



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 11:31 am GMT

PDB ID : 1A65
Title : TYPE-2 CU-DEPLETED LACCASE FROM COPRINUS CINEREUS
Authors : Ducros, V.; Brzozowski, W.
Deposited on : 1998-03-05
Resolution : 2.23 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

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

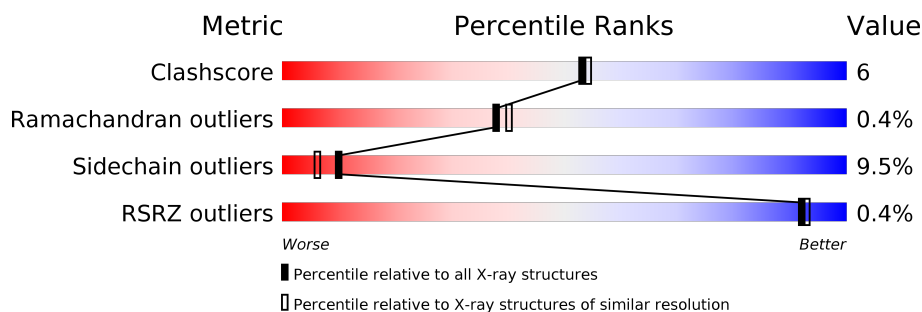
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.23 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))
Clashscore	112137	1957 (2.26-2.22)
Ramachandran outliers	110173	1916 (2.26-2.22)
Sidechain outliers	110143	1917 (2.26-2.22)
RSRZ outliers	101464	1809 (2.26-2.22)

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. 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	504	

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	NAG	A	800	X	-	-	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 4168 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 LACCASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	504	3848	2431	669	736	12	0	0	0

There is a discrepancy between the modelled and reference sequences:

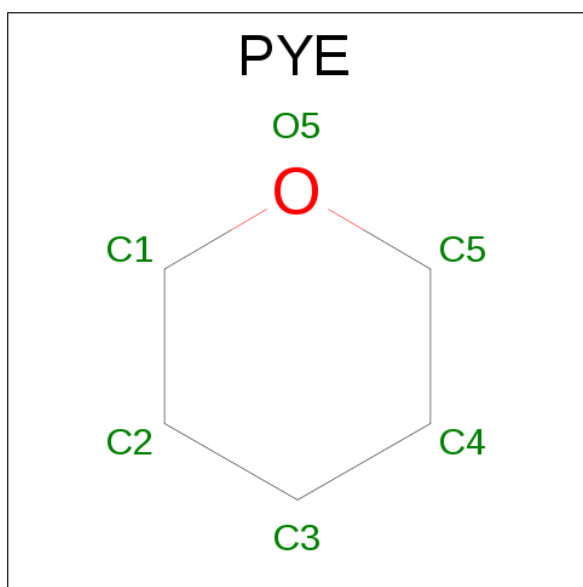
Chain	Residue	Modelled	Actual	Comment	Reference
A	225	GLU	GLN	CONFLICT	UNP Q9Y780

- Molecule 2 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 3 is TETRAHYDROPYRAN (three-letter code: PYE) (formula: $C_5H_{10}O$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	5	1		

- Molecule 4 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total	Cu	0	0
			3	3		

- Molecule 5 is OXYGEN ATOM (three-letter code: O) (formula: O).

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

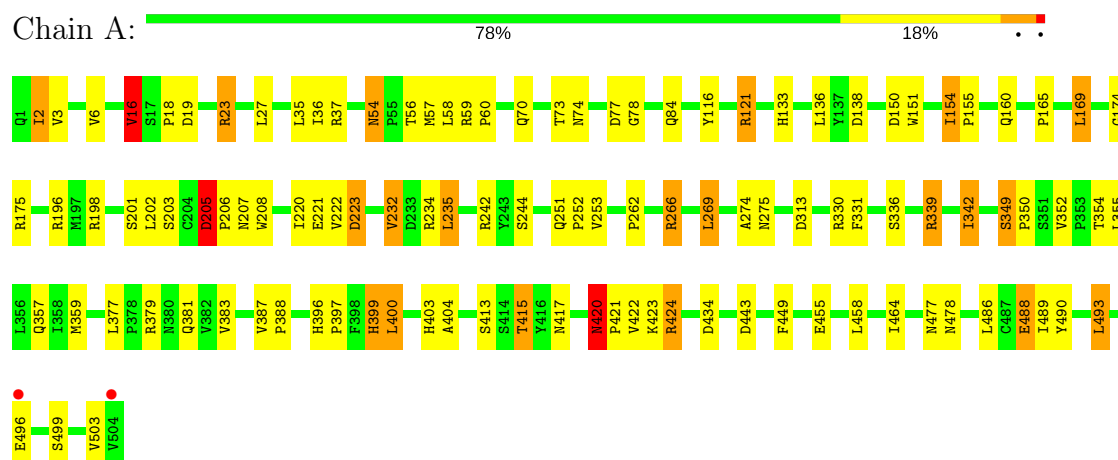
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	296	Total	O	0	0
			296	296		

