



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2018 – 05:33 pm 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 X-ray Structure 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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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 : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : 1.13  
EDS : trunk30967  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30967

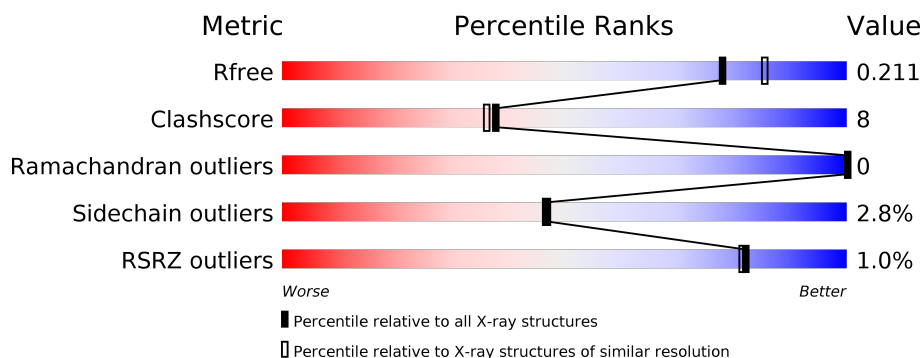
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 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))
$R_{free}$	111664	7193 (2.00-2.00)
Clashscore	122126	8267 (2.00-2.00)
Ramachandran outliers	120053	8166 (2.00-2.00)
Sidechain outliers	120020	8165 (2.00-2.00)
RSRZ outliers	108989	7011 (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. 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	498	<div> <div>82%</div> <div>14%</div> <div>••</div> </div>
1	B	498	<div> <div>%</div> <div>77%</div> <div>19%</div> <div>••</div> </div>
1	C	498	<div> <div>%</div> <div>82%</div> <div>14%</div> <div>••</div> </div>
1	D	498	<div> <div>2%</div> <div>80%</div> <div>17%</div> <div>••</div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	A	522	X	-	-	-
2	NAG	A	523	X	-	-	-
2	NAG	B	522	X	-	-	-
2	NAG	B	524	-	-	-	X
2	NAG	C	522	X	-	-	X
2	NAG	C	524	X	-	-	-
2	NAG	D	522	X	-	-	X
3	FUC	A	525	X	-	-	-
3	FUC	B	525	X	-	-	-
3	FUC	C	525	X	-	-	-
3	FUC	D	525	X	-	-	-
4	CIT	D	526	-	-	-	X

## 2 Entry composition [i](#)

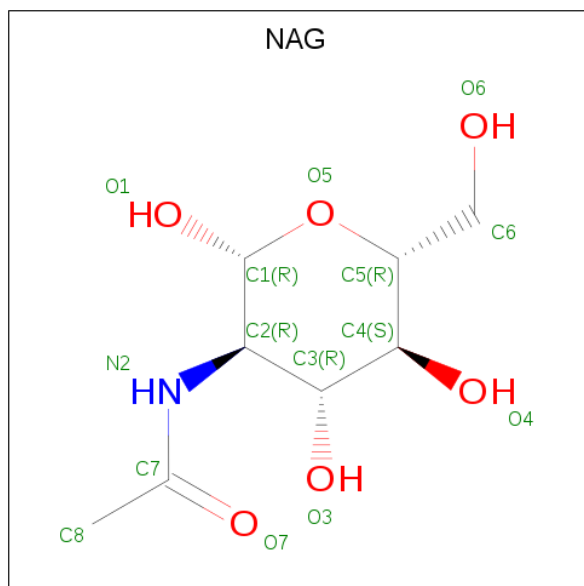
There are 6 unique types of molecules in this entry. The entry contains 17632 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 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 N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



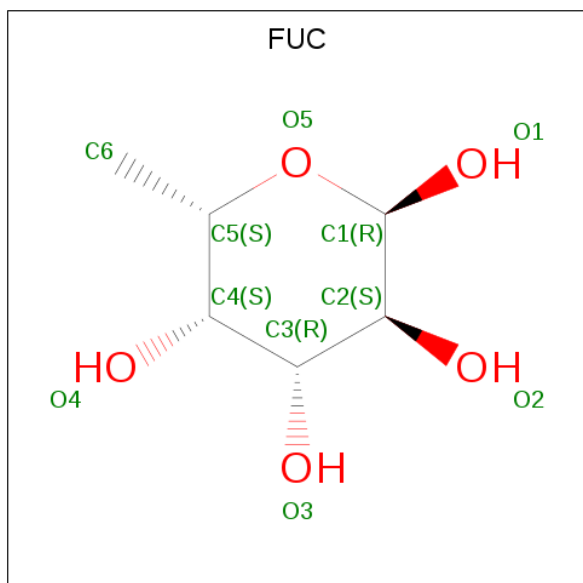
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

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

- Molecule 3 is ALPHA-L-FUCOSE (three-letter code: FUC) (formula: C<sub>6</sub>H<sub>12</sub>O<sub>5</sub>).



