



# wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 12:59 AM GMT

PDB ID : 1F8R  
Title : CRYSTAL STRUCTURE OF L-AMINO ACID OXIDASE FROM CALLOSE-  
LASMA RHODOSTOMA COMPLEXED WITH CITRATE  
Authors : Pawelek, P.D.; Cheah, J.; Coulombe, R.; Macheroux, P.; Ghisla, S.; Vrielink,  
A.  
Deposited on : 2000-07-04  
Resolution : 2.00 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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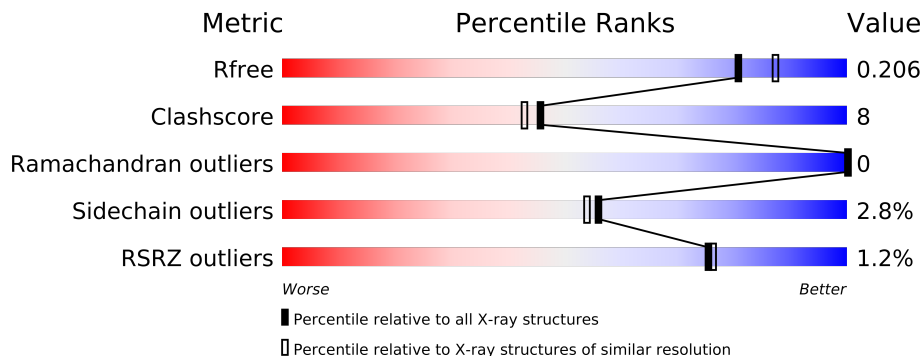
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.00 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))
$R_{free}$	66092	4888 (2.00-2.00)
Clashscore	79885	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (2.00-2.00)
RSRZ outliers	66119	4890 (2.00-2.00)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	498	
1	B	498	
1	C	498	
1	D	498	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	NAG	A	522	-	X
3	NAG	B	522	-	X
3	NAG	C	522	-	X
3	NAG	D	522	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
4	CIT	A	526	-	X
4	CIT	B	526	-	X
4	CIT	C	526	-	X
4	CIT	D	526	-	X

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 17632 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

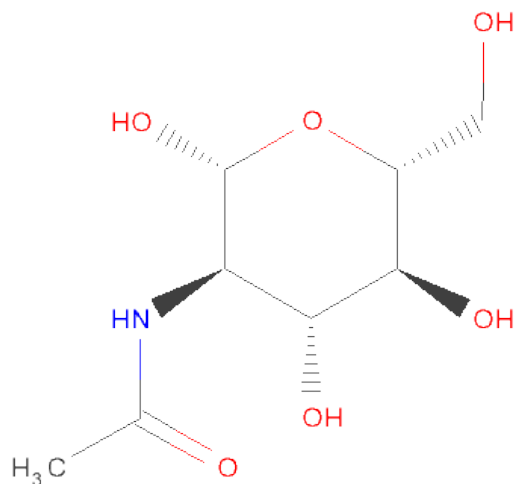
- Molecule 1 is a protein called L-AMINO ACID OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	483	Total	C	N	O	S	0	0	0
			3804	2434	640	718	12			
1	B	483	Total	C	N	O	S	0	0	0
			3847	2456	652	727	12			
1	C	483	Total	C	N	O	S	0	0	0
			3813	2437	644	720	12			
1	D	483	Total	C	N	O	S	0	0	0
			3827	2445	646	724	12			

- Molecule 2 is a polymer of unknown type called SUGAR (3-MER).

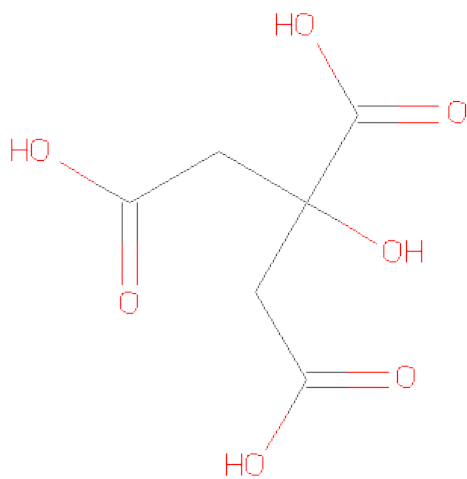
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	3	Total	C	N	O	0	0
			38	22	2	14		
2	B	3	Total	C	N	O	0	0
			38	22	2	14		
2	C	3	Total	C	N	O	0	0
			38	22	2	14		
2	D	3	Total	C	N	O	0	0
			38	22	2	14		

