-	expression tag	UNP L7P9J4

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	GLY	-	expression tag	UNP L7P9J4
C	0	SER	-	expression tag	UNP L7P9J4

- Molecule 2 is NITRATE ION (CCD ID: NO3) (formula: NO₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	N	O	0	0
			4	1	3		
2	B	1	Total	N	O	0	0
			4	1	3		
2	C	1	Total	N	O	0	0
			4	1	3		
2	C	1	Total	N	O	0	0
			4	1	3		

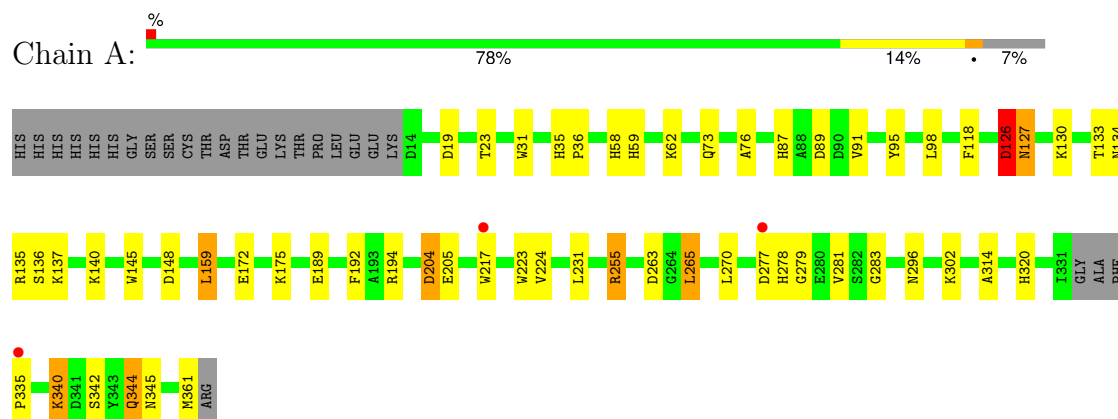
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	265	Total	O	0	0
			265	265		
3	B	260	Total	O	0	0
			260	260		
3	C	217	Total	O	0	0
			217	217		

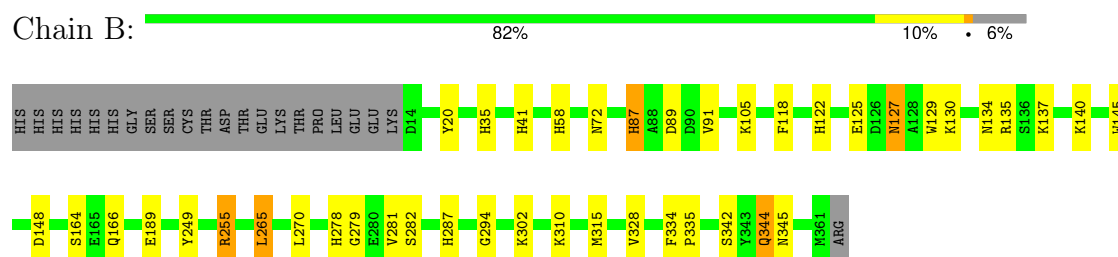
3 Residue-property plots

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.

