



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 07:47 PM GMT

PDB ID : 1H82
Title : STRUCTURE OF POLYAMINE OXIDASE IN COMPLEX WITH GUAZATINE
Authors : Binda, C.; Coda, A.; Angelini, R.; Federico, R.; Ascenzi, P.; Mattevi, A.
Deposited on : 2001-01-24
Resolution : 1.90 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
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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

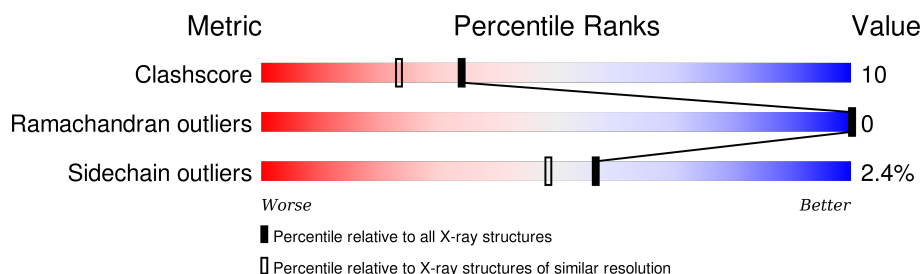
1 Overall quality at a glance

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))
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (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 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	472	 77% 19% ..
1	B	472	 76% 20% ..
1	C	472	 81% 15% ..

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
5	NAG	C	601	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	MAN	C	604	X	-	-	-

2 Entry composition [i](#)

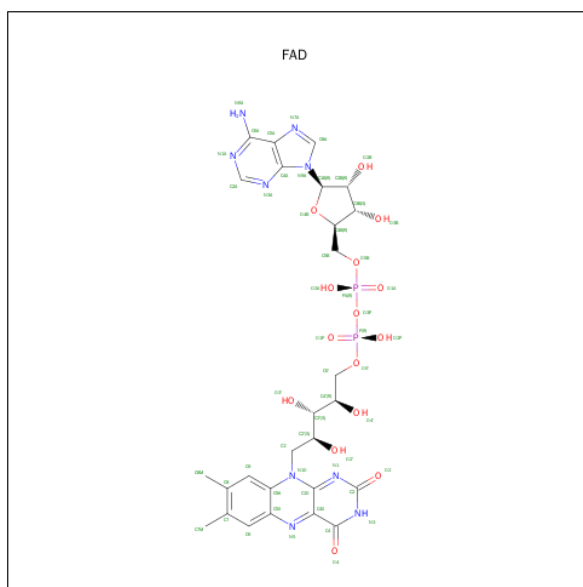
There are 7 unique types of molecules in this entry. The entry contains 12210 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 POLYAMINE OXIDASE.

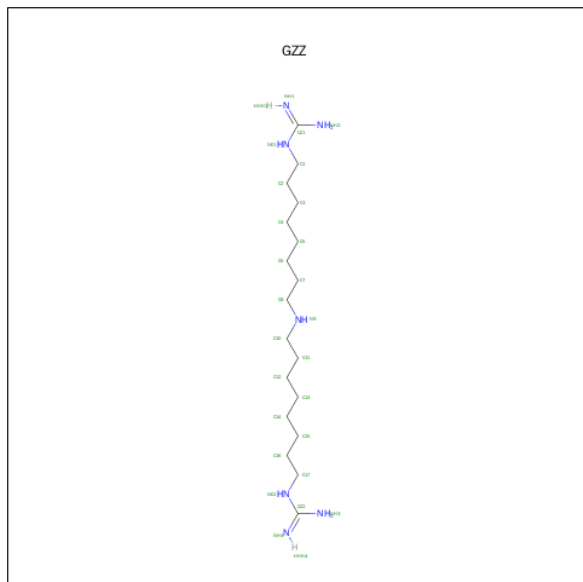
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	459	Total	C	N	O	S	54	0	0
			3684	2353	621	696	14			
1	B	462	Total	C	N	O	S	54	0	0
			3715	2374	627	700	14			
1	C	462	Total	C	N	O	S	41	0	0
			3715	2374	627	700	14			