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



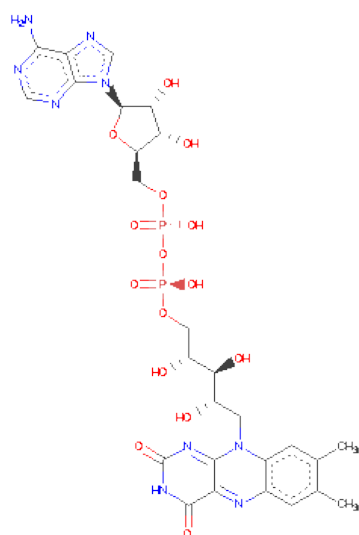
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is CITRIC ACID (three-letter code: CIT) (formula:  $C_6H_8O_7$ ).



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

- Molecule 5 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
5	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
5	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
5	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	466	Total	O	0	0
			466	466		

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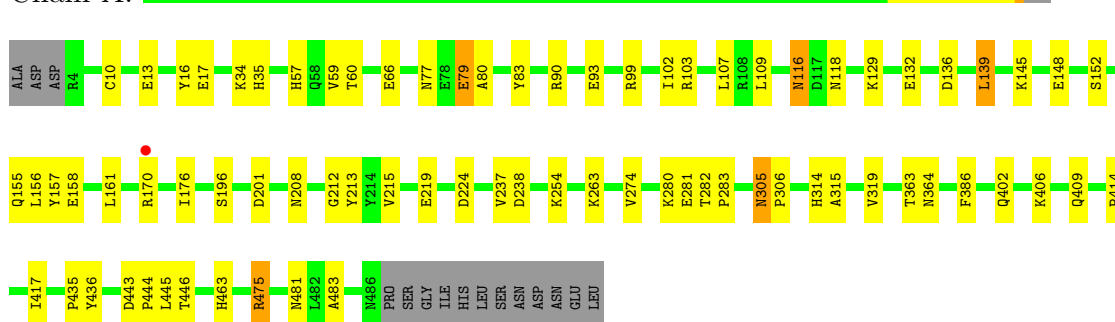
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	497	Total 497	O 497	0	0
6	C	461	Total 461	O 461	0	0
6	D	445	Total 445	O 445	0	0

### 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 errors 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.

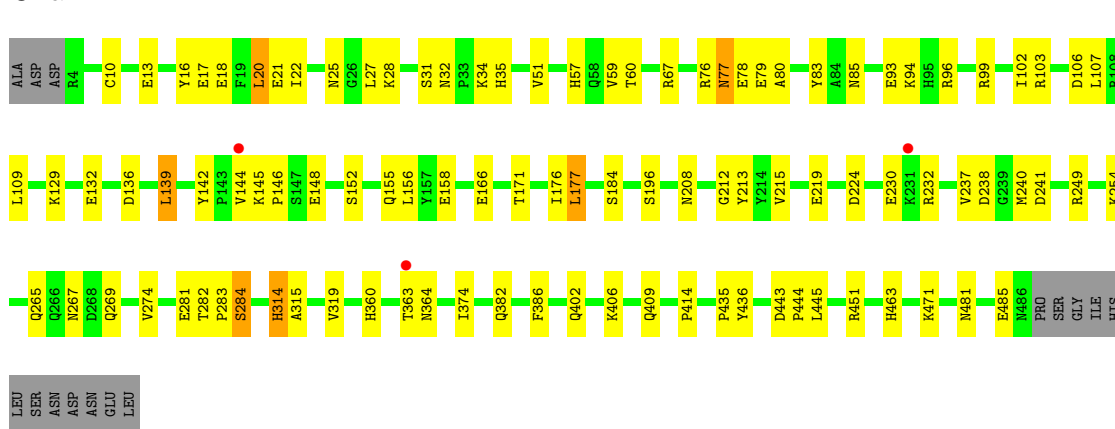
#### • Molecule 1: L-AMINO ACID OXIDASE

Chain A:



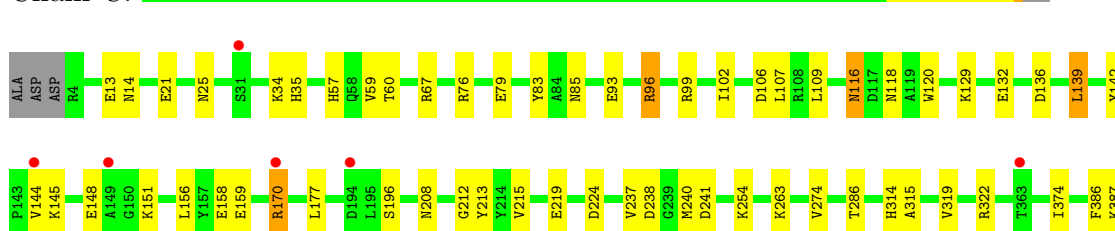
#### • Molecule 1: L-AMINO ACID OXIDASE

Chain B:



#### • Molecule 1: L-AMINO ACID OXIDASE

Chain C:

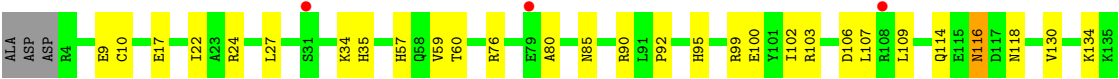






● Molecule 1: L-AMINO ACID OXIDASE

Chain D:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	79.50Å 154.96Å 102.95Å 90.00° 109.49° 90.00°	Depositor
Resolution (Å)	500.00 – 2.00 48.52 – 2.00	Depositor EDS
% Data completeness (in resolution range)	88.1 (500.00-2.00) 88.1 (48.52-2.00)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.58 (at 2.00Å)	Xtriage
Refinement program	CNS 0.5	Depositor
R, $R_{free}$	0.185 , 0.210 0.183 , 0.206	Depositor DCC
$R_{free}$ test set	13919 reflections (11.11%)	DCC
Wilson B-factor (Å <sup>2</sup> )	19.6	Xtriage
Anisotropy	0.517	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 44.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 139206 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	17632	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.41% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FUC, NAG, FAD, CIT

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	0/3895	0.59	0/5282
1	B	0.35	0/3938	0.60	0/5332
1	C	0.33	0/3903	0.59	0/5291
1	D	0.34	0/3918	0.59	0/5309
All	All	0.34	0/15654	0.59	0/21214

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	A	3	0
2	B	2	0
2	C	4	0
2	D	2	0
All	All	11	0

There are no bond length outliers.

There are no bond angle outliers.

5 of 11 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	523	NAG	C1
2	A	525	FUC	C3,C4
2	B	525	FUC	C3,C4
2	C	524	NAG	C1
2	C	525	FUC	C3,C1,C4

There are no planarity outliers.

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3804	0	3673	53	0
1	B	3847	0	3756	83	0
1	C	3813	0	3697	59	0
1	D	3827	0	3717	58	0
2	A	38	0	34	1	0
2	B	38	0	34	5	0
2	C	38	0	34	1	0
2	D	38	0	34	0	0
3	A	14	0	13	0	0
3	B	14	0	13	1	0
3	C	14	0	13	2	0
3	D	14	0	13	1	0
4	A	13	0	5	1	0
4	B	13	0	5	0	0
4	C	13	0	5	0	0
4	D	13	0	5	1	0
5	A	53	0	31	0	0
5	B	53	0	31	0	0
5	C	53	0	31	0	0
5	D	53	0	31	0	0
6	A	466	0	0	7	0
6	B	497	0	0	16	0
6	C	461	0	0	12	0
6	D	445	0	0	8	0
All	All	17632	0	15175	257	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 8.

The worst 5 of 257 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:144:VAL:CG1	1:C:148:GLU:HB2	1.87	1.05
1:B:265:GLN:HE21	1:B:267:ASN:HD21	1.01	0.98
1:A:446:THR:HB	1:A:475:ARG:HH22	1.32	0.93

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:144:VAL:HG12	1:B:148:GLU:HB2	1.51	0.91
1:B:13:GLU:OE1	1:B:471:LYS:HE2	1.74	0.87

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	481/498 (97%)	468 (97%)	13 (3%)	0	100	100
1	B	481/498 (97%)	467 (97%)	14 (3%)	0	100	100
1	C	481/498 (97%)	470 (98%)	11 (2%)	0	100	100
1	D	481/498 (97%)	467 (97%)	14 (3%)	0	100	100
All	All	1924/1992 (97%)	1872 (97%)	52 (3%)	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	398/427 (93%)	386 (97%)	12 (3%)	53	50
1	B	410/427 (96%)	399 (97%)	11 (3%)	57	56
1	C	402/427 (94%)	392 (98%)	10 (2%)	60	59
1	D	405/427 (95%)	392 (97%)	13 (3%)	51	47
All	All	1615/1708 (95%)	1569 (97%)	46 (3%)	56	54