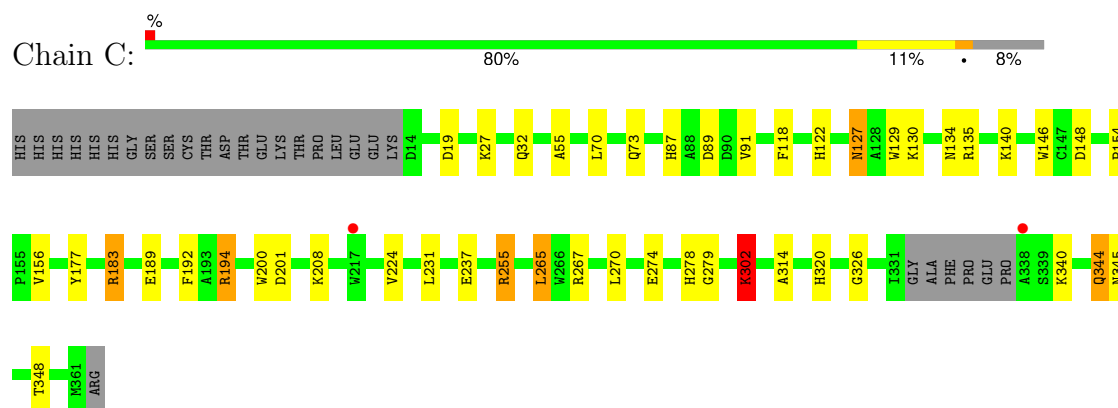
• Molecule 1: UNSATURATED 3S-RHAMNOGLYCURONYL HYDROLASE



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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	92.98Å 93.33Å 156.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.19 – 1.90 45.19 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.9 (45.19-1.90) 98.9 (45.19-1.90)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.69 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.162 , 0.207 0.164 , 0.209	Depositor DCC
R_{free} test set	5313 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	26.0	Xtriage
Anisotropy	0.040	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 41.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.023 for k,h,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	9354	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 3.31% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NO3

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	1.29	4/2962 (0.1%)	1.19	16/4017 (0.4%)
1	B	1.29	12/2967 (0.4%)	1.11	2/4025 (0.0%)
1	C	1.28	6/2953 (0.2%)	1.12	5/4004 (0.1%)
All	All	1.29	22/8882 (0.2%)	1.14	23/12046 (0.2%)

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	287	HIS	ND1-CE1	6.71	1.39	1.32
1	C	122	HIS	CG-CD2	6.14	1.42	1.35
1	A	58	HIS	CG-CD2	6.03	1.42	1.35
1	B	58	HIS	ND1-CE1	5.98	1.38	1.32
1	C	154	PRO	CA-C	5.84	1.57	1.52
1	C	122	HIS	ND1-CE1	5.82	1.38	1.32
1	C	183	ARG	CD-NE	-5.67	1.38	1.46
1	B	87	HIS	ND1-CE1	5.62	1.38	1.32
1	B	58	HIS	CG-CD2	5.61	1.42	1.35
1	C	326	GLY	N-CA	5.50	1.50	1.44
1	B	41	HIS	CG-CD2	5.49	1.41	1.35
1	A	145	TRP	CD2-CE2	5.34	1.50	1.41
1	B	278	HIS	CG-CD2	5.31	1.41	1.35
1	B	122	HIS	CG-ND1	-5.30	1.32	1.38
1	B	58	HIS	CE1-NE2	5.28	1.37	1.32
1	A	58	HIS	ND1-CE1	5.27	1.37	1.32
1	B	41	HIS	CE1-NE2	5.18	1.37	1.32
1	B	145	TRP	CD2-CE2	5.18	1.50	1.41
1	B	35	HIS	CE1-NE2	5.17	1.37	1.32
1	B	35	HIS	CG-CD2	5.15	1.41	1.35
1	C	177	TYR	N-CA	5.11	1.52	1.46
1	A	223	TRP	CD2-CE2	5.03	1.50	1.41