3 Residue-property plots

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: LACCASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	45.39Å 85.72Å 143.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	12.00 – 2.23 11.98 – 2.23	Depositor EDS
% Data completeness (in resolution range)	99.6 (12.00-2.23) 99.8 (11.98-2.23)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.94 (at 2.23Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.160 , 0.220 0.152 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	21.4	Xtriage
Anisotropy	0.239	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 58.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4168	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.40% 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: O, NAG, CU, PYE

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	0.59	1/3957 (0.0%)	1.44	45/5423 (0.8%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	420	ASN	CA-CB	5.30	1.67	1.53

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	23	ARG	NE-CZ-NH1	18.48	129.54	120.30
1	A	23	ARG	NE-CZ-NH2	-16.43	112.08	120.30
1	A	266	ARG	NE-CZ-NH1	12.94	126.77	120.30
1	A	23	ARG	CD-NE-CZ	10.69	138.57	123.60
1	A	121	ARG	NE-CZ-NH1	10.44	125.52	120.30
1	A	234	ARG	NE-CZ-NH2	-9.88	115.36	120.30
1	A	121	ARG	NE-CZ-NH2	-9.10	115.75	120.30
1	A	138	ASP	CB-CG-OD2	8.71	126.14	118.30
1	A	235	LEU	CA-CB-CG	8.61	135.09	115.30
1	A	266	ARG	NE-CZ-NH2	-8.49	116.05	120.30
1	A	339	ARG	NE-CZ-NH1	8.10	124.35	120.30
1	A	116	TYR	CA-CB-CG	8.07	128.73	113.40
1	A	379	ARG	NE-CZ-NH2	-7.78	116.41	120.30
1	A	420	ASN	N-CA-CB	-7.76	96.63	110.60
1	A	223	ASP	CB-CG-OD2	7.65	125.18	118.30
1	A	424	ARG	NE-CZ-NH1	-7.38	116.61	120.30
1	A	175	ARG	NE-CZ-NH2	-7.02	116.79	120.30
1	A	330	ARG	NE-CZ-NH2	-6.93	116.84	120.30
1	A	232	VAL	N-CA-CB	-6.91	96.30	111.50
1	A	379	ARG	NE-CZ-NH1	6.78	123.69	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	138	ASP	CB-CG-OD1	-6.76	112.22	118.30
1	A	150	ASP	CB-CG-OD1	6.35	124.02	118.30
1	A	349	SER	N-CA-CB	-6.30	101.05	110.50
1	A	399	HIS	CA-CB-CG	6.18	124.11	113.60
1	A	196	ARG	NE-CZ-NH2	-6.09	117.25	120.30
1	A	37	ARG	NE-CZ-NH1	5.99	123.29	120.30
1	A	205	ASP	CB-CG-OD1	5.95	123.65	118.30
1	A	198	ARG	NE-CZ-NH1	5.90	123.25	120.30
1	A	443	ASP	CB-CG-OD1	5.86	123.58	118.30
1	A	6	VAL	N-CA-CB	5.70	124.03	111.50
1	A	232	VAL	CG1-CB-CG2	5.65	119.94	110.90
1	A	16	VAL	N-CA-CB	-5.58	99.23	111.50
1	A	420	ASN	CB-CA-C	-5.56	99.28	110.40
1	A	266	ARG	CD-NE-CZ	5.46	131.25	123.60
1	A	383	VAL	CA-CB-CG2	5.45	119.07	110.90
1	A	424	ARG	CA-CB-CG	5.44	125.37	113.40
1	A	434	ASP	CB-CG-OD2	5.40	123.16	118.30
1	A	455	GLU	OE1-CD-OE2	-5.34	116.89	123.30
1	A	420	ASN	N-CA-C	5.30	125.31	111.00
1	A	16	VAL	CA-CB-CG1	5.11	118.56	110.90
1	A	388	PRO	N-CA-CB	5.11	109.43	103.30
1	A	404	ALA	N-CA-CB	5.07	117.20	110.10
1	A	387	VAL	CG1-CB-CG2	-5.06	102.80	110.90
1	A	359	MET	CA-CB-CG	5.02	121.84	113.30
1	A	77	ASP	CB-CG-OD1	5.01	122.81	118.30

