



# Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 02:32 pm BST

PDB ID : 4YTZ  
Title : Rat xanthine oxidoreductase, C-terminal deletion protein variant, crystal grown without dithiothreitol  
Authors : Nishino, T.; Okamoto, K.; Kawaguchi, Y.; Matsumura, T.; Eger, B.T.; Pai, E.F.; Nishino, T.  
Deposited on : 2015-03-18  
Resolution : 2.30 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](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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

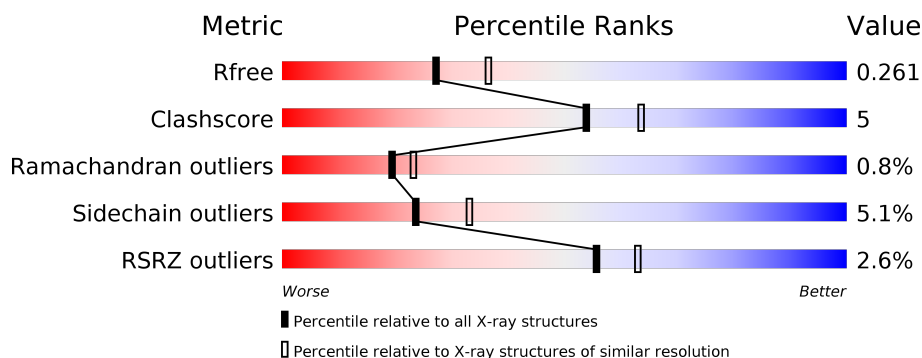
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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))
$R_{free}$	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 respectively. 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	1315	<div> <div>3%</div> <div> <div></div> <div>83%</div> <div>13%</div> <div>••</div> </div> </div>
1	B	1315	<div> <div>2%</div> <div> <div></div> <div>84%</div> <div>11%</div> <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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	URC	A	1404	-	X	-	-
4	URC	B	1404	-	X	-	-

## 2 Entry composition [i](#)

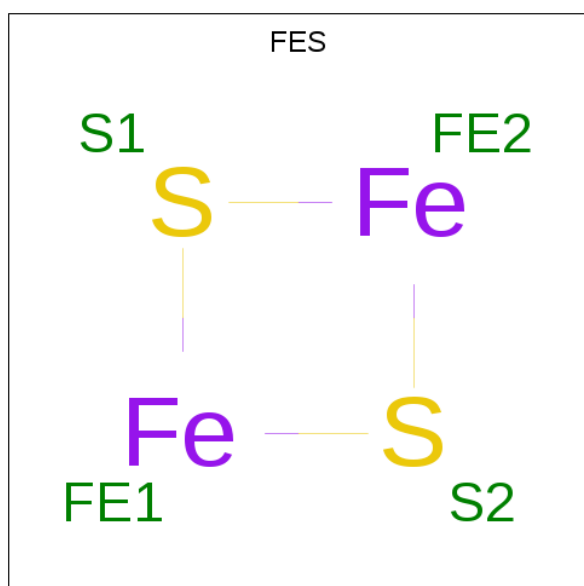
There are 7 unique types of molecules in this entry. The entry contains 20067 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Xanthine dehydrogenase/oxidase.

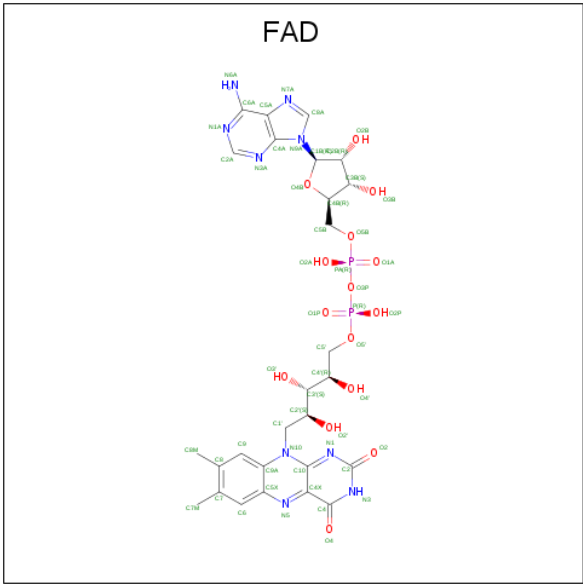
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1289	Total	C	N	O	S	0	0	0
			9964	6314	1714	1873	63			
1	B	1273	Total	C	N	O	S	0	0	0
			9840	6232	1696	1849	63			

- Molecule 2 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula:  $\text{Fe}_2\text{S}_2$ ).



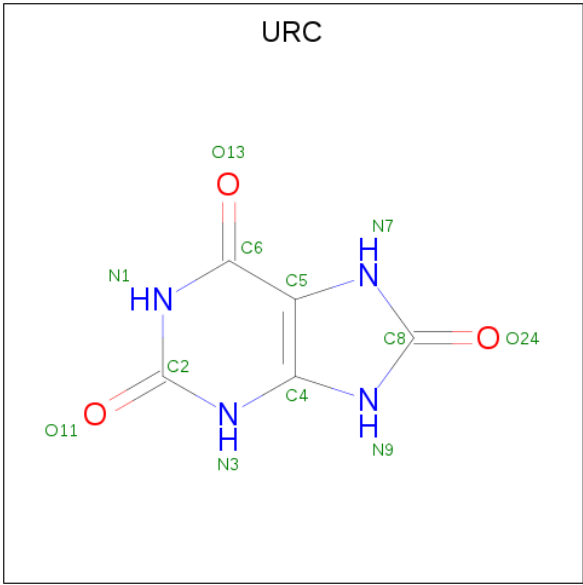
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	Fe	S	0	0
			4	2	2		
2	A	1	Total	Fe	S	0	0
			4	2	2		
2	B	1	Total	Fe	S	0	0
			4	2	2		
2	B	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C<sub>27</sub>H<sub>33</sub>N<sub>9</sub>O<sub>15</sub>P<sub>2</sub>).



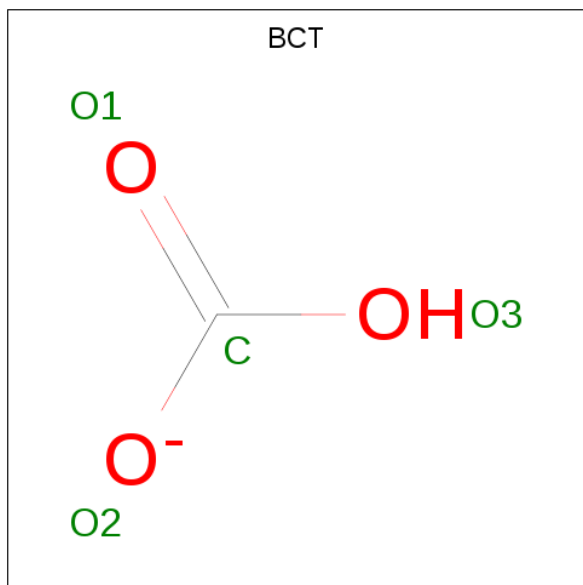
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 4 is URIC ACID (three-letter code: URC) (formula: C<sub>5</sub>H<sub>4</sub>N<sub>4</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			12	5	4	3		
4	B	1	Total	C	N	O	0	0
			12	5	4	3		

- Molecule 5 is BICARBONATE ION (three-letter code: BCT) (formula:  $\text{CHO}_3$ ).



