



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 07:55 PM UTC

PDB ID : 6RYX / pdb_00006ryx
Title : Copper oxidase from Colletotrichum graminicola
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Deposited on : 2019-06-12
Resolution : 2.65 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

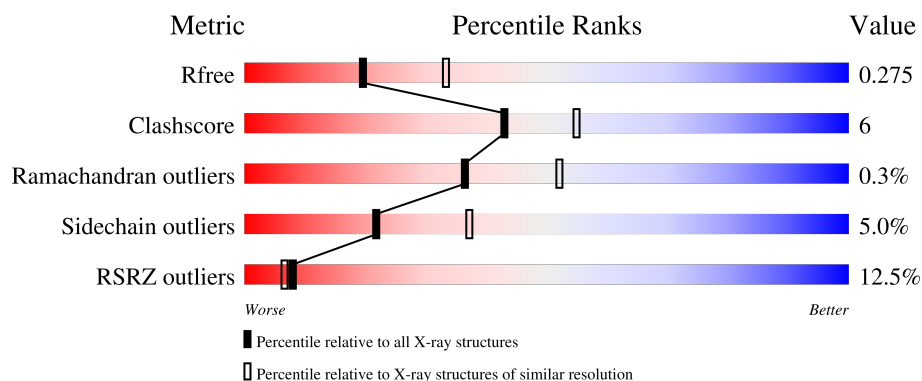
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	1110 (2.66-2.66)
Clashscore	190562	1141 (2.66-2.66)
Ramachandran outliers	187476	1126 (2.66-2.66)
Sidechain outliers	187428	1126 (2.66-2.66)
RSRZ outliers	180081	1110 (2.66-2.66)

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	714	11% 72% 15% • 12%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4620 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 Kelch domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	626	Total	C	N	O	S	0	2	0
			4587	2882	788	892	25			

There are 26 discrepancies between the modelled and reference sequences:

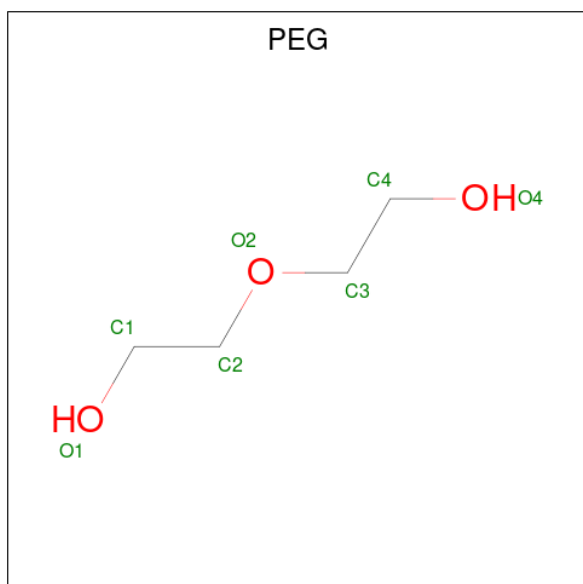
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLU	-	cloning artifact	UNP E3Q9X3
A	0	PHE	-	cloning artifact	UNP E3Q9X3
A	334	TRP	TYR	engineered mutation	UNP E3Q9X3
A	690	GLY	-	expression tag	UNP E3Q9X3
A	691	LEU	-	expression tag	UNP E3Q9X3
A	692	GLU	-	expression tag	UNP E3Q9X3
A	693	GLN	-	expression tag	UNP E3Q9X3
A	694	LYS	-	expression tag	UNP E3Q9X3
A	695	LEU	-	expression tag	UNP E3Q9X3
A	696	ILE	-	expression tag	UNP E3Q9X3
A	697	SER	-	expression tag	UNP E3Q9X3
A	698	GLU	-	expression tag	UNP E3Q9X3
A	699	GLU	-	expression tag	UNP E3Q9X3
A	700	ASP	-	expression tag	UNP E3Q9X3
A	701	LEU	-	expression tag	UNP E3Q9X3
A	702	ASN	-	expression tag	UNP E3Q9X3
A	703	SER	-	expression tag	UNP E3Q9X3
A	704	ALA	-	expression tag	UNP E3Q9X3
A	705	VAL	-	expression tag	UNP E3Q9X3
A	706	ASP	-	expression tag	UNP E3Q9X3
A	707	HIS	-	expression tag	UNP E3Q9X3
A	708	HIS	-	expression tag	UNP E3Q9X3
A	709	HIS	-	expression tag	UNP E3Q9X3
A	710	HIS	-	expression tag	UNP E3Q9X3
A	711	HIS	-	expression tag	UNP E3Q9X3
A	712	HIS	-	expression tag	UNP E3Q9X3

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 4 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cu	0	0
			1	1		

