



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 12:33 am GMT

PDB ID : 2XVF
Title : CRYSTAL STRUCTURE OF BACTERIAL FLAVIN-CONTAINING
MONOOXYGENASE
Authors : Cho, H.J.; Kang, B.S.
Deposited on : 2010-10-26
Resolution : 2.40 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 : 1.7.2 (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

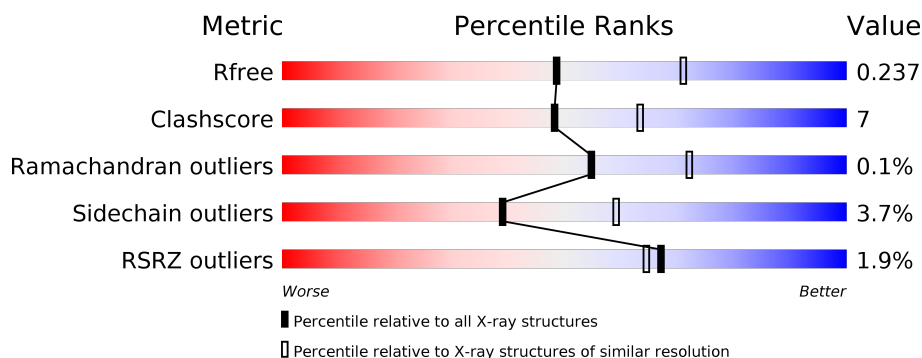
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	100719	3166 (2.40-2.40)
Clashscore	112137	3674 (2.40-2.40)
Ramachandran outliers	110173	3616 (2.40-2.40)
Sidechain outliers	110143	3617 (2.40-2.40)
RSRZ outliers	101464	3195 (2.40-2.40)

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	464	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 3%, orange 1%, yellow 1%, green 82%, grey 13%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 3% 82% 13% </div> </div>
1	B	464	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 81%, yellow 1%, orange 1%, grey 13%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 81% 13% </div> </div>
1	C	464	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 3%, orange 1%, yellow 1%, green 77%, grey 18%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 3% 77% 18% </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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NO3	A	1449	-	-	-	X
3	NO3	B	1447	-	-	-	X
4	GOL	B	1448	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11219 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 FLAVIN-CONTAINING MONOOXYGENASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	445	Total	C	N	O	S	Se	0	0	0
			3608	2321	597	670	7	13			
1	B	444	Total	C	N	O	S	Se	0	2	0
			3626	2330	604	672	7	13			
1	C	445	Total	C	N	O	S	Se	0	0	0
			3587	2298	591	678	7	13			

There are 24 discrepancies between the modelled and reference sequences:

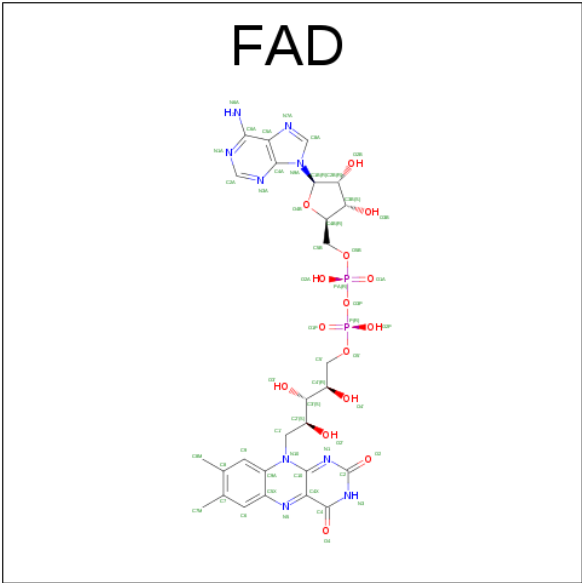
Chain	Residue	Modelled	Actual	Comment	Reference
A	457	LEU	-	EXPRESSION TAG	UNP Q83XK4
A	458	GLU	-	EXPRESSION TAG	UNP Q83XK4
A	459	HIS	-	EXPRESSION TAG	UNP Q83XK4
A	460	HIS	-	EXPRESSION TAG	UNP Q83XK4
A	461	HIS	-	EXPRESSION TAG	UNP Q83XK4
A	462	HIS	-	EXPRESSION TAG	UNP Q83XK4
A	463	HIS	-	EXPRESSION TAG	UNP Q83XK4
A	464	HIS	-	EXPRESSION TAG	UNP Q83XK4
B	457	LEU	-	EXPRESSION TAG	UNP Q83XK4
B	458	GLU	-	EXPRESSION TAG	UNP Q83XK4
B	459	HIS	-	EXPRESSION TAG	UNP Q83XK4
B	460	HIS	-	EXPRESSION TAG	UNP Q83XK4
B	461	HIS	-	EXPRESSION TAG	UNP Q83XK4
B	462	HIS	-	EXPRESSION TAG	UNP Q83XK4
B	463	HIS	-	EXPRESSION TAG	UNP Q83XK4
B	464	HIS	-	EXPRESSION TAG	UNP Q83XK4
C	457	LEU	-	EXPRESSION TAG	UNP Q83XK4
C	458	GLU	-	EXPRESSION TAG	UNP Q83XK4
C	459	HIS	-	EXPRESSION TAG	UNP Q83XK4
C	460	HIS	-	EXPRESSION TAG	UNP Q83XK4
C	461	HIS	-	EXPRESSION TAG	UNP Q83XK4
C	462	HIS	-	EXPRESSION TAG	UNP Q83XK4
C	463	HIS	-	EXPRESSION TAG	UNP Q83XK4

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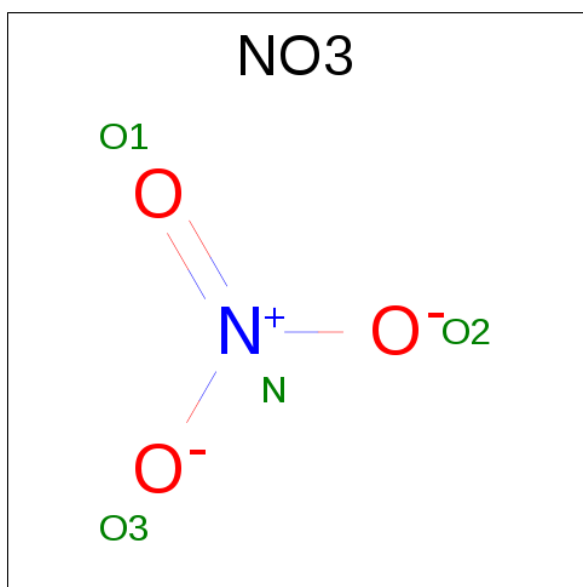
Chain	Residue	Modelled	Actual	Comment	Reference
C	464	HIS	-	EXPRESSION TAG	UNP Q83XK4

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).



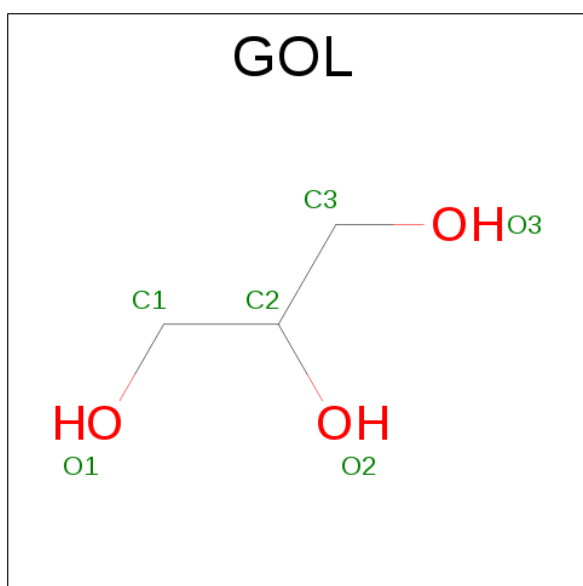
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 3 is NITRATE ION (three-letter code: NO3) (formula: NO₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	N	O	0	0
			4	1	3		
3	B	1	Total	N	O	0	0
			4	1	3		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