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

- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	2	Total	Ca	0	0
			2	2		
6	A	2	Total	Ca	0	0
			2	2		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	40	Total	O	0	0
			40	40		

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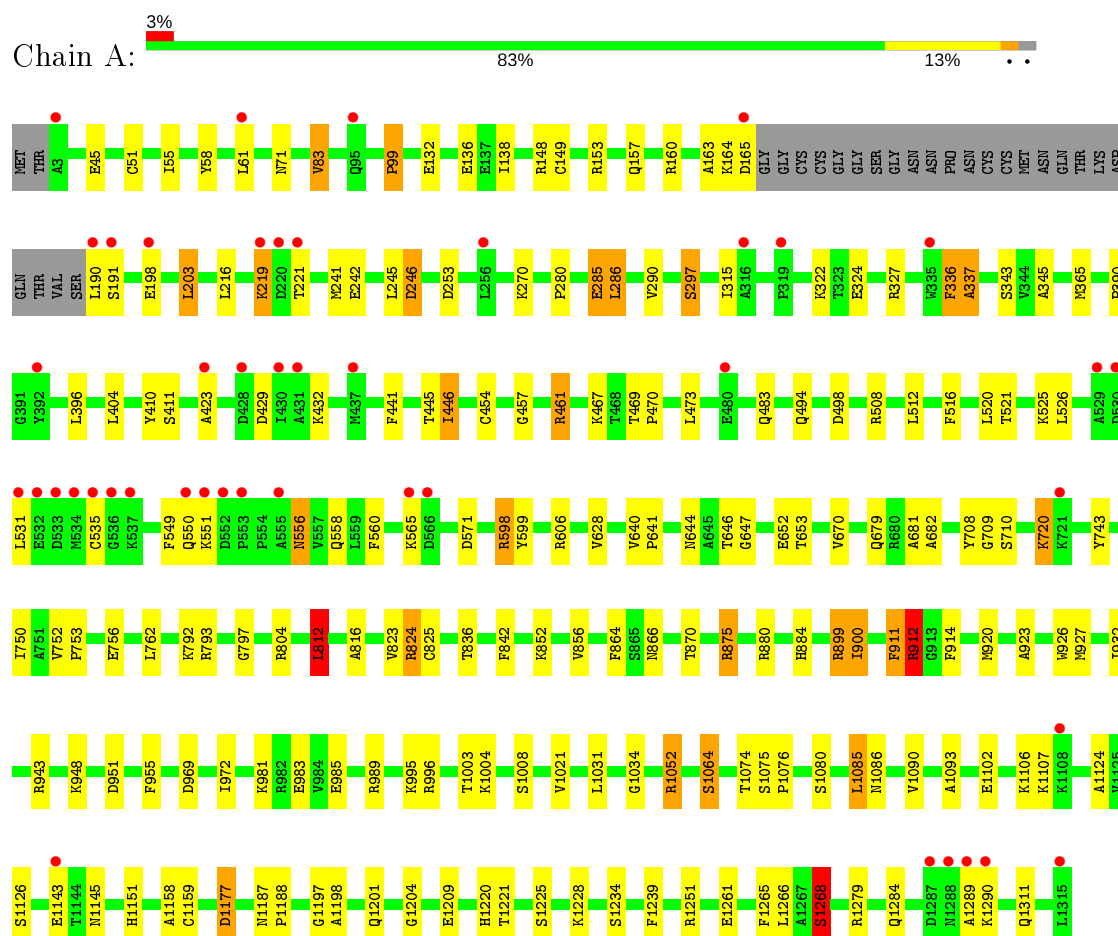
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	65	Total	O	0	0
			65	65		

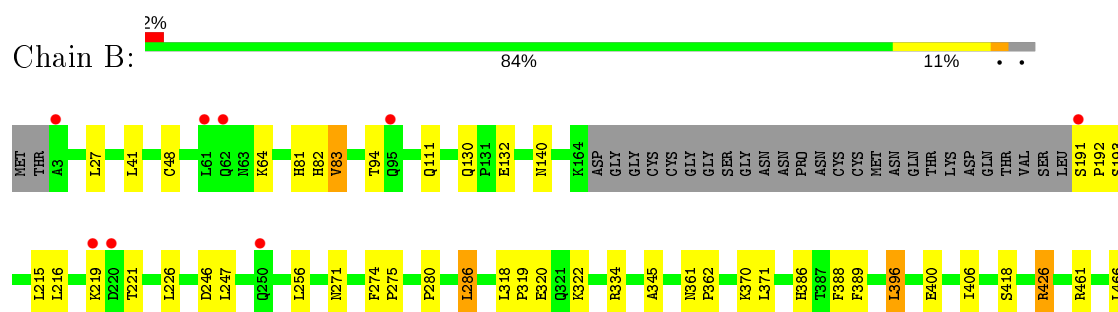
### 3 Residue-property plots

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.

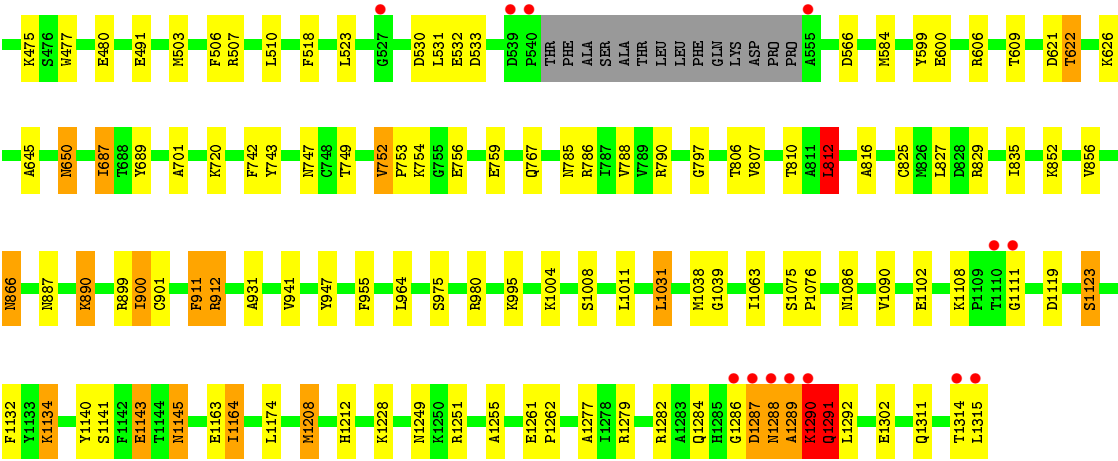
#### • Molecule 1: Xanthine dehydrogenase/oxidase



#### • Molecule 1: Xanthine dehydrogenase/oxidase







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	100.17Å 139.12Å 223.27Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.87 – 2.30 29.87 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.7 (29.87-2.30) 96.7 (29.87-2.30)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.76 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.5.0110	Depositor
R, $R_{free}$	0.207 , 0.265 0.206 , 0.261	Depositor DCC
$R_{free}$ test set	5404 reflections (4.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	36.5	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 28.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	20067	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.58% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BCT, CA, FES, FAD, URC

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	0.95	3/10174 (0.0%)	0.89	11/13767 (0.1%)
1	B	1.00	1/10045 (0.0%)	0.92	14/13588 (0.1%)
All	All	0.98	4/20219 (0.0%)	0.91	25/27355 (0.1%)

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	B	0	1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	890	LYS	CD-CE	5.26	1.64	1.51
1	A	136	GLU	CG-CD	5.12	1.59	1.51
1	A	1268	SER	CB-OG	-5.12	1.35	1.42
1	A	198	GLU	CG-CD	5.11	1.59	1.51