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	284	SER
1	C	116	ASN
1	D	269	GLN
1	B	314	HIS
1	C	96	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	314	HIS
1	C	57	HIS
1	D	269	GLN
1	B	342	HIS
1	B	409	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

12 carbohydrates 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	NAG	A	523	1,2	12,14,15	0.63	0	15,19,21	0.84	1 (6%)
2	NAG	A	524	2	12,14,15	0.45	0	15,19,21	0.76	0
2	FUC	A	525	2	9,10,11	0.57	0	10,14,16	2.19	2 (20%)
2	NAG	B	523	1,2	12,14,15	0.62	0	15,19,21	1.06	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAG	B	524	2	12,14,15	0.43	0	15,19,21	0.99	1 (6%)
2	FUC	B	525	2	9,10,11	0.60	0	10,14,16	1.83	2 (20%)
2	NAG	C	523	1,2	12,14,15	0.67	0	15,19,21	0.95	0
2	NAG	C	524	2	12,14,15	0.42	0	15,19,21	0.86	0
2	FUC	C	525	2	9,10,11	0.53	0	10,14,16	2.20	2 (20%)
2	NAG	D	523	1,2	12,14,15	0.53	0	15,19,21	0.77	0
2	NAG	D	524	2	12,14,15	0.38	0	15,19,21	1.01	1 (6%)
2	FUC	D	525	2	9,10,11	0.56	0	10,14,16	2.17	2 (20%)

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	523	1,2	1/1/5/7	0/6/23/26	0/1/1/1
2	NAG	A	524	2	-	0/6/23/26	0/1/1/1
2	FUC	A	525	2	2/2/4/5	0/0/17/20	0/1/1/1
2	NAG	B	523	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	524	2	-	0/6/23/26	0/1/1/1
2	FUC	B	525	2	2/2/4/5	0/0/17/20	0/1/1/1
2	NAG	C	523	1,2	-	0/6/23/26	0/1/1/1
2	NAG	C	524	2	1/1/5/7	0/6/23/26	0/1/1/1
2	FUC	C	525	2	3/3/4/5	0/0/17/20	0/1/1/1
2	NAG	D	523	1,2	-	0/6/23/26	0/1/1/1
2	NAG	D	524	2	-	0/6/23/26	0/1/1/1
2	FUC	D	525	2	2/2/4/5	0/0/17/20	0/1/1/1

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	525	FUC	C4-C3-C2	5.71	118.17	110.50
2	C	525	FUC	C4-C3-C2	5.56	117.97	110.50
2	D	525	FUC	C4-C3-C2	5.52	117.91	110.50
2	B	525	FUC	C4-C3-C2	4.46	116.49	110.50
2	C	525	FUC	C3-C4-C5	3.95	116.42	109.84

5 of 11 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	C	525	FUC	C3
2	C	525	FUC	C1
2	C	525	FUC	C4
2	A	523	NAG	C1
2	C	524	NAG	C1

There are no torsion outliers.

There are no ring outliers.

## 5.6 Ligand geometry ⓘ

12 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	$\# Z  > 2$
3	NAG	A	522	1	12,14,15	0.38	0	15,19,21	0.87	0
4	CIT	A	526	-	12,12,12	4.94	9 (75%)	17,17,17	2.11	5 (29%)
5	FAD	A	527	-	58,58,58	2.10	12 (20%)	85,89,89	1.60	12 (14%)
3	NAG	B	522	1	12,14,15	0.38	0	15,19,21	0.76	0
4	CIT	B	526	-	12,12,12	2.96	7 (58%)	17,17,17	2.34	8 (47%)
5	FAD	B	527	-	58,58,58	2.09	13 (22%)	85,89,89	1.55	12 (14%)
3	NAG	C	522	1	12,14,15	0.43	0	15,19,21	0.47	0
4	CIT	C	526	-	12,12,12	4.99	10 (83%)	17,17,17	2.38	8 (47%)
5	FAD	C	527	-	58,58,58	2.07	13 (22%)	85,89,89	1.52	12 (14%)
3	NAG	D	522	1	12,14,15	0.39	0	15,19,21	0.75	0
4	CIT	D	526	-	12,12,12	4.75	9 (75%)	17,17,17	2.24	7 (41%)
5	FAD	D	527	-	58,58,58	2.05	14 (24%)	85,89,89	1.55	12 (14%)