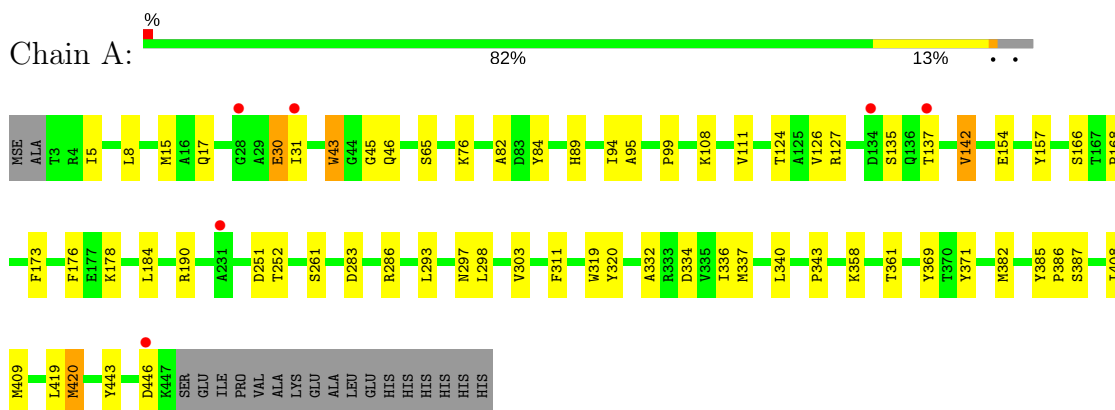
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	75	Total 75	O 75	0	0
5	B	108	Total 108	O 108	0	0
5	C	42	Total 42	O 42	0	0

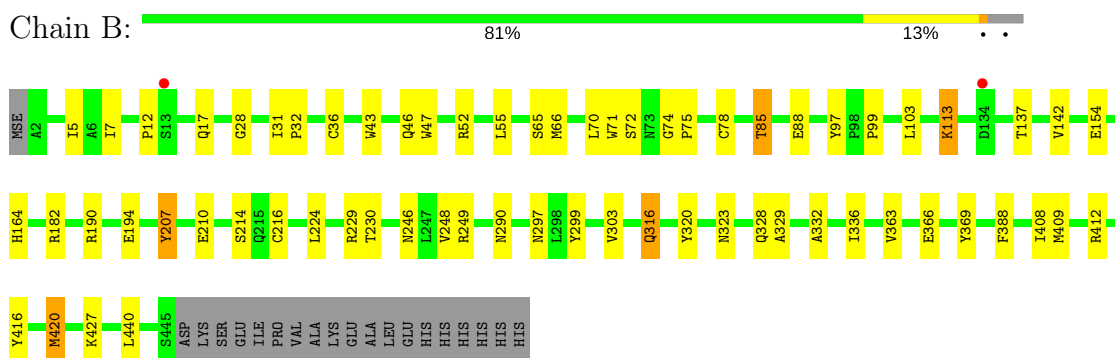
3 Residue-property plots [i](#)

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.

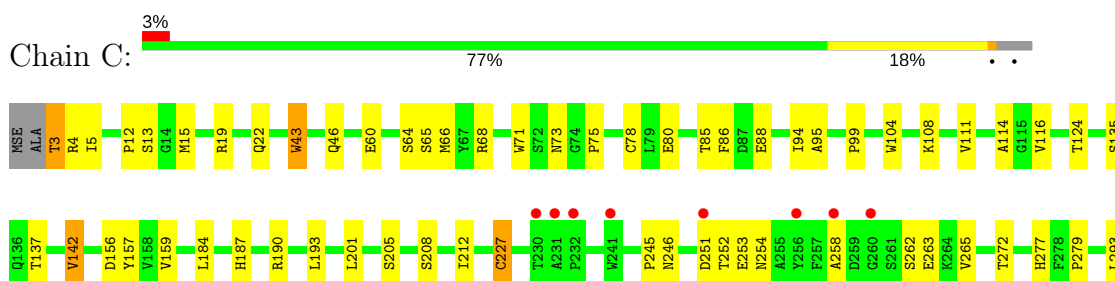
• Molecule 1: FLAVIN-CONTAINING MONOOXYGENASE