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	812	LEU	CA-CB-CG	-11.39	89.11	115.30
1	A	875	ARG	NE-CZ-NH2	-11.10	114.75	120.30
1	B	531	LEU	CA-CB-CG	10.23	138.83	115.30
1	B	812	LEU	CA-CB-CG	-9.37	93.75	115.30
1	B	812	LEU	CB-CG-CD2	-7.84	97.66	111.00
1	B	812	LEU	CB-CG-CD1	-7.82	97.72	111.00
1	A	989	ARG	NE-CZ-NH2	-6.79	116.90	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	507	ARG	NE-CZ-NH1	6.49	123.54	120.30
1	B	606	ARG	NE-CZ-NH2	-6.43	117.09	120.30
1	B	1291	GLN	N-CA-C	-6.37	93.79	111.00
1	A	812	LEU	CB-CG-CD2	-6.32	100.26	111.00
1	A	498	ASP	CB-CG-OD1	6.01	123.70	118.30
1	A	989	ARG	NE-CZ-NH1	5.75	123.18	120.30
1	A	1085	LEU	CB-CG-CD1	5.74	120.75	111.00
1	B	83	VAL	CG1-CB-CG2	5.65	119.94	110.90
1	B	1208	MET	CA-CB-CG	5.52	122.68	113.30
1	A	912	ARG	NE-CZ-NH2	-5.42	117.59	120.30
1	B	829	ARG	NE-CZ-NH1	5.41	123.01	120.30
1	B	790	ARG	NE-CZ-NH1	5.41	123.01	120.30
1	A	996	ARG	NE-CZ-NH2	-5.35	117.62	120.30
1	B	396	LEU	CA-CB-CG	5.31	127.51	115.30
1	A	598	ARG	NE-CZ-NH2	-5.29	117.65	120.30
1	B	621	ASP	CB-CG-OD1	5.23	123.00	118.30
1	A	875	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	B	426	ARG	NE-CZ-NH2	-5.05	117.78	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	1111	GLY	Peptide

## 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	9964	0	9968	110	0
1	B	9840	0	9841	107	0
2	A	8	0	0	0	0
2	B	8	0	0	0	0
3	A	53	0	31	2	0
3	B	53	0	31	2	0
4	A	12	0	4	0	0
4	B	12	0	4	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	4	0	0	0	0
5	B	4	0	0	0	0
6	A	2	0	0	0	0
6	B	2	0	0	0	0
7	A	40	0	0	0	0
7	B	65	0	0	0	0
All	All	20067	0	19879	209	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 5.