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



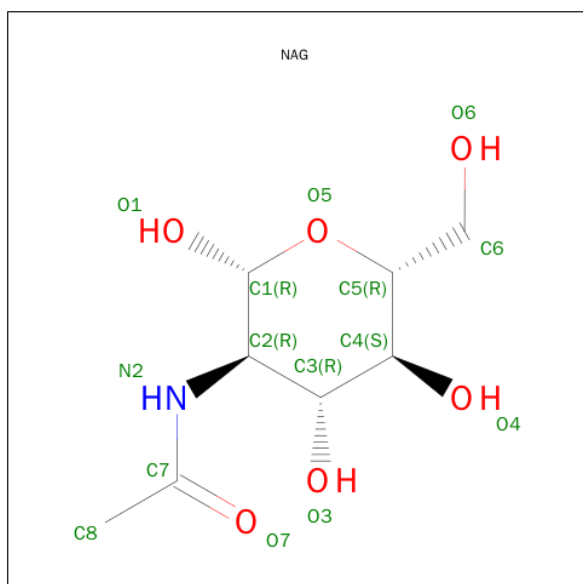
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 3 is N-{8-[(8-{[(E)-AMINO(IMINO)METHYL]AMINO}OCTYL)AMINO]OCTYL}GUANIDINE (three-letter code: GZZ) (formula: $C_{18}H_{41}N_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	N	0	0
			25	18	7		
3	B	1	Total	C	N	0	0
			25	18	7		
3	C	1	Total	C	N	0	0
			25	18	7		

- Molecule 4 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 5 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	C	2	Total	C	N	O	0	0
			24	14	1	9		

- Molecule 6 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	C	3	Total	C	N	O	0	0
			36	20	1	15		

- Molecule 7 is water.

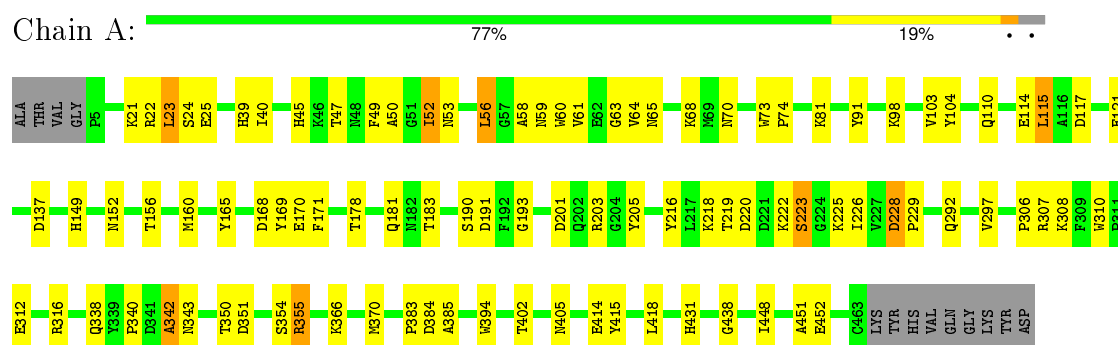
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	234	Total	O	0	0
			234	234		
7	B	243	Total	O	0	0
			243	243		
7	C	269	Total	O	0	0
			269	269		

3 Residue-property plots

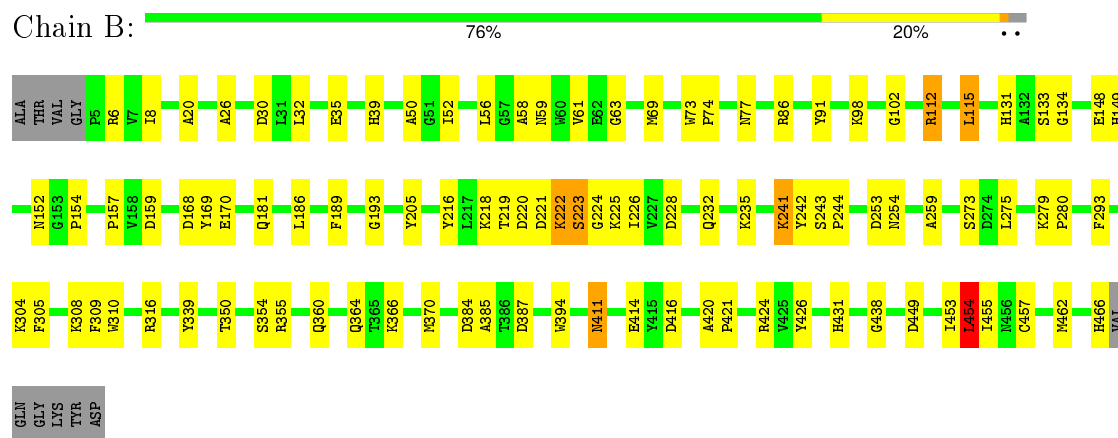
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