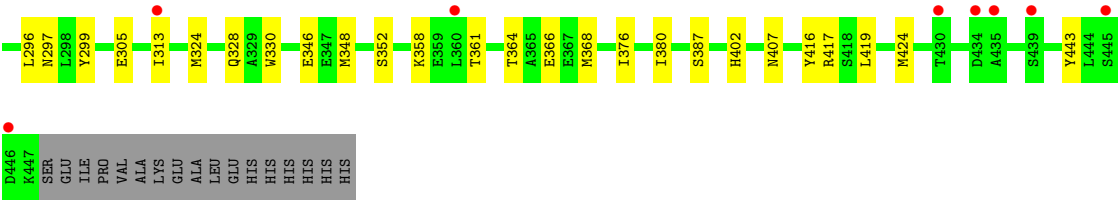


• Molecule 1: FLAVIN-CONTAINING MONOOXYGENASE



• Molecule 1: FLAVIN-CONTAINING MONOOXYGENASE





R446	50.0	Allowed
R447	50.0	Allowed
SER	50.0	Allowed
GLU	50.0	Allowed
ILE	50.0	Allowed
PRO	50.0	Allowed
VAL	50.0	Allowed
ALA	50.0	Allowed
LYS	50.0	Allowed
GLU	50.0	Allowed
ALA	50.0	Allowed
LEU	50.0	Allowed
GLU	50.0	Allowed
HIS	50.0	Allowed
HIS	50.0	Allowed
HIS	50.0	Allowed
HIS	50.0	Allowed
HIS	50.0	Allowed
HIS	50.0	Allowed

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	158.62Å 70.08Å 140.96Å 90.00° 90.71° 90.00°	Depositor
Resolution (Å)	34.38 – 2.40 34.38 – 2.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (34.38-2.40) 84.7 (34.38-2.40)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	44.13 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, R_{free}	0.184 , 0.236 0.187 , 0.237	Depositor DCC
R_{free} test set	2627 reflections (5.37%)	DCC
Wilson B-factor (Å ²)	41.2	Xtriage
Anisotropy	0.012	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 36.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.021 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11219	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.03% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, FAD, NO3

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	0.54	1/3709 (0.0%)	0.59	1/5023 (0.0%)
1	B	0.51	0/3734	0.59	0/5055
1	C	0.50	0/3688	0.55	0/5004
All	All	0.52	1/11131 (0.0%)	0.58	1/15082 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	320	TYR	CD1-CE1	-6.02	1.30	1.39

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	190	ARG	NE-CZ-NH2	-5.41	117.60	120.30

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	3608	0	3356	43	0
1	B	3626	0	3393	49	0
1	C	3587	0	3274	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	53	0	31	1	0
2	B	53	0	31	1	0
2	C	53	0	31	3	0
3	A	4	0	0	0	0
3	B	4	0	0	0	0
4	B	6	0	8	0	0
5	A	75	0	0	0	0
5	B	108	0	0	3	0
5	C	42	0	0	1	0
All	All	11219	0	10124	146	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 7.

The worst 5 of 146 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:B:388:PHE:HB3	1:B:420:MSE:HE1	1.46	0.96
1:C:305:GLU:HG2	1:C:348:MSE:HE2	1.48	0.96
1:B:388:PHE:CB	1:B:420:MSE:HE1	1.96	0.95
1:A:46:GLN:NE2	1:A:65:SER:H	1.65	0.94
1:A:31:ILE:HG22	1:A:337:MSE:CE	1.99	0.93

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	443/464 (96%)	423 (96%)	19 (4%)	1 (0%)	51 67
1	B	444/464 (96%)	429 (97%)	15 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	443/464 (96%)	419 (95%)	24 (5%)	0	100	100
All	All	1330/1392 (96%)	1271 (96%)	58 (4%)	1 (0%)	55	72