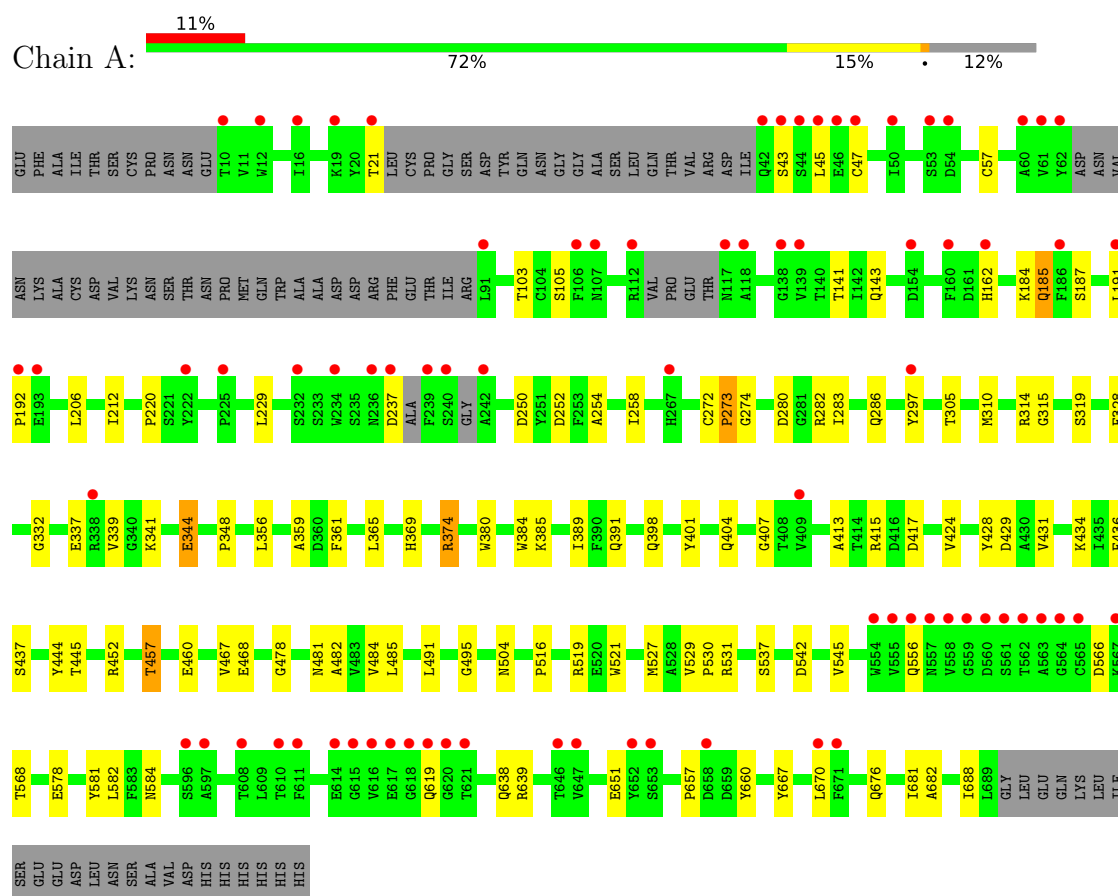
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	10	Total	O	0	1
			11	11		

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: Kelch domain-containing protein



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, α , β , γ	172.04Å 172.04Å 172.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	121.65 – 2.65 121.65 – 2.65	Depositor EDS
% Data completeness (in resolution range)	100.0 (121.65-2.65) 100.0 (121.65-2.65)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.98 (at 2.65Å)	Xtriage
Refinement program	REFMAC 5.8.0253	Depositor
R, R_{free}	0.221 , 0.280 0.221 , 0.275	Depositor DCC
R_{free} test set	1230 reflections (3.08%)	wwPDB-VP
Wilson B-factor (Å ²)	65.7	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 86.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.030 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4620	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.81% 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: NAG, PEG, CU

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	1.10	1/4700 (0.0%)	1.45	8/6425 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	348	PRO	C-O	-5.19	1.18	1.24

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	407	GLY	CA-C-O	-6.03	117.41	122.29
1	A	274	GLY	CA-C-O	-5.80	116.36	121.58
1	A	45	LEU	N-CA-C	-5.71	106.40	113.19
1	A	401	TYR	CA-C-O	-5.27	115.16	121.11
1	A	344	GLU	CB-CA-C	5.24	119.74	110.16
1	A	273	PRO	CB-CA-C	-5.23	102.93	111.56
1	A	584	ASN	CA-C-O	-5.03	115.73	121.82
1	A	460	GLU	CB-CA-C	5.01	115.93	108.87