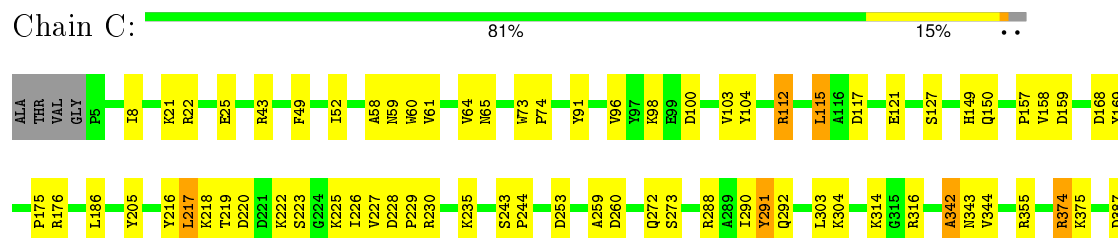
• Molecule 1: POLYAMINE OXIDASE



• Molecule 1: POLYAMINE OXIDASE



• Molecule 1: POLYAMINE OXIDASE



R412	L418	R424	H431	E434	G438	L454	H466	VAL	GLN	GLY	LYS	TYR	ASP
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4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	184.97Å 184.97Å 282.24Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 1.90	Depositor
% Data completeness (in resolution range)	94.3 (50.00-1.90)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT 5D	Depositor
R, R_{free}	0.199 , 0.231	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	12210	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FCA, GZZ, NAG, FAD, MAN

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	0.66	0/3775	1.17	13/5116 (0.3%)
1	B	0.66	0/3808	1.18	17/5160 (0.3%)
1	C	0.68	0/3808	1.17	16/5160 (0.3%)
All	All	0.67	0/11391	1.17	46/15436 (0.3%)

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
1	A	1	0
1	C	0	1
6	C	1	0
All	All	2	1

There are no bond length outliers.

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	355	ARG	NE-CZ-NH2	-11.84	114.38	120.30
1	A	342	ALA	N-CA-C	8.13	132.95	111.00
1	C	112	ARG	NE-CZ-NH1	7.75	124.17	120.30
1	B	112	ARG	NE-CZ-NH1	7.31	123.96	120.30
1	C	115	LEU	CB-CG-CD1	-6.55	99.86	111.00

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	341	ASP	CA

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Mol	Chain	Res	Type	Atom
6	C	604	MAN	C1

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	291	TYR	Sidechain

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	3684	0	3585	66	0
1	B	3715	0	3614	87	0
1	C	3715	0	3614	55	0
2	A	53	0	31	4	0
2	B	53	0	31	2	0
2	C	53	0	31	2	0
3	A	25	0	39	7	0
3	B	25	0	39	4	0
3	C	25	0	39	2	0
4	A	28	0	26	2	0
4	B	28	0	26	4	0
5	C	24	0	22	8	0
6	C	36	0	31	6	0
7	A	234	0	0	5	0
7	B	243	0	0	5	0
7	C	269	0	0	9	0
All	All	12210	0	11128	221	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 10.

The worst 5 of 221 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:272:GLN:HA	7:C:2151:HOH:O	1.25	1.28

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:220:ASP:HB3	1:A:223:SER:HB2	1.25	1.12
1:A:308:LYS:HZ3	1:A:312:GLU:HG3	0.94	1.10
1:C:219:THR:HG22	1:C:226:ILE:HA	1.43	1.00
1:B:220:ASP:HB3	1:B:223:SER:HB2	1.44	0.98

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	457/472 (97%)	437 (96%)	20 (4%)	0	100	100
1	B	460/472 (98%)	441 (96%)	19 (4%)	0	100	100
1	C	460/472 (98%)	443 (96%)	17 (4%)	0	100	100
All	All	1377/1416 (97%)	1321 (96%)	56 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	394/404 (98%)	384 (98%)	10 (2%)	55	47
1	B	397/404 (98%)	388 (98%)	9 (2%)	58	51
1	C	397/404 (98%)	387 (98%)	10 (2%)	55	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1188/1212 (98%)	1159 (98%)	29 (2%)	57 49

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	168	ASP
1	B	293	PHE
1	C	205	TYR
1	B	205	TYR
1	B	411	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	152	ASN
1	B	292	GLN
1	B	466	HIS
1	B	131	HIS
1	C	360	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 ⓘ