All (209) 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:1291:GLN:HG3	1:B:1291:GLN:O	1.64	0.96
1:B:1282:ARG:HE	1:B:1290:LYS:CB	1.76	0.96
1:B:1282:ARG:HE	1:B:1290:LYS:HB3	1.30	0.96
1:A:191:SER:HB2	1:A:560:PHE:O	1.71	0.90
1:A:461:ARG:HH11	1:A:461:ARG:HG3	1.38	0.88
1:B:1290:LYS:O	1:B:1291:GLN:O	1.91	0.87
1:A:1265:PHE:O	1:A:1268:SER:HB2	1.75	0.86
1:A:955:PHE:HA	1:A:1145:ASN:HD21	1.42	0.85
1:A:710:SER:HA	1:A:899:ARG:NH2	1.91	0.85
1:B:955:PHE:HA	1:B:1145:ASN:HD21	1.43	0.81
1:A:710:SER:HA	1:A:899:ARG:HH21	1.48	0.79
1:B:1164:ILE:HD13	1:B:1277:ALA:HB1	1.67	0.76
1:A:753:PRO:HD3	1:A:816:ALA:HB1	1.67	0.75
1:B:216:LEU:O	1:B:219:LYS:HG2	1.86	0.75
1:B:1164:ILE:HD13	1:B:1277:ALA:CB	2.20	0.72
1:B:1282:ARG:HE	1:B:1290:LYS:HB2	1.54	0.71
1:B:687:ILE:HG12	1:B:689:TYR:CZ	2.26	0.71
1:A:1289:ALA:HB1	1:A:1290:LYS:HA	1.72	0.70
1:B:388:PHE:CD1	1:B:396:LEU:CD2	2.77	0.68
1:B:752:VAL:HG22	1:B:754:LYS:HE2	1.74	0.68
1:A:242:GLU:O	1:A:246:ASP:HB2	1.94	0.67
1:A:710:SER:O	1:A:875:ARG:NH2	2.27	0.67
1:A:55:ILE:HG23	1:A:83:VAL:HG13	1.78	0.66
1:A:467:LYS:O	1:A:470:PRO:HD2	1.96	0.66
1:B:1141:SER:OG	1:B:1143:GLU:HG2	1.95	0.66
1:A:606:ARG:HD3	1:A:679:GLN:HA	1.79	0.65
1:A:432:LYS:O	1:A:457:GLY:HA3	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:756:GLU:HB3	1:B:584:MET:SD	2.37	0.65
1:B:767:GLN:HG2	1:B:1038:MET:HE2	1.77	0.65
1:A:58:TYR:CE2	1:A:219:LYS:HD3	2.32	0.64
1:B:1290:LYS:O	1:B:1291:GLN:C	2.37	0.63
1:B:1291:GLN:O	1:B:1291:GLN:CG	2.44	0.62
1:B:1289:ALA:H	1:B:1290:LYS:HZ3	1.46	0.62
1:A:920:MET:HE3	1:A:1265:PHE:CG	2.36	0.61
1:A:598:ARG:O	1:B:600:GLU:HG2	2.00	0.61
1:A:920:MET:HE3	1:A:1265:PHE:CD2	2.35	0.61
1:B:1286:GLY:O	1:B:1287:ASP:HB2	2.01	0.60
1:B:749:THR:HG22	1:B:812:LEU:HD22	1.81	0.60
1:A:324:GLU:HB2	1:A:411:SER:HB3	1.83	0.59
1:A:216:LEU:O	1:A:219:LYS:HG2	2.02	0.59
1:B:1282:ARG:NE	1:B:1290:LYS:CB	2.59	0.58
1:A:216:LEU:O	1:A:219:LYS:CG	2.52	0.58
1:B:1289:ALA:N	1:B:1290:LYS:HZ3	2.00	0.58
1:B:318:LEU:HB3	1:B:319:PRO:HD2	1.84	0.58
1:B:1290:LYS:HZ3	1:B:1290:LYS:H	1.52	0.57
1:A:932:ILE:HG12	1:A:1279:ARG:NE	2.19	0.57
1:A:1102:GLU:HG3	1:A:1106:LYS:HE2	1.85	0.57
1:B:1279:ARG:HH12	1:B:1291:GLN:N	2.03	0.57
1:B:1287:ASP:HA	1:B:1288:ASN:O	2.04	0.57
1:B:900:ILE:HD12	1:B:900:ILE:C	2.23	0.57
1:B:389:PHE:O	1:B:461:ARG:NH1	2.36	0.57
1:A:708:TYR:CD2	1:A:900:ILE:HD11	2.39	0.57
1:B:388:PHE:CD1	1:B:396:LEU:HD22	2.39	0.56
1:A:812:LEU:HD11	1:A:825:CYS:HB3	1.87	0.56
1:B:318:LEU:HB3	1:B:319:PRO:CD	2.36	0.56
1:B:191:SER:HB2	1:B:192:PRO:CD	2.36	0.56
1:B:1140:TYR:OH	1:B:1145:ASN:ND2	2.39	0.56
1:B:111:GLN:HB3	1:B:1039:GLY:O	2.07	0.55
1:B:1249:ASN:O	1:B:1255:ALA:HA	2.06	0.55
1:B:1290:LYS:HD2	1:B:1290:LYS:C	2.27	0.55
1:B:426:ARG:HD3	1:B:1212:HIS:CG	2.42	0.55
1:A:461:ARG:NH1	1:A:461:ARG:HG3	2.15	0.54
1:B:995:LYS:NZ	1:B:1284:GLN:HE21	2.05	0.54
1:A:995:LYS:HZ2	1:A:1284:GLN:HE21	1.55	0.54
1:B:1291:GLN:HA	1:B:1292:LEU:HD23	1.90	0.54
1:A:948:LYS:HG2	1:A:951:ASP:OD2	2.08	0.54
1:B:1086:ASN:O	1:B:1090:VAL:HG23	2.07	0.53
1:B:955:PHE:HA	1:B:1145:ASN:ND2	2.19	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1282:ARG:NE	1:B:1290:LYS:HB2	2.20	0.53
1:A:132:GLU:HB3	1:A:165:ASP:HB2	1.89	0.53
1:A:483:GLN:HE22	1:A:1311:GLN:HE22	1.55	0.53
1:A:995:LYS:NZ	1:A:1284:GLN:HE21	2.07	0.53
1:A:521:THR:HG22	1:A:525:LYS:HD2	1.91	0.52
1:B:1287:ASP:OD2	1:B:1290:LYS:NZ	2.43	0.52
1:B:191:SER:CB	1:B:192:PRO:CD	2.88	0.52
1:A:812:LEU:HD11	1:A:825:CYS:CB	2.40	0.52
1:B:645:ALA:HB1	1:B:650:ASN:ND2	2.24	0.52
1:B:812:LEU:HD11	1:B:825:CYS:HB3	1.91	0.52
1:A:812:LEU:CD1	1:A:825:CYS:HB3	2.40	0.52
1:B:753:PRO:HD3	1:B:816:ALA:HB1	1.91	0.52
1:B:1279:ARG:HH12	1:B:1291:GLN:CA	2.23	0.51
1:A:670:VAL:HG11	1:A:681:ALA:HB3	1.92	0.51
1:A:157:GLN:HE22	1:A:558:GLN:HE22	1.58	0.51
1:A:880:ARG:HD2	1:A:914:PHE:O	2.11	0.51
1:B:388:PHE:CD1	1:B:396:LEU:HD21	2.46	0.51
1:B:747:ASN:HB2	1:B:827:LEU:HD12	1.93	0.50
1:B:1119:ASP:O	1:B:1123:SER:HB3	2.12	0.50
1:B:975:SER:O	1:B:980:ARG:HD3	2.11	0.50
1:A:1158:ALA:HA	1:A:1177:ASP:O	2.11	0.50
1:B:1286:GLY:O	1:B:1287:ASP:CB	2.60	0.50
1:B:806:THR:O	1:B:810:THR:HG23	2.12	0.50
1:B:1163:GLU:HB2	1:B:1174:LEU:HD11	1.94	0.49
1:A:995:LYS:NZ	1:A:1284:GLN:NE2	2.61	0.49
1:A:290:VAL:HG13	1:A:297:SER:HB2	1.93	0.49
1:A:923:ALA:HA	1:A:926:TRP:NE1	2.28	0.49
1:A:793:ARG:NH1	1:B:756:GLU:OE2	2.35	0.49
1:B:1279:ARG:NH1	1:B:1291:GLN:HB3	2.27	0.49
1:A:132:GLU:HB3	1:A:165:ASP:CB	2.43	0.48
1:B:400:GLU:CD	1:B:400:GLU:H	2.16	0.48
1:B:27:LEU:HD21	1:B:41:LEU:HB2	1.95	0.48
1:A:599:TYR:HA	1:B:599:TYR:HA	1.94	0.48
1:B:622:THR:CG2	1:B:626:LYS:HE3	2.44	0.48
1:B:191:SER:CB	1:B:192:PRO:HD3	2.44	0.47
1:A:708:TYR:HB2	1:A:900:ILE:HG13	1.96	0.47
1:B:1290:LYS:O	1:B:1290:LYS:HD2	2.14	0.47
1:A:345:ALA:HB1	3:A:1403:FAD:H4'	1.97	0.47
1:B:812:LEU:HD11	1:B:825:CYS:CB	2.45	0.47
1:B:386:HIS:CG	1:B:466:LEU:HD11	2.49	0.47
1:B:477:TRP:HD1	1:B:523:LEU:HD23	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:880:ARG:HB3	1:A:914:PHE:O	2.14	0.47
1:B:1075:SER:HB3	1:B:1076:PRO:HD2	1.96	0.47
1:B:1282:ARG:NE	1:B:1290:LYS:HB3	2.13	0.47
1:B:191:SER:HB2	1:B:192:PRO:HD3	1.96	0.47
1:A:911:PHE:O	1:A:912:ARG:C	2.52	0.46
1:A:322:LYS:HD3	1:A:410:TYR:HB3	1.97	0.46
1:A:884:HIS:HB3	1:A:920:MET:HG3	1.97	0.46
1:A:99:PRO:HG2	1:A:203:LEU:HD13	1.98	0.46
1:A:708:TYR:HD2	1:A:900:ILE:HD11	1.81	0.46
1:B:1290:LYS:HZ3	1:B:1290:LYS:N	2.13	0.46
1:B:503:MET:HG2	1:B:1302:GLU:CD	2.36	0.46
1:B:418:SER:HB2	1:B:518:PHE:CD1	2.51	0.46
1:A:792:LYS:NZ	1:A:1064:SER:O	2.44	0.46
1:A:138:ILE:HD12	1:A:163:ALA:HB2	1.98	0.46
1:A:241:MET:HE2	1:A:285:GLU:HG2	1.98	0.46
1:A:153:ARG:HG2	1:A:556:ASN:ND2	2.32	0.46
1:A:1187:ASN:HA	1:A:1188:PRO:HD2	1.81	0.45
1:B:866:ASN:C	1:B:866:ASN:HD22	2.19	0.45
1:A:1003:THR:HG22	1:A:1266:LEU:HD21	1.98	0.45
1:A:1151:HIS:NE2	1:A:1251:ARG:O	2.48	0.45
1:B:475:LYS:HA	1:B:475:LYS:HD3	1.73	0.45
1:B:1290:LYS:O	1:B:1291:GLN:HG3	2.16	0.45
1:B:900:ILE:HD12	1:B:901:CYS:N	2.31	0.45
1:A:280:PRO:HB2	1:A:286:LEU:HD23	1.99	0.45
1:A:969:ASP:HA	1:A:972:ILE:HG12	1.97	0.45
1:B:995:LYS:HZ1	1:B:1284:GLN:HE21	1.63	0.45
1:A:446:ILE:HD11	1:A:535:CYS:HB3	1.99	0.45
1:A:1034:GLY:HA3	1:A:1074:THR:HG21	1.99	0.45
1:A:241:MET:O	1:A:245:LEU:HG	2.17	0.45
1:A:516:PHE:CE2	1:A:520:LEU:HD11	2.51	0.45
1:B:361:ASN:N	1:B:362:PRO:CD	2.80	0.45
1:A:1204:GLY:HA3	1:A:1209:GLU:OE2	2.17	0.45
1:A:58:TYR:CZ	1:A:219:LYS:HD3	2.52	0.44
1:B:767:GLN:HG2	1:B:1038:MET:CE	2.46	0.44
1:A:549:PHE:CE2	1:A:551:LYS:HG3	2.52	0.44
1:A:926:TRP:CE3	1:A:927:MET:N	2.85	0.44
1:B:1261:GLU:N	1:B:1262:PRO:CD	2.80	0.44
1:B:911:PHE:O	1:B:912:ARG:C	2.55	0.44
1:A:51:CYS:SG	1:A:71:ASN:HB3	2.58	0.44
1:A:216:LEU:O	1:A:219:LYS:HG3	2.17	0.44
1:A:336:PHE:O	1:A:337:ALA:O	2.36	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:792:LYS:HE3	1:B:756:GLU:OE1	2.17	0.44
1:A:55:ILE:HG23	1:A:83:VAL:CG1	2.46	0.44
1:A:762:LEU:N	1:A:762:LEU:HD12	2.33	0.44
1:B:785:ASN:OD1	1:B:786:ARG:NH1	2.49	0.44
1:A:324:GLU:HB2	1:A:411:SER:CB	2.48	0.43
1:A:812:LEU:HD21	1:A:823:VAL:O	2.18	0.43
1:B:81:HIS:O	1:B:82:HIS:HB2	2.16	0.43
1:A:652:GLU:HB2	1:A:870:THR:HG21	2.00	0.43
1:A:469:THR:N	1:A:470:PRO:CD	2.81	0.43
1:B:1279:ARG:HH12	1:B:1291:GLN:CB	2.32	0.43
1:A:720:LYS:HA	1:A:720:LYS:HD3	1.57	0.43
1:B:931:ALA:HA	1:B:941:VAL:HG21	2.00	0.43
1:A:1080:SER:OG	1:A:1261:GLU:HG3	2.18	0.43
1:B:1279:ARG:HH12	1:B:1291:GLN:HB3	1.83	0.43
1:A:646:THR:HG23	1:A:647:GLY:N	2.34	0.42
1:B:701:ALA:CB	1:B:901:CYS:HB3	2.49	0.42
1:A:750:ILE:HG12	1:A:824:ARG:HB2	2.01	0.42
1:A:1124:ALA:HB3	1:B:1134:LYS:HD2	2.00	0.42
1:B:1289:ALA:C	1:B:1290:LYS:O	2.57	0.42
1:A:516:PHE:CZ	1:A:520:LEU:HD11	2.55	0.42
1:A:191:SER:CB	1:A:560:PHE:O	2.54	0.42
1:A:640:VAL:HA	1:A:641:PRO:HD3	1.89	0.42
1:B:609:THR:HG21	1:B:835:ILE:HD11	2.01	0.42
1:B:345:ALA:HB1	3:B:1403:FAD:H4'	2.01	0.42
1:A:315:ILE:HD13	1:A:327:ARG:HG2	2.00	0.42
1:A:792:LYS:NZ	1:B:759:GLU:OE1	2.49	0.42
1:B:645:ALA:HB1	1:B:650:ASN:HD22	1.85	0.42
1:A:1086:ASN:O	1:A:1090:VAL:HG23	2.19	0.42
1:A:337:ALA:HB2	3:A:1403:FAD:C6	2.50	0.42
1:A:148:ARG:NE	1:A:1201:GLN:HE21	2.17	0.42
1:A:441:PHE:CE2	1:A:526:LEU:HD21	2.55	0.42
1:A:644:ASN:O	1:A:653:THR:HA	2.20	0.42
1:B:1208:MET:HG2	1:B:1228:LYS:O	2.20	0.42
1:A:1075:SER:HB3	1:A:1076:PRO:HD2	2.02	0.41
1:A:995:LYS:HZ1	1:A:1284:GLN:NE2	2.18	0.41
1:B:506:PHE:CZ	1:B:510:LEU:HD11	2.55	0.41
1:A:1021:VAL:HG12	1:A:1093:ALA:HB1	2.03	0.41
1:A:365:MET:HG2	1:A:454:CYS:SG	2.61	0.41
1:B:256:LEU:O	3:B:1403:FAD:H2B	2.20	0.41
1:B:899:ARG:HD2	1:B:899:ARG:HA	1.92	0.41
1:A:670:VAL:HG21	1:A:682:ALA:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:274:PHE:HA	1:B:275:PRO:HD3	1.87	0.41
1:B:130:GLN:HE21	1:B:132:GLU:H	1.68	0.41
1:B:280:PRO:HB2	1:B:286:LEU:HD23	2.03	0.41
1:B:371:LEU:HD12	1:B:388:PHE:CE1	2.55	0.41
1:A:912:ARG:NH2	1:A:1198:ALA:HB2	2.36	0.40
1:A:1228:LYS:HA	1:A:1228:LYS:HD2	1.83	0.40
1:A:842:PHE:HA	1:A:864:PHE:O	2.21	0.40
1:A:149:CYS:O	1:A:1197:GLY:HA3	2.22	0.40
1:A:45:GLU:OE2	1:A:1225:SER:HB3	2.21	0.40
1:A:628:VAL:HG21	1:A:681:ALA:HA	2.02	0.40
1:A:1126:SER:HB2	1:B:1132:PHE:CG	2.56	0.40
1:A:571:ASP:OD2	1:A:1052:ARG:HD2	2.21	0.40
1:B:1031:LEU:HB3	1:B:1063:ILE:HG12	2.03	0.40
1:B:215:LEU:HD23	1:B:215:LEU:HA	1.81	0.40
1:B:81:HIS:CD2	1:B:226:LEU:HD11	2.57	0.40
1:A:709:GLY:O	1:A:899:ARG:NH2	2.51	0.40
1:A:804:ARG:HG3	1:A:836:THR:O	2.21	0.40
1:B:890:LYS:HB3	1:B:890:LYS:HE2	1.81	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	1285/1315 (98%)	1218 (95%)	59 (5%)	8 (1%)	25	31
1	B	1267/1315 (96%)	1213 (96%)	42 (3%)	12 (1%)	17	20
All	All	2552/2630 (97%)	2431 (95%)	101 (4%)	20 (1%)	19	23