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	3848	0	3651	47	0
2	A	14	0	13	1	0
3	A	6	0	9	0	0
4	A	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	1	0	0	0	0
6	A	296	0	0	1	0
All	All	4168	0	3673	47	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 (47) 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:54:ASN:HD22	1:A:56:THR:H	1.18	0.86
1:A:54:ASN:ND2	1:A:56:THR:H	1.78	0.80
1:A:274:ALA:O	1:A:275:ASN:HB2	1.89	0.73
1:A:121:ARG:HD2	1:A:202:LEU:HB3	1.77	0.66
1:A:154:ILE:HB	1:A:155:PRO:HD2	1.80	0.64
1:A:205:ASP:HB3	1:A:206:PRO:HD3	1.80	0.64
1:A:262:PRO:HG3	1:A:269:LEU:HD13	1.80	0.64
1:A:400:LEU:HD13	1:A:403:HIS:HB2	1.81	0.63
1:A:342:ILE:HG21	1:A:464:ILE:HG23	1.79	0.63
1:A:151:TRP:HB2	1:A:169:LEU:HD22	1.81	0.62
1:A:16:VAL:HG13	1:A:18:PRO:HD3	1.85	0.58
1:A:331:PHE:CG	1:A:342:ILE:HD11	2.38	0.58
1:A:205:ASP:HB3	1:A:206:PRO:CD	2.35	0.55
1:A:417:ASN:HD21	1:A:420:ASN:HB3	1.71	0.55
1:A:3:VAL:HG22	1:A:36:ILE:HG12	1.88	0.55
1:A:331:PHE:HB3	1:A:342:ILE:HD11	1.90	0.53
1:A:251:GLN:HB3	1:A:252:PRO:HD2	1.90	0.52
1:A:74:ASN:H	1:A:477:ASN:ND2	2.09	0.51
1:A:488:GLU:HG3	1:A:489:ILE:N	2.25	0.51
1:A:203:SER:HB2	1:A:208:TRP:CZ3	2.45	0.51
1:A:331:PHE:HB3	1:A:342:ILE:CD1	2.41	0.50
1:A:352:VAL:O	1:A:357:GLN:NE2	2.42	0.49
1:A:222:VAL:HG11	1:A:422:VAL:CG2	2.42	0.49
1:A:331:PHE:CD1	1:A:342:ILE:HD11	2.48	0.49
1:A:2:ILE:HD13	1:A:35:LEU:HD23	1.96	0.48
1:A:221:GLU:HB3	1:A:244:SER:HB2	1.94	0.48
1:A:413:SER:OG	1:A:415:THR:HG23	2.15	0.47
1:A:59:ARG:N	1:A:60:PRO:CD	2.77	0.47
1:A:251:GLN:HB3	1:A:252:PRO:CD	2.45	0.46
1:A:490:TYR:HA	1:A:493:LEU:HD22	1.98	0.46
1:A:54:ASN:ND2	1:A:56:THR:OG1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:349:SER:HA	1:A:350:PRO:HD2	1.85	0.45
1:A:420:ASN:N	1:A:421:PRO:CD	2.79	0.45
1:A:223:ASP:OD2	1:A:424:ARG:HB2	2.17	0.45
1:A:313:ASP:O	1:A:423:LYS:NZ	2.51	0.44
1:A:133:HIS:CD2	1:A:220:ILE:HB	2.53	0.44
1:A:59:ARG:H	1:A:60:PRO:CD	2.30	0.43
1:A:331:PHE:CE1	2:A:800:NAG:H82	2.54	0.43
1:A:205:ASP:CB	1:A:206:PRO:CD	2.96	0.42
1:A:78:GLY:HA2	1:A:84:GLN:HE21	1.84	0.42
1:A:165:PRO:HG3	1:A:206:PRO:HG3	2.02	0.42
1:A:396:HIS:HA	1:A:397:PRO:HD3	1.78	0.42
1:A:420:ASN:HD22	1:A:420:ASN:HA	1.31	0.41
1:A:19:ASP:HA	1:A:174:GLY:O	2.19	0.41
1:A:342:ILE:HB	6:A:1072:HOH:O	2.21	0.40
1:A:331:PHE:CB	1:A:342:ILE:HD11	2.51	0.40
1:A:70:GLN:NE2	1:A:73:THR:OG1	2.54	0.40