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	255	ARG	CG-CD-NE	-8.53	93.24	112.00
1	A	255	ARG	NE-CZ-NH2	-8.48	111.57	119.20
1	A	281	VAL	N-CA-C	7.54	118.34	110.72
1	C	183	ARG	NE-CZ-NH2	-7.16	112.76	119.20
1	C	255	ARG	CG-CD-NE	-6.85	96.94	112.00
1	A	31	TRP	N-CA-C	-6.58	104.19	111.36
1	C	183	ARG	CB-CG-CD	-6.34	96.72	111.30
1	A	126	ASP	CB-CA-C	6.13	122.25	109.68
1	A	204	ASP	N-CA-C	6.04	118.83	111.82
1	A	255	ARG	CD-NE-CZ	5.89	132.65	124.40
1	B	281	VAL	N-CA-C	5.82	117.34	111.00
1	C	194	ARG	CA-CB-CG	5.78	125.66	114.10
1	A	263	ASP	CA-C-N	-5.58	116.80	123.44
1	A	263	ASP	C-N-CA	-5.58	116.80	123.44
1	B	255	ARG	CG-CD-NE	-5.50	99.91	112.00
1	A	277	ASP	CB-CA-C	5.28	119.85	109.72
1	A	76	ALA	N-CA-C	-5.24	105.74	111.82
1	C	156	VAL	N-CA-C	-5.19	105.34	111.00
1	A	23	THR	N-CA-C	-5.15	105.75	111.36
1	A	283	GLY	N-CA-C	-5.04	106.65	112.50
1	A	35	HIS	CA-C-N	-5.02	114.61	119.78
1	A	35	HIS	C-N-CA	-5.02	114.61	119.78
1	A	342	SER	CB-CA-C	5.02	118.02	109.84

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	2868	0	2713	28	0
1	B	2873	0	2719	20	0
1	C	2855	0	2702	23	0
2	A	4	0	0	0	0
2	B	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	8	0	0	0	0
3	A	265	0	0	6	0
3	B	260	0	0	2	1
3	C	217	0	0	3	1
All	All	9354	0	8134	70	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 4.