5 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
5	NAG	C	601	1,5,6	14,14,15	1.28	2 (14%)	15,19,21	1.61	5 (33%)
6	NAG	C	602	5,6	14,14,15	0.97	1 (7%)	15,19,21	1.58	1 (6%)
5	FCA	C	603	5	10,10,11	1.23	1 (10%)	14,14,16	1.81	5 (35%)
6	MAN	C	604	6	11,11,12	0.64	0	14,15,17	2.66	3 (21%)
6	MAN	C	605	6	11,11,12	0.57	0	14,15,17	1.59	3 (21%)

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
5	NAG	C	601	1,5,6	-	0/6/23/26	0/1/1/1
6	NAG	C	602	5,6	-	0/6/23/26	0/1/1/1
5	FCA	C	603	5	-	0/0/17/20	0/1/1/1
6	MAN	C	604	6	1/1/4/5	0/2/19/22	0/1/1/1
6	MAN	C	605	6	-	0/2/19/22	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	601	NAG	O5-C1	-2.77	1.39	1.43
5	C	603	FCA	C2-C3	-2.77	1.48	1.52
6	C	602	NAG	O5-C1	-2.75	1.39	1.43
5	C	601	NAG	C1-C2	-2.62	1.48	1.52

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	602	NAG	C2-N2-C7	-5.32	116.21	123.04
6	C	605	MAN	C1-C2-C3	-3.53	105.36	109.54
6	C	605	MAN	C2-C3-C4	-2.83	106.24	111.04
5	C	601	NAG	O4-C4-C3	-2.50	104.71	110.34
5	C	603	FCA	O5-C1-C2	-2.31	107.10	110.86

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	C	604	MAN	C1

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	601	NAG	7	0
6	C	602	NAG	6	0
5	C	603	FCA	3	0

5.6 Ligand geometry [i](#)

10 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	FAD	A	579	-	48,58,58	0.99	1 (2%)	54,89,89	2.15	10 (18%)
3	GZZ	A	590	-	18,24,24	1.03	2 (11%)	17,25,25	1.44	3 (17%)
4	NAG	A	601	1,4	14,14,15	0.94	1 (7%)	15,19,21	1.68	4 (26%)
4	NAG	A	602	4	14,14,15	0.90	0	15,19,21	1.85	3 (20%)
2	FAD	B	579	-	48,58,58	0.95	1 (2%)	54,89,89	1.88	5 (9%)
3	GZZ	B	590	-	18,24,24	1.25	2 (11%)	17,25,25	1.37	2 (11%)
4	NAG	B	601	1,4	14,14,15	1.26	3 (21%)	15,19,21	2.49	3 (20%)
4	NAG	B	602	4	14,14,15	0.96	1 (7%)	15,19,21	1.37	2 (13%)
2	FAD	C	579	-	48,58,58	1.01	2 (4%)	54,89,89	2.24	10 (18%)
3	GZZ	C	590	-	18,24,24	1.21	2 (11%)	17,25,25	0.98	1 (5%)

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	FAD	A	579	-	-	0/30/50/50	0/6/6/6
3	GZZ	A	590	-	-	0/18/22/22	0/0/0/0
4	NAG	A	601	1,4	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	A	602	4	-	0/6/23/26	0/1/1/1
2	FAD	B	579	-	-	0/30/50/50	0/6/6/6
3	GZZ	B	590	-	-	0/18/22/22	0/0/0/0
4	NAG	B	601	1,4	-	0/6/23/26	0/1/1/1
4	NAG	B	602	4	-	0/6/23/26	0/1/1/1
2	FAD	C	579	-	-	0/30/50/50	0/6/6/6
3	GZZ	C	590	-	-	0/18/22/22	0/0/0/0

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	601	NAG	O5-C1	-2.74	1.39	1.43
4	B	601	NAG	C1-C2	-2.29	1.49	1.52
4	B	602	NAG	O5-C1	-2.18	1.40	1.43
4	A	601	NAG	O3-C3	2.05	1.47	1.43
3	A	590	GZZ	C8-N9	2.27	1.54	1.46

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	579	FAD	C4X-C10-N10	-8.29	115.64	120.52
4	B	601	NAG	C2-N2-C7	-7.29	113.67	123.04
2	A	579	FAD	C4X-C4-N3	-6.38	114.86	123.59
2	A	579	FAD	C4X-C10-N10	-6.26	116.83	120.52
2	B	579	FAD	C4X-C4-N3	-5.79	115.67	123.59

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	579	FAD	4	0
3	A	590	GZZ	7	0
4	A	601	NAG	2	0
4	A	602	NAG	2	0
2	B	579	FAD	2	0
3	B	590	GZZ	4	0
4	B	601	NAG	4	0
4	B	602	NAG	4	0
2	C	579	FAD	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	590	GZZ	2	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.