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	4587	0	4124	54	0
2	A	14	0	13	0	0
3	A	7	0	10	0	0
4	A	1	0	0	0	0
5	A	11	0	0	1	0
All	All	4620	0	4147	54	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 (54) 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:481:ASN:HB3	1:A:537:SER:HB3	1.62	0.80
1:A:374:ARG:HD3	1:A:444:TYR:CB	2.27	0.64
1:A:310:MET:HE1	1:A:314:ARG:HD2	1.82	0.61
1:A:272:CYS:N	1:A:273:PRO:HD3	2.17	0.60
1:A:141:THR:HB	1:A:143:GLN:OE1	2.06	0.55
1:A:468:GLU:OE1	1:A:519[B]:ARG:NH1	2.26	0.55
1:A:212:ILE:HD12	1:A:237:ASP:HA	1.90	0.53
1:A:380:TRP:CD1	1:A:380:TRP:N	2.77	0.51
1:A:478:GLY:O	1:A:495:GLY:HA2	2.10	0.51
1:A:436:PHE:HZ	1:A:521:TRP:CZ2	2.29	0.51
1:A:280:ASP:OD2	1:A:282:ARG:HD3	2.11	0.51
1:A:339:VAL:O	1:A:341:LYS:HE3	2.11	0.50
1:A:384:TRP:CG	1:A:385:LYS:H	2.30	0.50
1:A:315:GLY:O	1:A:332:GLY:HA2	2.11	0.50
1:A:542:ASP:OD1	1:A:542:ASP:C	2.55	0.50
1:A:527:MET:HE3	1:A:531:ARG:HG2	1.94	0.50
1:A:516:PRO:O	1:A:519[A]:ARG:NH1	2.45	0.49
1:A:481:ASN:HB3	1:A:537:SER:CB	2.37	0.49
1:A:374:ARG:HD3	1:A:444:TYR:HB2	1.94	0.49
1:A:657:PRO:HG3	5:A:904:HOH:O	2.13	0.49
1:A:566:ASP:OD1	1:A:568:THR:OG1	2.20	0.48
1:A:57:CYS:O	1:A:184:LYS:HE2	2.14	0.48
1:A:250:ASP:OD1	1:A:250:ASP:C	2.56	0.48
1:A:272:CYS:N	1:A:273:PRO:CD	2.78	0.47
1:A:434:LYS:HD3	1:A:457:THR:HG23	1.96	0.47
1:A:280:ASP:OD2	1:A:282:ARG:CD	2.63	0.47
1:A:356:LEU:O	1:A:359:ALA:HB3	2.14	0.46
1:A:398:GLN:HE21	1:A:413:ALA:HB3	1.80	0.46
1:A:220:PRO:HB3	1:A:667:TYR:CG	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:328:PHE:CD2	1:A:389:ILE:HG12	2.51	0.46
1:A:162:HIS:HE2	1:A:187:SER:HG	1.57	0.46
1:A:578:GLU:HG2	1:A:582:LEU:HD12	1.98	0.45
1:A:527:MET:HE3	1:A:529:VAL:O	2.16	0.45
1:A:429:ASP:HB3	1:A:434:LYS:HB2	1.99	0.45
1:A:424:VAL:HB	1:A:482:ALA:HB2	1.99	0.45
1:A:286:GLN:HE22	1:A:319:SER:HB3	1.82	0.45
1:A:670:LEU:O	1:A:682:ALA:HA	2.16	0.45
1:A:252:ASP:OD1	1:A:254:ALA:HB3	2.18	0.44
1:A:428:TYR:HA	1:A:484:VAL:HG21	1.99	0.44
1:A:415:ARG:HA	1:A:467:VAL:HG11	1.99	0.44
1:A:283:ILE:HB	1:A:297:TYR:HB3	2.00	0.44
1:A:185:GLN:O	1:A:185:GLN:HG3	2.18	0.43
1:A:191:LEU:O	1:A:192:PRO:C	2.62	0.43
1:A:374:ARG:HD3	1:A:444:TYR:HB3	1.99	0.43
1:A:491:LEU:CD2	1:A:545:VAL:HG21	2.48	0.42
1:A:676[B]:GLN:CD	1:A:676[B]:GLN:N	2.77	0.42
1:A:229:LEU:HD23	1:A:229:LEU:HA	1.91	0.42
1:A:660:TYR:OH	1:A:688:ILE:O	2.36	0.42
1:A:361:PHE:HD1	1:A:365:LEU:HD21	1.85	0.41
1:A:504:ASN:HB3	1:A:530:PRO:HG3	2.02	0.41
1:A:250:ASP:O	1:A:258:ILE:HA	2.20	0.41
1:A:417:ASP:CG	1:A:452:ARG:HH12	2.28	0.41
1:A:380:TRP:O	1:A:391:GLN:HA	2.21	0.41
1:A:337:GLU:HB2	1:A:339:VAL:HG22	2.02	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	616/714 (86%)	577 (94%)	37 (6%)	2 (0%)	36	52