All (70) 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:62:LYS:HE2	3:A:2064:HOH:O	1.07	1.24
1:A:126:ASP:HB2	3:A:2139:HOH:O	1.36	1.23
1:C:27:LYS:HE3	3:C:2005:HOH:O	1.75	0.86
1:A:278:HIS:HD2	1:A:279:GLY:O	1.72	0.72
1:A:189:GLU:OE1	1:A:255:ARG:NH2	2.24	0.70
1:A:335:PRO:HD3	3:A:2263:HOH:O	1.92	0.69
1:B:189:GLU:OE1	1:B:255:ARG:NH2	2.25	0.69
1:A:127:ASN:HD22	1:A:127:ASN:C	2.04	0.65
1:C:87:HIS:HD2	1:C:89:ASP:H	1.45	0.63
1:C:265:LEU:HD13	1:C:314:ALA:HB3	1.82	0.61
1:A:172:GLU:OE2	1:A:175:LYS:HE2	2.03	0.58
1:A:126:ASP:CB	3:A:2139:HOH:O	2.14	0.58
1:B:310:LYS:NZ	3:B:2212:HOH:O	2.37	0.57
1:B:127:ASN:ND2	1:B:130:LYS:H	2.02	0.57
1:C:140:LYS:NZ	3:C:2124:HOH:O	2.38	0.57
1:A:265:LEU:HB3	1:A:279:GLY:HA3	1.89	0.55
1:C:134:ASN:ND2	1:C:140:LYS:H	2.05	0.55
1:A:98:LEU:HD13	1:A:159:LEU:HB3	1.89	0.54
1:C:302:LYS:HE3	1:C:302:LYS:HA	1.90	0.54
1:A:265:LEU:HD13	1:A:314:ALA:HB3	1.88	0.54
1:C:55:ALA:HA	1:C:70:LEU:HD11	1.89	0.54
1:B:134:ASN:ND2	1:B:140:LYS:H	2.06	0.53
1:A:344:GLN:HE21	1:A:345:ASN:H	1.57	0.53
1:C:265:LEU:HD13	1:C:314:ALA:CB	2.39	0.53
1:C:265:LEU:HB3	1:C:279:GLY:HA3	1.90	0.52
1:A:87:HIS:HD2	1:A:89:ASP:H	1.58	0.51
1:C:344:GLN:HE21	1:C:345:ASN:H	1.59	0.51
1:C:278:HIS:HD2	1:C:279:GLY:O	1.94	0.51
1:C:189:GLU:OE1	1:C:255:ARG:NH2	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:164:SER:CB	1:B:166:GLN:HE21	2.25	0.50
1:B:342:SER:HB2	3:B:2249:HOH:O	2.12	0.50
1:A:62:LYS:CE	3:A:2064:HOH:O	1.92	0.49
1:A:127:ASN:C	1:A:127:ASN:ND2	2.71	0.49
1:C:32:GLN:HB2	1:C:348:THR:HG21	1.93	0.49
1:A:127:ASN:ND2	1:A:130:LYS:H	2.11	0.48
1:B:334:PHE:HB2	1:B:335:PRO:HD2	1.96	0.48
1:C:320:HIS:HE1	1:C:340:LYS:O	1.97	0.48
1:B:334:PHE:HB2	1:B:335:PRO:CD	2.43	0.47
1:B:344:GLN:HE21	1:B:345:ASN:H	1.63	0.47
1:B:87:HIS:HD2	1:B:89:ASP:H	1.63	0.47
1:A:59:HIS:HD2	3:A:2060:HOH:O	1.97	0.47
1:B:265:LEU:HB3	1:B:279:GLY:HA3	1.98	0.46
1:B:282:SER:HB3	1:B:328:VAL:HG13	1.98	0.45
1:C:237:GLU:HB2	3:C:2178:HOH:O	2.16	0.45
1:C:200:TRP:CZ2	1:C:208:LYS:HG2	2.52	0.45
1:A:36:PRO:HG2	1:B:72[B]:ASN:ND2	2.32	0.45
1:A:91:VAL:HB	1:A:118:PHE:CE1	2.52	0.45
1:A:194:ARG:HB2	1:A:217[A]:TRP:HD1	1.82	0.44
1:C:127:ASN:C	1:C:127:ASN:HD22	2.25	0.44
1:B:127:ASN:HD22	1:B:129:TRP:H	1.65	0.44
1:A:344:GLN:HE21	1:A:345:ASN:N	2.16	0.44
1:B:249:TYR:OH	1:B:294:GLY:HA3	2.18	0.44
1:A:320:HIS:HE1	1:A:340:LYS:O	2.01	0.43
1:A:192:PHE:CE1	1:A:224:VAL:HG11	2.52	0.43
1:A:134:ASN:ND2	1:A:136:SER:H	2.17	0.42
1:A:296:ASN:OD1	1:A:361:MET:HA	2.19	0.42
1:B:91:VAL:HB	1:B:118:PHE:CE1	2.53	0.42
1:B:20:TYR:CD2	1:B:20:TYR:C	2.97	0.42
1:B:127:ASN:HD22	1:B:129:TRP:N	2.17	0.42
1:C:91:VAL:HB	1:C:118:PHE:CE1	2.55	0.42
1:B:105:LYS:HD2	1:B:105:LYS:HA	1.79	0.42
1:C:127:ASN:ND2	1:C:130:LYS:H	2.17	0.42
1:A:134:ASN:ND2	1:A:140:LYS:H	2.17	0.41
1:C:265:LEU:O	1:C:267:ARG:NH1	2.51	0.41
1:C:192:PHE:CE1	1:C:224:VAL:HG11	2.55	0.41
1:B:265:LEU:HD12	1:B:265:LEU:HA	1.94	0.41
1:C:146:TRP:HA	1:C:194:ARG:O	2.21	0.41
1:C:127:ASN:HD22	1:C:129:TRP:H	1.68	0.40
1:A:265:LEU:HD13	1:A:314:ALA:CB	2.52	0.40
1:A:95:TYR:CE2	1:A:159:LEU:HD22	2.57	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)
3:B:2103:HOH:O	3:C:2178:HOH:O[3_655]	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	344/370 (93%)	339 (98%)	5 (2%)	0	100	100
1	B	348/370 (94%)	338 (97%)	10 (3%)	0	100	100
1	C	343/370 (93%)	335 (98%)	7 (2%)	1 (0%)	36	29
All	All	1035/1110 (93%)	1012 (98%)	22 (2%)	1 (0%)	48	40