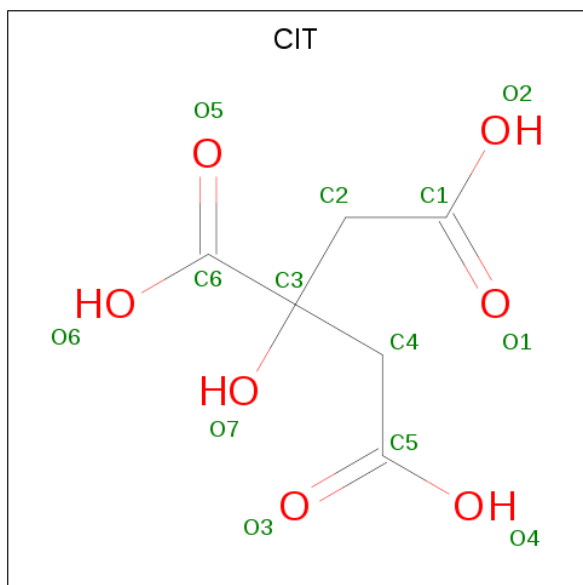
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			10	6	4		

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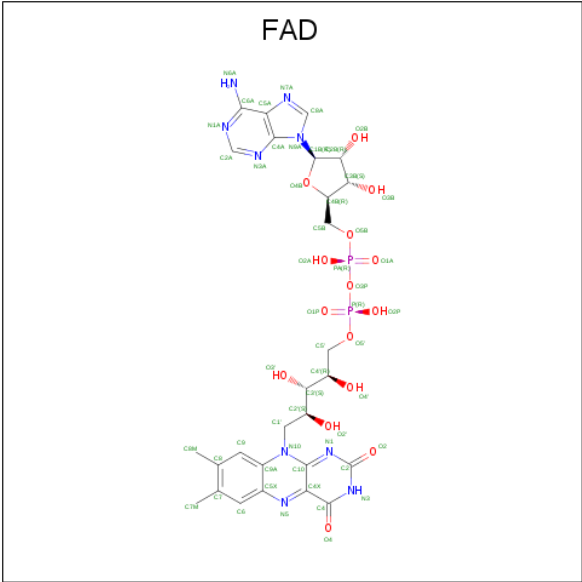
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			10	6	4		
3	C	1	Total	C	O	0	0
			10	6	4		
3	D	1	Total	C	O	0	0
			10	6	4		

- 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		

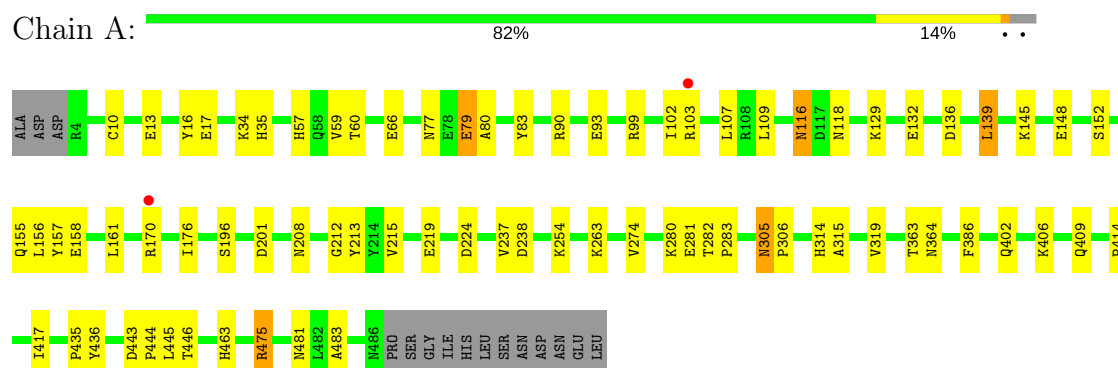
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	466	Total	O	0	0
			466	466		
6	B	497	Total	O	0	0
			497	497		
6	C	461	Total	O	0	0
			461	461		
6	D	445	Total	O	0	0
			445	445		