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	43	SER
1	A	556	GLN

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	445/589 (76%)	423 (95%)	22 (5%)	22	38

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	THR
1	A	47	CYS
1	A	103	THR
1	A	105	SER
1	A	185	GLN
1	A	206	LEU
1	A	305	THR
1	A	344	GLU
1	A	369	HIS
1	A	374	ARG
1	A	404	GLN
1	A	431	VAL
1	A	437	SER
1	A	445	THR
1	A	457	THR
1	A	485	LEU
1	A	581	TYR
1	A	619	GLN
1	A	638	GLN
1	A	639	ARG
1	A	651	GLU
1	A	681	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	185	GLN
1	A	286	GLN
1	A	377	ASN
1	A	532	ASN

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](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	PEG	A	802	-	6,6,6	0.34	0	5,5,5	0.29	0
2	NAG	A	801	1	14,14,15	0.40	0	17,19,21	2.24	5 (29%)

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
3	PEG	A	802	-	-	1/4/4/4	-
2	NAG	A	801	1	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	NAG	C4-C3-C2	-6.62	101.32	111.02
2	A	801	NAG	C1-O5-C5	3.46	116.83	112.19
2	A	801	NAG	O3-C3-C2	3.11	115.86	109.40
2	A	801	NAG	C1-C2-N2	2.91	115.01	110.43
2	A	801	NAG	O5-C1-C2	-2.46	107.49	111.29

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	NAG	C1-C2-N2-C7
2	A	801	NAG	O7-C7-N2-C2
2	A	801	NAG	C8-C7-N2-C2
3	A	802	PEG	O2-C3-C4-O4
2	A	801	NAG	C3-C2-N2-C7

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	626/714 (87%)	0.90	78 (12%) 8 6	21, 54, 76, 109	138 (22%)

All (78) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	563	ALA	15.1
1	A	562	THR	14.3
1	A	192	PRO	12.9
1	A	561	SER	12.7
1	A	560	ASP	12.2
1	A	557	ASN	11.8
1	A	240	SER	11.5
1	A	43	SER	10.8
1	A	555	VAL	10.7
1	A	558	VAL	10.4
1	A	554	TRP	10.1
1	A	239	PHE	10.0
1	A	46	GLU	9.8
1	A	236	ASN	9.5
1	A	559	GLY	9.3
1	A	616	VAL	9.2
1	A	556	GLN	9.2
1	A	564	GLY	8.7
1	A	42	GLN	8.4
1	A	62	TYR	8.4
1	A	44	SER	8.2
1	A	45	LEU	7.6
1	A	618	GLY	7.3
1	A	242	ALA	7.2
1	A	565	CYS	7.1
1	A	234	TRP	6.8
1	A	193	GLU	6.5

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Mol	Chain	Res	Type	RSRZ
1	A	620	GLY	6.2
1	A	138	GLY	6.1
1	A	617	GLU	6.0
1	A	647	VAL	5.6
1	A	61	VAL	5.3
1	A	60	ALA	4.9
1	A	19	LYS	4.9
1	A	597	ALA	4.8
1	A	596	SER	4.6
1	A	139	VAL	4.5
1	A	652	TYR	4.4
1	A	567	LYS	4.3
1	A	615	GLY	4.1
1	A	621	THR	4.0
1	A	614	GLU	3.9
1	A	154	ASP	3.8
1	A	12	TRP	3.8
1	A	619	GLN	3.7
1	A	117	ASN	3.7
1	A	16	ILE	3.6
1	A	10	THR	3.4
1	A	237	ASP	3.3
1	A	658	ASP	3.3
1	A	611	PHE	3.1
1	A	112	ARG	3.0
1	A	160	PHE	3.0
1	A	21	THR	3.0
1	A	191	LEU	2.9
1	A	670	LEU	2.9
1	A	222	TYR	2.7
1	A	232	SER	2.5
1	A	338	ARG	2.5
1	A	608	THR	2.5
1	A	671	PHE	2.5
1	A	653	SER	2.4
1	A	162	HIS	2.4
1	A	186	PHE	2.4
1	A	107	ASN	2.3
1	A	225	PRO	2.3
1	A	53	SER	2.2
1	A	54	ASP	2.2
1	A	50	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	646	THR	2.2
1	A	106	PHE	2.1
1	A	610	THR	2.1
1	A	47	CYS	2.1
1	A	91	LEU	2.1
1	A	409	VAL	2.1
1	A	118	ALA	2.1
1	A	267	HIS	2.1
1	A	297	TYR	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	NAG	A	801	14/15	0.80	0.21	49,67,71,73	14
3	PEG	A	802	7/7	0.92	0.12	61,73,83,83	0
4	CU	A	803	1/1	0.97	0.04	84,84,84,84	0

6.5 Other polymers [i](#)

There are no such residues in this entry.