There are no symmetry-related clashes.

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	502/504 (100%)	491 (98%)	9 (2%)	2 (0%)	38	40

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	205	ASP
1	A	420	ASN

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	410/411 (100%)	371 (90%)	39 (10%)	10 6

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

Mol	Chain	Res	Type
1	A	2	ILE
1	A	16	VAL
1	A	23	ARG
1	A	27	LEU
1	A	54	ASN
1	A	57	MET
1	A	58	LEU
1	A	136	LEU
1	A	154	ILE
1	A	160	GLN
1	A	169	LEU
1	A	201	SER
1	A	207	ASN
1	A	232	VAL
1	A	235	LEU
1	A	242	ARG
1	A	253	VAL
1	A	266	ARG
1	A	269	LEU
1	A	336	SER
1	A	339	ARG
1	A	342	ILE
1	A	354	THR
1	A	355	LEU
1	A	377	LEU
1	A	381	GLN
1	A	399	HIS
1	A	400	LEU
1	A	415	THR
1	A	420	ASN

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Mol	Chain	Res	Type
1	A	449	PHE
1	A	458	LEU
1	A	478	ASN
1	A	486	LEU
1	A	488	GLU
1	A	493	LEU
1	A	496	GLU
1	A	499	SER
1	A	503	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	ASN
1	A	54	ASN
1	A	70	GLN
1	A	84	GLN
1	A	115	GLN
1	A	164	GLN
1	A	207	ASN
1	A	236	GLN
1	A	267	ASN
1	A	278	ASN
1	A	332	GLN
1	A	366	ASN
1	A	380	ASN
1	A	420	ASN
1	A	477	ASN
1	A	478	ASN
1	A	485	GLN
1	A	501	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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 4 are 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	$\# Z > 2$
2	NAG	A	800	1	14,14,15	1.24	1 (7%)	15,19,21	1.79	3 (20%)
3	PYE	A	900	1	6,6,6	0.53	0	6,6,6	1.66	1 (16%)

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	NAG	A	800	1	1/1/5/7	0/6/23/26	0/1/1/1
3	PYE	A	900	1	-	0/0/6/6	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	800	NAG	O7-C7	-3.16	1.15	1.23

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	800	NAG	C1-C2-N2	-2.12	106.87	110.49
3	A	900	PYE	C3-C4-C5	2.40	115.65	110.28
2	A	800	NAG	C1-O5-C5	3.26	116.66	112.17
2	A	800	NAG	O5-C1-C2	4.15	117.25	111.47

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	800	NAG	C1

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	800	NAG	1	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 [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	504/504 (100%)	-0.76	2 (0%) 92 93	10, 21, 37, 62	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	504	VAL	2.7
1	A	496	GLU	2.5

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	PYE	A	900	6/6	0.80	0.24	0.55	58,59,59,60	0
2	NAG	A	800	14/15	0.92	0.13	0.53	30,33,36,39	0
5	O	A	904	1/1	0.99	0.08	-0.04	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	CU	A	901	1/1	0.99	0.04	-2.24	29,29,29,29	0
4	CU	A	903	1/1	1.00	0.02	-2.39	21,21,21,21	0
4	CU	A	902	1/1	0.99	0.03	-2.91	27,27,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.