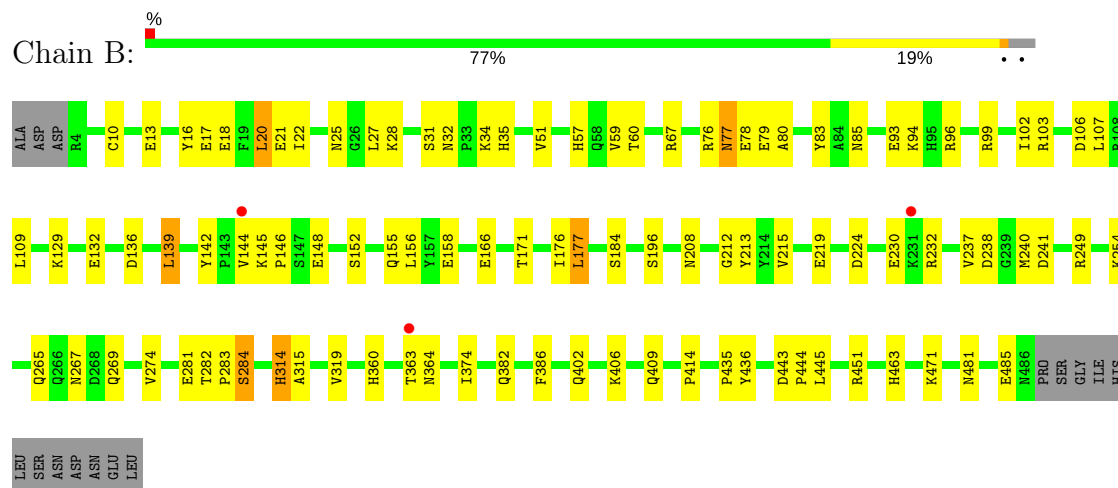
### 3 Residue-property plots [i](#)

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.

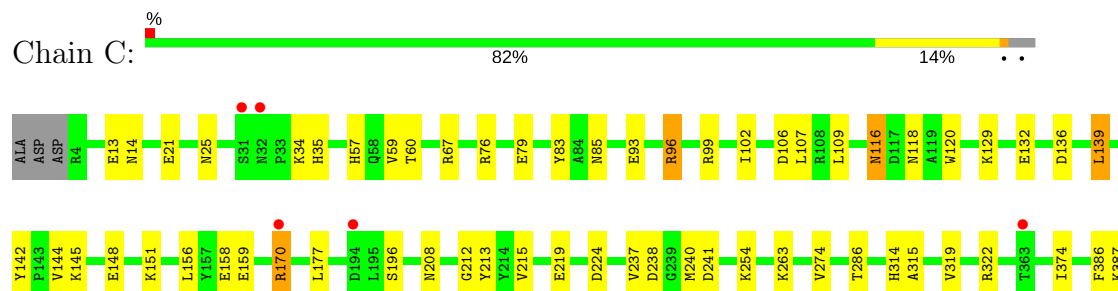
#### • Molecule 1: L-AMINO ACID OXIDASE



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



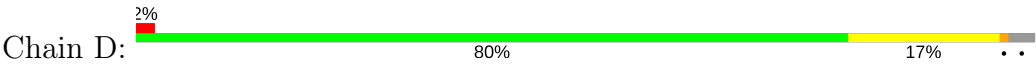
#### • Molecule 1: L-AMINO ACID OXIDASE







● Molecule 1: L-AMINO ACID OXIDASE



## 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 0.186 , 0.211	Depositor DCC
$R_{free}$ test set	13919 reflections (10.00%)	wwPDB-VP
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> )	0.38 , 57.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	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.

<sup>2</sup>Theoretical 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: 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

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	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	42	0	37	0	0
2	B	42	0	37	5	0
2	C	42	0	37	3	0
2	D	42	0	37	1	0
3	A	10	0	10	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	10	0	10	3	0
3	C	10	0	10	1	0
3	D	10	0	10	0	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

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 8.