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	343	PRO

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	373/391 (95%)	361 (97%)	12 (3%)	44	65
1	B	379/391 (97%)	368 (97%)	11 (3%)	48	68
1	C	369/391 (94%)	351 (95%)	18 (5%)	29	46
All	All	1121/1173 (96%)	1080 (96%)	41 (4%)	39	59

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	297	ASN
1	B	427	LYS
1	C	387	SER
1	B	316	GLN
1	B	363	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	297	ASN
1	B	323	ASN
1	C	403	HIS
1	B	316	GLN

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Mol	Chain	Res	Type
1	B	377	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

6 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	1448	-	51,58,58	1.24	5 (9%)	54,89,89	2.12	7 (12%)
3	NO3	A	1449	-	1,3,3	4.47	1 (100%)	0,3,3	0.00	-
2	FAD	B	1446	-	51,58,58	1.19	5 (9%)	54,89,89	1.99	7 (12%)
3	NO3	B	1447	-	1,3,3	4.48	1 (100%)	0,3,3	0.00	-
4	GOL	B	1448	-	5,5,5	0.33	0	5,5,5	0.19	0
2	FAD	C	1448	-	51,58,58	1.31	6 (11%)	54,89,89	1.93	6 (11%)

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	1448	-	-	0/28/50/50	0/6/6/6
3	NO3	A	1449	-	-	0/0/0/0	0/0/0/0
2	FAD	B	1446	-	-	0/28/50/50	0/6/6/6
3	NO3	B	1447	-	-	0/0/0/0	0/0/0/0
4	GOL	B	1448	-	-	0/4/4/4	0/0/0/0
2	FAD	C	1448	-	-	0/28/50/50	0/6/6/6

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1448	FAD	C1'-N10	2.14	1.50	1.48
2	B	1446	FAD	C2A-N1A	2.18	1.38	1.33
2	C	1448	FAD	C2A-N1A	2.23	1.38	1.33
2	B	1446	FAD	C4-N3	2.39	1.37	1.33
2	A	1448	FAD	C4-N3	2.54	1.37	1.33

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1448	FAD	N3A-C2A-N1A	-11.42	118.92	128.86
2	B	1446	FAD	N3A-C2A-N1A	-11.00	119.28	128.86
2	C	1448	FAD	N3A-C2A-N1A	-10.40	119.80	128.86
2	A	1448	FAD	C4X-C4-N3	-2.95	119.29	123.48
2	C	1448	FAD	C4X-C4-N3	-2.41	120.06	123.48

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1448	FAD	1	0
2	B	1446	FAD	1	0
2	C	1448	FAD	3	0

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 [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	432/464 (93%)	-0.11	6 (1%) 75 74	24, 45, 68, 85	0
1	B	431/464 (92%)	-0.29	2 (0%) 90 89	21, 41, 60, 76	0
1	C	432/464 (93%)	0.07	16 (3%) 42 41	34, 55, 95, 113	0
All	All	1295/1392 (93%)	-0.11	24 (1%) 67 64	21, 46, 83, 113	0

The worst 5 of 24 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	232	PRO	3.3
1	C	430	THR	3.3
1	A	134	ASP	2.9
1	B	134	ASP	2.7
1	C	446	ASP	2.7

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(\AA^2)	Q<0.9
4	GOL	B	1448	6/6	0.85	0.44	7.02	93,93,94,94	0
3	NO3	A	1449	4/4	0.95	0.26	6.37	74,75,75,75	0
3	NO3	B	1447	4/4	0.89	0.24	4.00	59,60,60,60	0
2	FAD	A	1448	53/53	0.98	0.25	1.66	31,35,39,42	0
2	FAD	C	1448	53/53	0.96	0.22	0.82	40,44,51,52	0
2	FAD	B	1446	53/53	0.98	0.23	0.80	31,33,34,36	0

6.5 Other polymers [i](#)

There are no such residues in this entry.