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	337	ALA
1	A	1008	SER
1	B	1008	SER
1	B	1287	ASP
1	B	1288	ASN
1	B	1289	ALA
1	B	1290	LYS
1	B	532	GLU
1	B	797	GLY
1	B	912	ARG
1	B	947	TYR
1	A	164	LYS
1	A	912	ARG
1	A	423	ALA
1	A	797	GLY
1	B	530	ASP
1	B	1291	GLN
1	A	390	PRO
1	A	556	ASN
1	B	887	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	1088/1109 (98%)	1030 (95%)	58 (5%)	22	31
1	B	1074/1109 (97%)	1022 (95%)	52 (5%)	25	36
All	All	2162/2218 (98%)	2052 (95%)	110 (5%)	24	33

All (110) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	61	LEU
1	A	83	VAL
1	A	99	PRO
1	A	160	ARG

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Mol	Chain	Res	Type
1	A	190	LEU
1	A	203	LEU
1	A	219	LYS
1	A	221	THR
1	A	246	ASP
1	A	253	ASP
1	A	270	LYS
1	A	285	GLU
1	A	286	LEU
1	A	297	SER
1	A	336	PHE
1	A	343	SER
1	A	396	LEU
1	A	404	LEU
1	A	429	ASP
1	A	445	THR
1	A	446	ILE
1	A	461	ARG
1	A	473	LEU
1	A	494	GLN
1	A	508	ARG
1	A	512	LEU
1	A	531	LEU
1	A	550	GLN
1	A	565	LYS
1	A	720	LYS
1	A	743	TYR
1	A	752	VAL
1	A	812	LEU
1	A	824	ARG
1	A	852	LYS
1	A	856	VAL
1	A	866	ASN
1	A	899	ARG
1	A	900	ILE
1	A	911	PHE
1	A	943	ARG
1	A	981	LYS
1	A	983	GLU
1	A	985	GLU
1	A	1004	LYS
1	A	1031	LEU

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Mol	Chain	Res	Type
1	A	1052	ARG
1	A	1064	SER
1	A	1085	LEU
1	A	1107	LYS
1	A	1143	GLU
1	A	1159	CYS
1	A	1177	ASP
1	A	1220	HIS
1	A	1221	THR
1	A	1234	SER
1	A	1239	PHE
1	A	1268	SER
1	B	48	CYS
1	B	64	LYS
1	B	83	VAL
1	B	94	THR
1	B	140	ASN
1	B	193	SER
1	B	221	THR
1	B	246	ASP
1	B	247	LEU
1	B	271	ASN
1	B	286	LEU
1	B	320	GLU
1	B	322	LYS
1	B	334	ARG
1	B	370	LYS
1	B	406	ILE
1	B	480	GLU
1	B	491	GLU
1	B	533	ASP
1	B	566	ASP
1	B	622	THR
1	B	650	ASN
1	B	687	ILE
1	B	720	LYS
1	B	742	PHE
1	B	743	TYR
1	B	752	VAL
1	B	788	VAL
1	B	807	VAL
1	B	812	LEU