The worst 5 of 257 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: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
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 [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	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%)	44	44
1	B	410/427 (96%)	399 (97%)	11 (3%)	48	49
1	C	402/427 (94%)	392 (98%)	10 (2%)	50	52
1	D	405/427 (95%)	392 (97%)	13 (3%)	42	41
All	All	1615/1708 (95%)	1569 (97%)	46 (3%)	47	47

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

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Mol	Chain	Res	Type
1	B	342	HIS
1	B	409	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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

24 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	NAG	A	522	1	14,14,15	0.74	0	17,19,21	1.03	1 (5%)
2	NAG	A	523	1,3,2	14,14,15	0.90	0	17,19,21	0.96	1 (5%)
2	NAG	A	524	2	14,14,15	0.60	0	17,19,21	0.80	0
3	FUC	A	525	2	9,10,11	0.70	0	13,14,16	2.28	3 (23%)
4	CIT	A	526	-	3,12,12	5.51	2 (66%)	3,17,17	4.69	1 (33%)
5	FAD	A	527	-	51,58,58	2.04	14 (27%)	57,89,89	1.80	7 (12%)
2	NAG	B	522	1	14,14,15	0.61	0	17,19,21	0.65	0
2	NAG	B	523	1,3,2	14,14,15	0.52	0	17,19,21	1.02	1 (5%)
2	NAG	B	524	2	14,14,15	0.68	0	17,19,21	2.10	3 (17%)
3	FUC	B	525	2	9,10,11	0.65	0	13,14,16	1.82	3 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	CIT	B	526	-	3,12,12	3.08	2 (66%)	3,17,17	4.73	1 (33%)
5	FAD	B	527	-	51,58,58	2.07	15 (29%)	57,89,89	1.81	7 (12%)
2	NAG	C	522	1	14,14,15	0.57	0	17,19,21	0.60	0
2	NAG	C	523	1,3,2	14,14,15	0.76	0	17,19,21	0.98	0
2	NAG	C	524	2	14,14,15	0.70	1 (7%)	17,19,21	0.85	1 (5%)
3	FUC	C	525	2	9,10,11	0.65	0	13,14,16	2.08	3 (23%)
4	CIT	C	526	-	3,12,12	6.92	2 (66%)	3,17,17	3.58	1 (33%)
5	FAD	C	527	-	51,58,58	2.04	15 (29%)	57,89,89	1.75	8 (14%)
2	NAG	D	522	1	14,14,15	0.65	0	17,19,21	0.69	0
2	NAG	D	523	1,3,2	14,14,15	0.66	0	17,19,21	0.70	0
2	NAG	D	524	2	14,14,15	0.56	0	17,19,21	0.92	1 (5%)
3	FUC	D	525	2	9,10,11	0.71	0	13,14,16	2.18	3 (23%)
4	CIT	D	526	-	3,12,12	5.42	2 (66%)	3,17,17	5.08	1 (33%)
5	FAD	D	527	-	51,58,58	2.00	14 (27%)	57,89,89	1.75	7 (12%)

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	522	1	1/1/5/7	0/6/23/26	0/1/1/1
2	NAG	A	523	1,3,2	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
3	FUC	A	525	2	2/2/4/5	0/0/17/20	0/1/1/1
4	CIT	A	526	-	-	0/6/16/16	0/0/0/0
5	FAD	A	527	-	-	0/28/50/50	0/6/6/6
2	NAG	B	522	1	1/1/5/7	0/6/23/26	0/1/1/1
2	NAG	B	523	1,3,2	-	0/6/23/26	0/1/1/1
2	NAG	B	524	2	-	0/6/23/26	0/1/1/1
3	FUC	B	525	2	2/2/4/5	0/0/17/20	0/1/1/1
4	CIT	B	526	-	-	0/6/16/16	0/0/0/0
5	FAD	B	527	-	-	0/28/50/50	0/6/6/6
2	NAG	C	522	1	1/1/5/7	0/6/23/26	0/1/1/1
2	NAG	C	523	1,3,2	-	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
3	FUC	C	525	2	3/3/4/5	0/0/17/20	0/1/1/1
4	CIT	C	526	-	-	0/6/16/16	0/0/0/0
5	FAD	C	527	-	-	0/28/50/50	0/6/6/6
2	NAG	D	522	1	1/1/5/7	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	D	523	1,3,2	-	0/6/23/26	0/1/1/1
2	NAG	D	524	2	-	0/6/23/26	0/1/1/1
3	FUC	D	525	2	2/2/4/5	0/0/17/20	0/1/1/1
4	CIT	D	526	-	-	0/6/16/16	0/0/0/0
5	FAD	D	527	-	-	0/28/50/50	0/6/6/6