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	302	LYS

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	298/317 (94%)	281 (94%)	17 (6%)	18	11
1	B	298/317 (94%)	288 (97%)	10 (3%)	32	25
1	C	297/317 (94%)	284 (96%)	13 (4%)	25	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	893/951 (94%)	853 (96%)	40 (4%)	24	17

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	ASP
1	A	73	GLN
1	A	126	ASP
1	A	127	ASN
1	A	133	THR
1	A	135	ARG
1	A	137	LYS
1	A	148	ASP
1	A	159	LEU
1	A	204	ASP
1	A	205	GLU
1	A	231	LEU
1	A	265	LEU
1	A	270	LEU
1	A	302	LYS
1	A	340	LYS
1	A	344	GLN
1	B	125	GLU
1	B	127	ASN
1	B	135	ARG
1	B	137	LYS
1	B	148	ASP
1	B	265	LEU
1	B	270	LEU
1	B	302	LYS
1	B	315	MET
1	B	344	GLN
1	C	19	ASP
1	C	73	GLN
1	C	127	ASN
1	C	135	ARG
1	C	148	ASP
1	C	183	ARG
1	C	201	ASP
1	C	231	LEU
1	C	265	LEU
1	C	270	LEU

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Mol	Chain	Res	Type
1	C	274	GLU
1	C	302	LYS
1	C	344	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	73	GLN
1	A	87	HIS
1	A	108	ASN
1	A	127	ASN
1	A	134	ASN
1	A	166	GLN
1	A	247	ASN
1	A	278	HIS
1	A	287	HIS
1	A	320	HIS
1	A	344	GLN
1	B	87	HIS
1	B	108	ASN
1	B	127	ASN
1	B	134	ASN
1	B	166	GLN
1	B	287	HIS
1	B	344	GLN
1	C	73	GLN
1	C	87	HIS
1	C	127	ASN
1	C	134	ASN
1	C	278	HIS
1	C	287	HIS
1	C	344	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	NO3	C	1363	-	1,3,3	3.28	1 (100%)	0,3,3	-	-
2	NO3	B	1362	-	1,3,3	3.26	1 (100%)	0,3,3	-	-
2	NO3	A	1362	-	1,3,3	3.66	1 (100%)	0,3,3	-	-
2	NO3	C	1362	-	1,3,3	3.38	1 (100%)	0,3,3	-	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1362	NO3	O1-N	3.66	1.42	1.24
2	C	1362	NO3	O1-N	3.38	1.41	1.24
2	C	1363	NO3	O1-N	3.28	1.40	1.24
2	B	1362	NO3	O1-N	3.26	1.40	1.24

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 ⓘ

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	345/370 (93%)	-0.46	3 (0%) 81 83	11, 26, 45, 89	3 (0%)
1	B	348/370 (94%)	-0.50	0 100 100	12, 25, 41, 57	2 (0%)
1	C	342/370 (92%)	-0.43	2 (0%) 85 87	12, 25, 48, 76	5 (1%)
All	All	1035/1110 (93%)	-0.46	5 (0%) 87 89	11, 25, 46, 89	10 (0%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	335	PRO	4.0
1	C	217[A]	TRP	3.5
1	A	217[A]	TRP	3.1
1	A	277	ASP	2.9
1	C	338	ALA	2.3

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	NO3	A	1362	4/4	0.82	0.13	58,62,67,70	0
2	NO3	C	1363	4/4	0.88	0.07	61,61,65,70	0
2	NO3	C	1362	4/4	0.89	0.10	56,64,64,66	0
2	NO3	B	1362	4/4	0.89	0.10	64,69,70,74	0

6.5 Other polymers [i](#)

There are no such residues in this entry.