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Mol	Chain	Res	Type
1	B	852	LYS
1	B	856	VAL
1	B	866	ASN
1	B	900	ILE
1	B	911	PHE
1	B	964	LEU
1	B	1004	LYS
1	B	1011	LEU
1	B	1031	LEU
1	B	1102	GLU
1	B	1108	LYS
1	B	1123	SER
1	B	1134	LYS
1	B	1143	GLU
1	B	1145	ASN
1	B	1164	ILE
1	B	1251	ARG
1	B	1290	LYS
1	B	1291	GLN
1	B	1311	GLN
1	B	1314	THR
1	B	1315	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	130	GLN
1	A	223	GLN
1	A	558	GLN
1	A	583	ASN
1	A	585	GLN
1	A	650	ASN
1	A	866	ASN
1	A	1086	ASN
1	A	1088	GLN
1	A	1145	ASN
1	A	1284	GLN
1	A	1285	HIS
1	A	1288	ASN
1	A	1311	GLN
1	B	130	GLN
1	B	140	ASN

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Mol	Chain	Res	Type
1	B	223	GLN
1	B	271	ASN
1	B	350	ASN
1	B	583	ASN
1	B	642	ASN
1	B	650	ASN
1	B	866	ASN
1	B	1088	GLN
1	B	1145	ASN
1	B	1284	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 ⓘ

Of 14 ligands modelled in this entry, 4 are monoatomic - leaving 10 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	$\# Z  > 2$
3	FAD	A	1403	-	51,58,58	1.43	6 (11%)	60,89,89	1.88	11 (18%)
5	BCT	B	1405	-	0,3,3	0.00	-	0,3,3	0.00	-
2	FES	A	1402	1	0,4,4	0.00	-	-		
2	FES	B	1402	1	0,4,4	0.00	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	FES	A	1401	1	0,4,4	0.00	-	-		
3	FAD	B	1403	-	51,58,58	1.35	4 (7%)	60,89,89	2.07	17 (28%)
5	BCT	A	1405	-	0,3,3	0.00	-	0,3,3	0.00	-
4	URC	B	1404	-	13,13,13	5.41	8 (61%)	11,19,19	7.42	9 (81%)
4	URC	A	1404	-	13,13,13	5.27	6 (46%)	11,19,19	8.49	8 (72%)
2	FES	B	1401	1	0,4,4	0.00	-	-		

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	FAD	A	1403	-	-	0/30/50/50	0/6/6/6
2	FES	A	1402	1	-	-	0/1/1/1
2	FES	B	1402	1	-	-	0/1/1/1
3	FAD	B	1403	-	-	2/30/50/50	0/6/6/6
2	FES	A	1401	1	-	-	0/1/1/1
4	URC	B	1404	-	-	-	0/2/2/2
4	URC	A	1404	-	-	-	0/2/2/2
2	FES	B	1401	1	-	-	0/1/1/1

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1404	URC	O24-C8	11.76	1.48	1.23
4	A	1404	URC	O24-C8	11.63	1.47	1.23
4	B	1404	URC	C4-N3	-8.31	1.35	1.46
4	A	1404	URC	C4-N3	-8.20	1.36	1.46
4	A	1404	URC	O13-C6	8.12	1.39	1.23
4	B	1404	URC	O13-C6	7.27	1.37	1.23
4	B	1404	URC	C4-N9	-6.63	1.36	1.44
4	B	1404	URC	O11-C2	6.21	1.36	1.23
4	A	1404	URC	C4-N9	-6.06	1.37	1.44
4	A	1404	URC	O11-C2	5.49	1.34	1.23
4	B	1404	URC	C5-N7	-4.96	1.35	1.45
3	A	1403	FAD	C10-N1	4.95	1.39	1.33
4	A	1404	URC	C5-N7	-4.15	1.37	1.45
3	B	1403	FAD	C1'-N10	4.09	1.52	1.48
3	B	1403	FAD	C4X-N5	3.76	1.38	1.33
3	A	1403	FAD	C2A-N3A	3.47	1.37	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1403	FAD	C4-N3	3.28	1.38	1.33
3	B	1403	FAD	C2A-N1A	3.06	1.39	1.33
3	B	1403	FAD	C2A-N3A	2.83	1.36	1.32
3	A	1403	FAD	C2A-N1A	2.71	1.38	1.33
3	A	1403	FAD	C2B-C1B	-2.37	1.50	1.53
3	A	1403	FAD	C4X-N5	2.29	1.36	1.33
4	B	1404	URC	C5-C6	-2.28	1.48	1.52
4	B	1404	URC	C5-C4	-2.11	1.40	1.53

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1404	URC	C5-C4-N9	18.34	111.13	102.64
4	A	1404	URC	C4-N9-C8	-16.93	101.39	112.89
4	B	1404	URC	C5-C4-N9	15.78	109.94	102.64
4	B	1404	URC	C4-N9-C8	-14.90	102.77	112.89
4	A	1404	URC	N7-C8-N9	8.47	116.71	108.76
4	A	1404	URC	N1-C2-N3	7.47	123.99	116.12
3	A	1403	FAD	C4-N3-C2	7.26	121.27	115.14
4	B	1404	URC	N1-C2-N3	7.05	123.54	116.12
4	B	1404	URC	N7-C8-N9	6.95	115.28	108.76
3	B	1403	FAD	C1'-N10-C9A	6.63	123.51	118.29
3	B	1403	FAD	N3A-C2A-N1A	-6.01	119.28	128.68
3	A	1403	FAD	C1'-N10-C9A	5.64	122.73	118.29
3	B	1403	FAD	C4-N3-C2	5.38	119.69	115.14
3	B	1403	FAD	C5X-C9A-N10	5.19	121.48	117.72
3	A	1403	FAD	N3A-C2A-N1A	-4.80	121.17	128.68
4	A	1404	URC	O24-C8-N7	-4.07	120.10	125.94
3	A	1403	FAD	C4X-C4-N3	-3.73	118.33	123.43
4	B	1404	URC	C6-N1-C2	-3.60	121.44	126.25
3	A	1403	FAD	C4X-N5-C5X	3.42	120.19	116.77
3	B	1403	FAD	C9A-N10-C10	-3.41	117.44	121.91
4	A	1404	URC	C6-N1-C2	-3.27	121.88	126.25
3	B	1403	FAD	C4X-N5-C5X	2.97	119.74	116.77
3	B	1403	FAD	C6-C5X-C9A	2.79	122.70	119.05
3	A	1403	FAD	O3'-C3'-C2'	-2.78	102.10	108.81
4	B	1404	URC	O24-C8-N7	-2.69	122.07	125.94
3	A	1403	FAD	C4A-C5A-N7A	-2.56	106.73	109.40
3	B	1403	FAD	C5A-C6A-N6A	2.54	124.22	120.35
3	B	1403	FAD	C1B-N9A-C4A	-2.47	122.30	126.64
3	B	1403	FAD	C9A-C5X-N5	-2.44	118.54	122.36
3	A	1403	FAD	C6-C5X-C9A	2.41	122.21	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1404	URC	O11-C2-N3	-2.39	118.17	122.92
3	B	1403	FAD	C5'-C4'-C3'	-2.32	107.72	112.20
4	B	1404	URC	O24-C8-N9	-2.30	122.64	125.94
3	B	1403	FAD	O3'-C3'-C2'	-2.28	103.30	108.81
3	A	1403	FAD	C1B-N9A-C4A	-2.28	122.64	126.64
4	B	1404	URC	O11-C2-N3	-2.24	118.46	122.92
3	B	1403	FAD	C2A-N1A-C6A	2.22	122.56	118.75
3	A	1403	FAD	C1'-C2'-C3'	-2.22	103.58	109.79
3	B	1403	FAD	C4A-C5A-N7A	-2.17	107.14	109.40
4	A	1404	URC	O11-C2-N1	-2.11	117.83	121.82
3	B	1403	FAD	C4X-C4-N3	-2.07	120.60	123.43
3	A	1403	FAD	C6-C5X-N5	-2.07	116.77	119.05
3	B	1403	FAD	O4'-C4'-C3'	2.06	114.10	109.10
4	B	1404	URC	O11-C2-N1	-2.03	118.00	121.82
3	B	1403	FAD	O3B-C3B-C4B	-2.02	105.21	111.05

There are no chirality outliers.