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	NAG	A	522	1	1/1/5/7	0/6/23/26	0/1/1/1
4	CIT	A	526	-	-	0/16/16/16	0/0/0/0
5	FAD	A	527	-	-	0/34/50/50	0/1/6/6
3	NAG	B	522	1	1/1/5/7	0/6/23/26	0/1/1/1
4	CIT	B	526	-	-	0/16/16/16	0/0/0/0
5	FAD	B	527	-	-	0/34/50/50	0/1/6/6
3	NAG	C	522	1	1/1/5/7	0/6/23/26	0/1/1/1
4	CIT	C	526	-	-	0/16/16/16	0/0/0/0
5	FAD	C	527	-	-	0/34/50/50	0/1/6/6
3	NAG	D	522	1	1/1/5/7	0/6/23/26	0/1/1/1
4	CIT	D	526	-	-	0/16/16/16	0/0/0/0
5	FAD	D	527	-	-	0/34/50/50	0/1/6/6

The worst 5 of 87 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	526	CIT	C2-C3	12.85	1.70	1.53
4	D	526	CIT	C2-C3	8.88	1.65	1.53
4	A	526	CIT	C4-C3	8.32	1.64	1.53
4	A	526	CIT	C2-C3	8.25	1.64	1.53
4	A	526	CIT	C3-C6	7.81	1.61	1.53

The worst 5 of 76 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	527	FAD	O4B-C1B-N9A	-6.79	102.12	108.44
5	C	527	FAD	O4B-C1B-N9A	-6.25	102.63	108.44
5	D	527	FAD	O4B-C1B-N9A	-6.11	102.76	108.44
5	B	527	FAD	O4B-C1B-N9A	-6.05	102.82	108.44
4	D	526	CIT	C3-C2-C1	5.93	128.13	113.77

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	B	522	NAG	C1
3	D	522	NAG	C1
3	A	522	NAG	C1
3	C	522	NAG	C1

There are no torsion outliers.

There are no ring outliers.

## 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 ⓘ

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	483/498 (96%)	-0.22	1 (0%) 93 94	13, 22, 35, 57	8 (1%)
1	B	483/498 (96%)	-0.27	3 (0%) 86 88	12, 21, 35, 58	7 (1%)
1	C	483/498 (96%)	-0.25	7 (1%) 72 72	12, 22, 35, 59	5 (1%)
1	D	483/498 (96%)	-0.23	9 (1%) 64 64	12, 22, 36, 59	4 (0%)
All	All	1932/1992 (96%)	-0.24	20 (1%) 75 80	12, 22, 35, 59	24 (1%)

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	363	THR	6.2
1	D	486	ASN	5.4
1	C	194	ASP	4.3
1	C	486	ASN	4.0
1	D	146	PRO	3.9

### 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates ⓘ

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, 95<sup>th</sup> 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAG	B	523	14/15	0.19	28.04	47,53,59,59	0
2	FUC	B	525	10/11	0.38	3.71	61,62,63,63	0
2	NAG	C	523	14/15	0.21	3.03	45,51,54,55	0
2	FUC	C	525	10/11	0.26	1.34	56,56,57,57	0
2	FUC	D	525	10/11	0.24	0.84	45,46,47,48	0
2	FUC	A	525	10/11	0.32	0.80	53,55,55,56	0
2	NAG	D	523	14/15	0.15	0.79	38,42,44,48	0
2	NAG	A	523	14/15	0.13	-0.41	40,43,49,51	0
2	NAG	A	524	14/15	0.29	-	52,53,56,57	0
2	NAG	B	524	14/15	0.57	-	62,64,65,66	0
2	NAG	C	524	14/15	0.34	-	57,59,60,61	0
2	NAG	D	524	14/15	0.33	-	51,54,57,58	0

## 6.4 Ligands ⓘ

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, 95<sup>th</sup> 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NAG	C	522	14/15	0.45	9.08	57,61,62,62	0
4	CIT	D	526	13/13	0.50	8.34	79,82,83,84	0
4	CIT	A	526	13/13	0.41	6.94	63,66,68,69	0
4	CIT	B	526	13/13	0.40	6.33	61,64,67,68	0
4	CIT	C	526	13/13	0.40	6.20	65,68,70,70	0
3	NAG	B	522	14/15	0.29	5.75	52,54,57,57	0
3	NAG	A	522	14/15	0.35	5.64	51,54,56,57	0
3	NAG	D	522	14/15	0.47	4.37	59,63,64,65	0
5	FAD	D	527	53/53	0.10	0.41	11,14,16,18	0
5	FAD	C	527	53/53	0.09	-0.13	10,12,15,16	0
5	FAD	A	527	53/53	0.09	-0.25	13,14,16,17	0
5	FAD	B	527	53/53	0.08	-0.49	10,13,15,16	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.