The worst 5 of 67 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	527	FAD	PA-O2A	-3.77	1.36	1.55
5	C	527	FAD	PA-O2A	-3.77	1.36	1.55
5	B	527	FAD	PA-O2A	-3.69	1.37	1.55
5	D	527	FAD	PA-O2A	-3.66	1.37	1.55
5	B	527	FAD	P-O2P	-3.30	1.39	1.55

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	527	FAD	C4X-C4-N3	-4.57	116.97	123.47
5	B	527	FAD	C4B-O4B-C1B	-4.52	105.12	109.83
5	B	527	FAD	C4X-C4-N3	-4.51	117.05	123.47
5	A	527	FAD	C4X-C4-N3	-4.42	117.18	123.47
5	C	527	FAD	C4X-C4-N3	-4.39	117.22	123.47

5 of 15 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	525	FUC	C3
3	A	525	FUC	C4
2	C	522	NAG	C1
2	B	522	NAG	C1
3	C	525	FUC	C3

There are no torsion outliers.

There are no ring outliers.

11 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	525	FUC	1	0
4	A	526	CIT	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	522	NAG	1	0
2	B	523	NAG	1	0
2	B	524	NAG	4	0
3	B	525	FUC	3	0
2	C	522	NAG	2	0
2	C	523	NAG	1	0
3	C	525	FUC	1	0
2	D	522	NAG	1	0
4	D	526	CIT	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, 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%)	-0.31	2 (0%) 92 92	13, 22, 35, 57	8 (1%)
1	B	483/498 (96%)	-0.31	3 (0%) 89 88	12, 21, 35, 58	7 (1%)
1	C	483/498 (96%)	-0.31	6 (1%) 79 78	12, 22, 35, 59	5 (1%)
1	D	483/498 (96%)	-0.30	8 (1%) 70 68	12, 22, 36, 59	4 (0%)
All	All	1932/1992 (96%)	-0.30	19 (0%) 82 81	12, 22, 35, 59	24 (1%)

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	363	THR	6.1
1	D	486	ASN	5.4
1	C	486	ASN	4.6
1	C	194	ASP	4.5
1	D	146	PRO	4.2

### 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. 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	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAG	C	522	14/15	0.49	0.44	57,61,62,62	0
2	NAG	D	522	14/15	0.51	0.48	59,63,64,65	0
4	CIT	B	526	13/13	0.59	0.39	61,64,67,68	0
2	NAG	B	524	14/15	0.63	0.57	62,64,65,66	0
4	CIT	A	526	13/13	0.63	0.40	63,66,68,69	0
4	CIT	C	526	13/13	0.65	0.39	65,68,70,70	0
4	CIT	D	526	13/13	0.66	0.47	79,82,83,84	0
2	NAG	A	522	14/15	0.70	0.32	51,54,56,57	0
2	NAG	D	524	14/15	0.72	0.31	51,54,57,58	0
2	NAG	B	522	14/15	0.73	0.26	52,54,57,57	0
3	FUC	A	525	10/11	0.77	0.29	53,55,55,56	0
2	NAG	C	523	14/15	0.80	0.19	45,51,54,55	0
3	FUC	C	525	10/11	0.80	0.28	56,56,57,57	0
2	NAG	B	523	14/15	0.81	0.21	47,53,59,59	0
3	FUC	D	525	10/11	0.82	0.21	45,46,47,48	0
2	NAG	A	524	14/15	0.82	0.28	52,53,56,57	0
2	NAG	C	524	14/15	0.82	0.29	57,59,60,61	0
2	NAG	D	523	14/15	0.83	0.15	38,42,44,48	0
3	FUC	B	525	10/11	0.84	0.39	61,62,63,63	0
2	NAG	A	523	14/15	0.85	0.13	40,43,49,51	0
5	FAD	C	527	53/53	0.98	0.08	10,12,15,16	0
5	FAD	A	527	53/53	0.98	0.08	13,14,16,17	0
5	FAD	D	527	53/53	0.98	0.09	11,14,16,18	0
5	FAD	B	527	53/53	0.98	0.08	10,13,15,16	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.