All (2) torsion outliers are listed below:

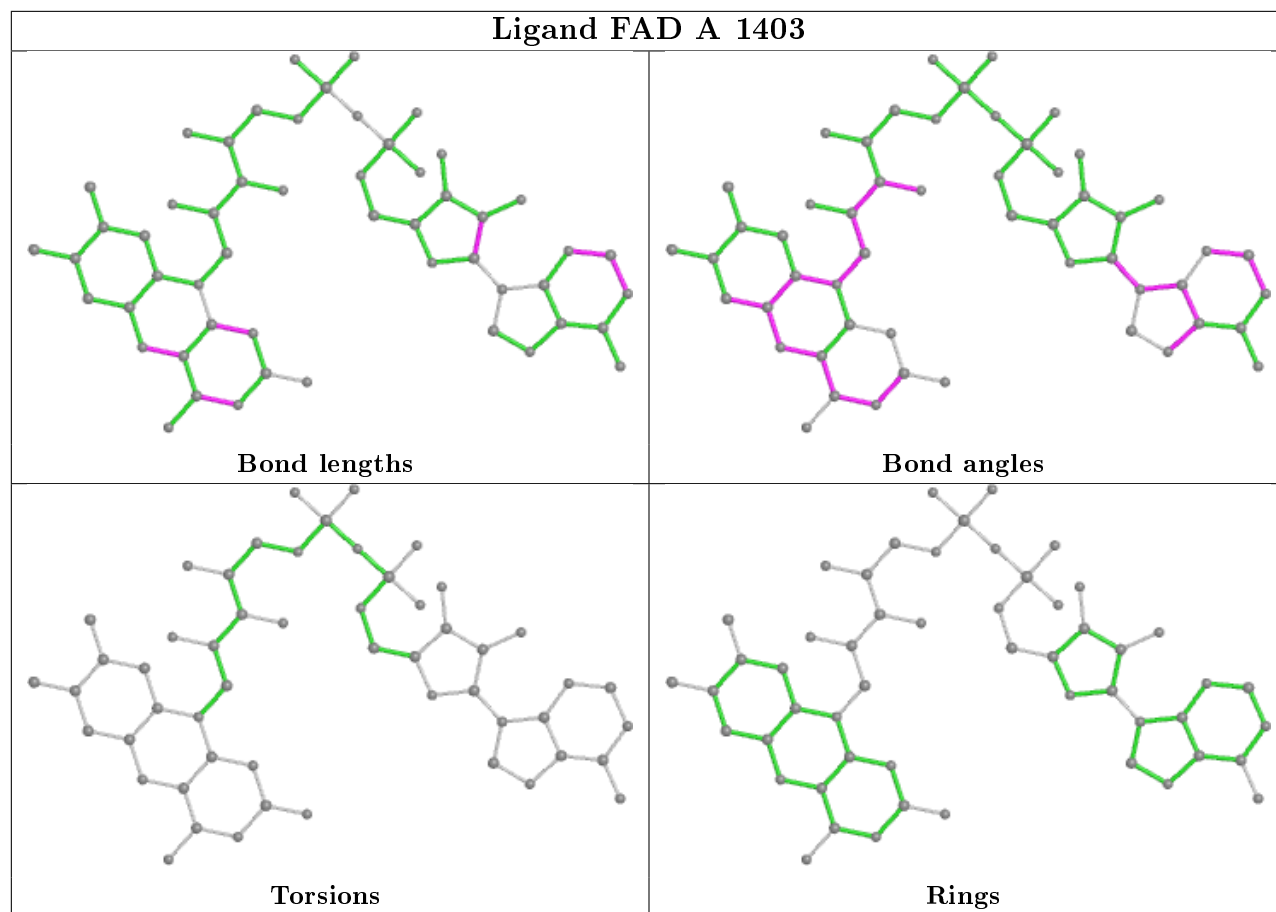
Mol	Chain	Res	Type	Atoms
3	B	1403	FAD	O4B-C4B-C5B-O5B
3	B	1403	FAD	C3B-C4B-C5B-O5B

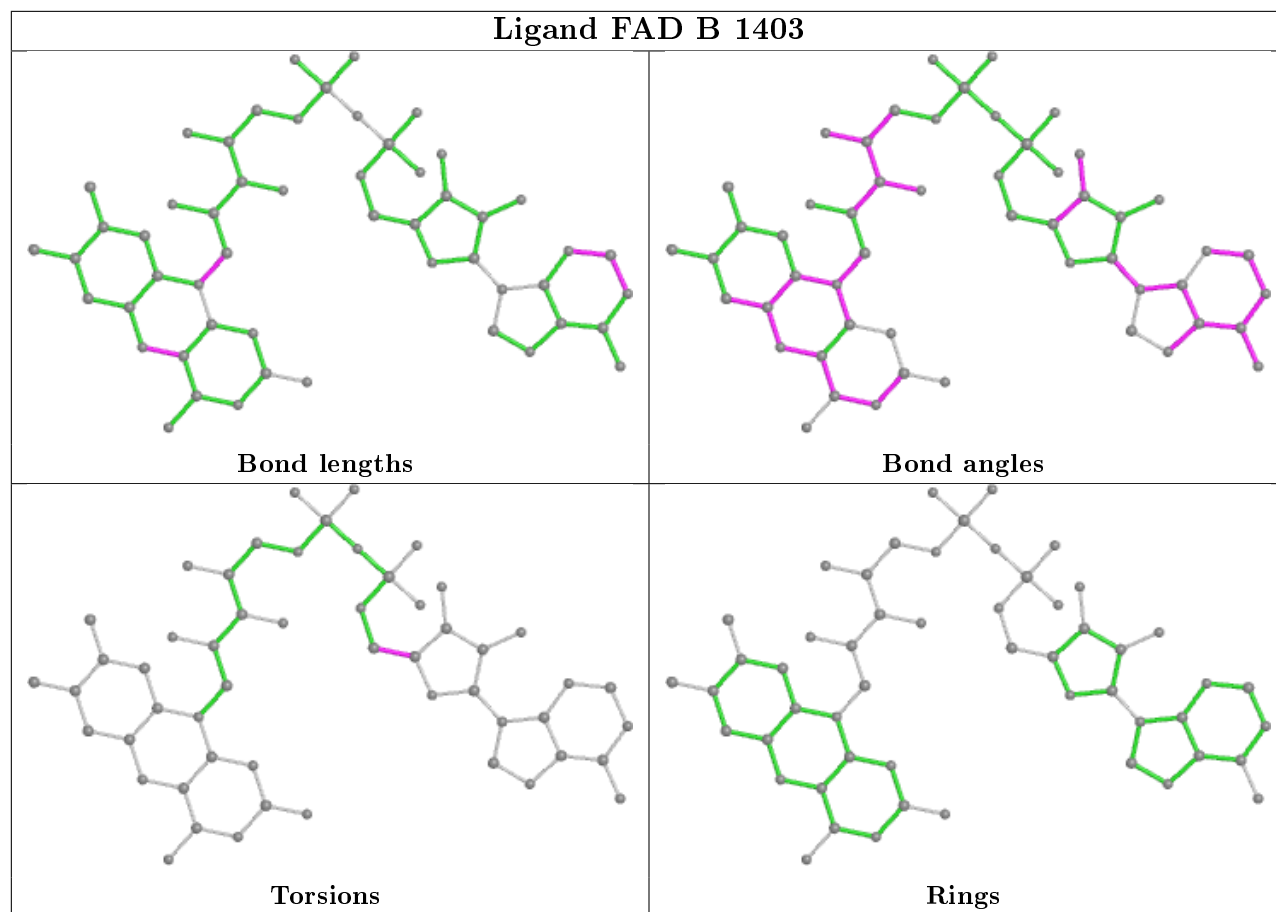
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1403	FAD	2	0
3	B	1403	FAD	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





## 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 ⓘ

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	1289/1315 (98%)	-0.12	45 (3%) 44 51	20, 35, 59, 94	0
1	B	1273/1315 (96%)	-0.32	21 (1%) 72 77	18, 30, 48, 75	0
All	All	2562/2630 (97%)	-0.22	66 (2%) 56 63	18, 32, 56, 94	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	534	MET	7.2
1	A	1315	LEU	7.0
1	B	1315	LEU	6.0
1	A	535	CYS	5.9
1	A	165	ASP	5.6
1	A	61	LEU	5.3
1	B	540	PRO	5.3
1	B	1287	ASP	5.3
1	A	533	ASP	5.1
1	B	1286	GLY	4.8
1	A	423	ALA	4.2
1	B	61	LEU	4.2
1	A	1287	ASP	4.1
1	A	536	GLY	4.0
1	B	191	SER	3.9
1	A	3	ALA	3.9
1	A	1288	ASN	3.8
1	B	1288	ASN	3.8
1	A	530	ASP	3.7
1	A	1289	ALA	3.7
1	A	552	ASP	3.5
1	B	1289	ALA	3.4
1	A	550	GLN	3.4
1	A	553	PRO	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	1111	GLY	3.3
1	A	551	LYS	3.3
1	B	1110	THR	3.2
1	A	220	ASP	3.2
1	A	431	ALA	3.1
1	A	95	GLN	3.1
1	A	221	THR	3.1
1	B	1314	THR	3.1
1	B	539	ASP	2.8
1	A	531	LEU	2.7
1	A	191	SER	2.7
1	A	566	ASP	2.7
1	A	555	ALA	2.6
1	A	219	LYS	2.6
1	A	721	LYS	2.6
1	B	250	GLN	2.5
1	B	3	ALA	2.5
1	A	190	LEU	2.5
1	B	1290	LYS	2.5
1	B	555	ALA	2.4
1	A	335	TRP	2.4
1	A	428	ASP	2.4
1	A	529	ALA	2.4
1	B	95	GLN	2.4
1	A	537	LYS	2.3
1	A	316	ALA	2.3
1	A	1290	LYS	2.3
1	A	392	TYR	2.3
1	A	256	LEU	2.2
1	A	480	GLU	2.2
1	B	220	ASP	2.2
1	B	62	GLN	2.2
1	A	198	GLU	2.2
1	A	532	GLU	2.1
1	A	1143	GLU	2.1
1	A	430	ILE	2.1
1	A	1108	LYS	2.1
1	B	527	GLY	2.1
1	A	319	PRO	2.1
1	A	565	LYS	2.1
1	A	437	MET	2.0
1	B	219	LYS	2.0

## 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 ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

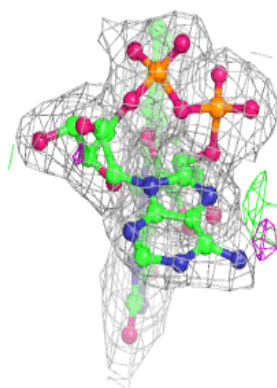
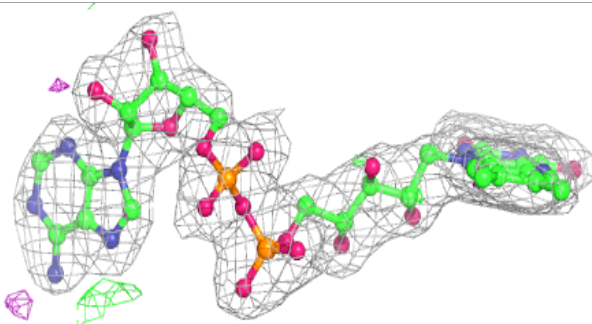
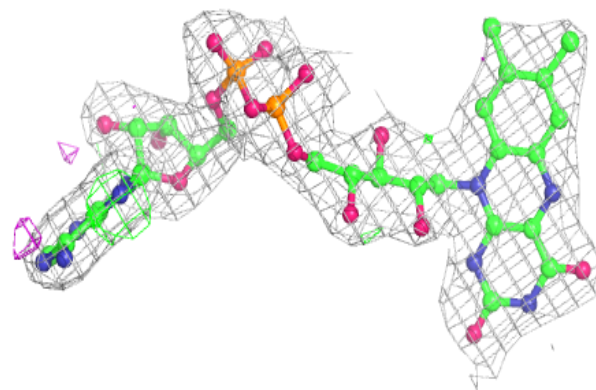
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
4	URC	A	1404	12/12	0.93	0.13	36,39,41,41	0
3	FAD	A	1403	53/53	0.95	0.14	28,35,40,44	0
4	URC	B	1404	12/12	0.96	0.10	31,34,37,38	0
3	FAD	B	1403	53/53	0.97	0.11	20,25,28,31	0
5	BCT	B	1405	4/4	0.98	0.10	23,24,24,25	0
5	BCT	A	1405	4/4	0.98	0.08	30,33,33,34	0
2	FES	B	1402	4/4	0.99	0.07	23,24,25,25	0
2	FES	A	1401	4/4	0.99	0.05	31,33,34,35	0
6	CA	B	1406	1/1	0.99	0.05	27,27,27,27	0
6	CA	A	1406	1/1	0.99	0.06	31,31,31,31	0
6	CA	B	1407	1/1	0.99	0.10	29,29,29,29	0
2	FES	A	1402	4/4	0.99	0.06	25,26,26,27	0
6	CA	A	1407	1/1	0.99	0.07	32,32,32,32	0
2	FES	B	1401	4/4	0.99	0.05	30,31,32,33	0

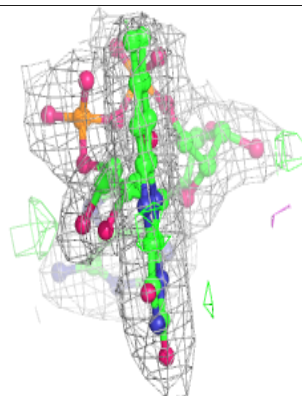
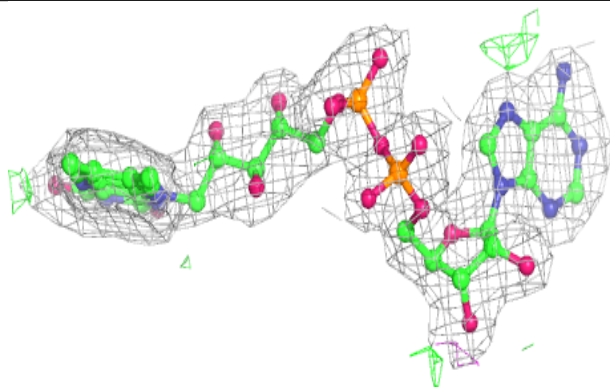
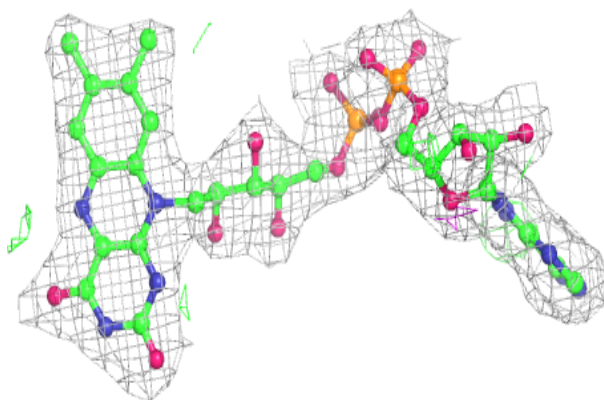
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around FAD A 1403:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around FAD B 1403:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





## 6.5 Other polymers ⓘ

There are no such residues in this entry.