



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 11:44 PM UTC

PDB ID : 5EA9 / pdb_00005ea9
Title : Crystal Structure of Trypanosoma cruzi Dihydroorotate Dehydrogenase in Complex with Neq0130
Authors : Rocha, J.R.; Inaoka, D.K.; Cheleski, J.; Shiba, T.; Harada, S.; Montanari, C.A.; Kita, K.
Deposited on : 2015-10-15
Resolution : 1.71 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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtrriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

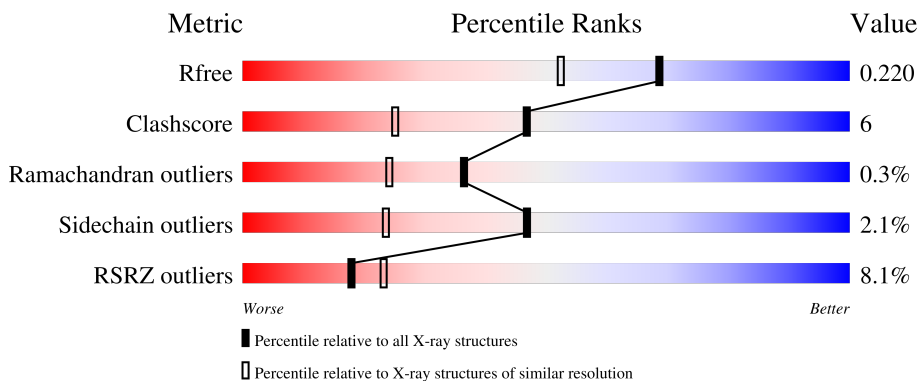
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.71 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}	180053	1039 (1.72-1.72)
Clashscore	190562	1049 (1.72-1.72)
Ramachandran outliers	187476	1041 (1.72-1.72)
Sidechain outliers	187428	1041 (1.72-1.72)
RSRZ outliers	180081	1039 (1.72-1.72)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 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	314	
1	B	314	

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	GOL	A	408	-	X	-	-
5	EDO	A	414	-	X	-	-

2 Entry composition i

There are 7 unique types of molecules in this entry. The entry contains 5574 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.

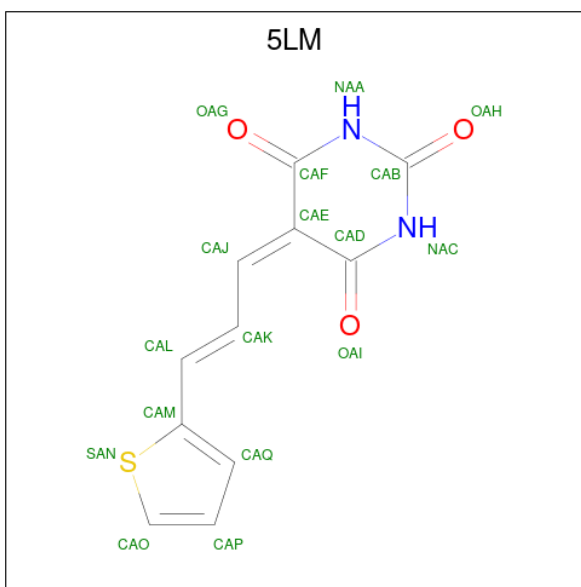
- Molecule 1 is a protein called Dihydroorotate dehydrogenase (fumarate).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	313	2397	1535	397	447	18	0	2	0
1	B	313	2409	1544	400	446	19	0	4	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	SER	-	expression tag	UNP Q4D3W2
B	-1	SER	-	expression tag	UNP Q4D3W2

- Molecule 2 is 5-[(E)-3-thiophen-2-ylprop-2-enylidene]-1,3-diazinane-2,4,6-trione (CCD ID: 5LM) (formula: C₁₁H₈N₂O₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	17	11	2	3	1	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	B	1	17	11	2	3	1	0	0

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



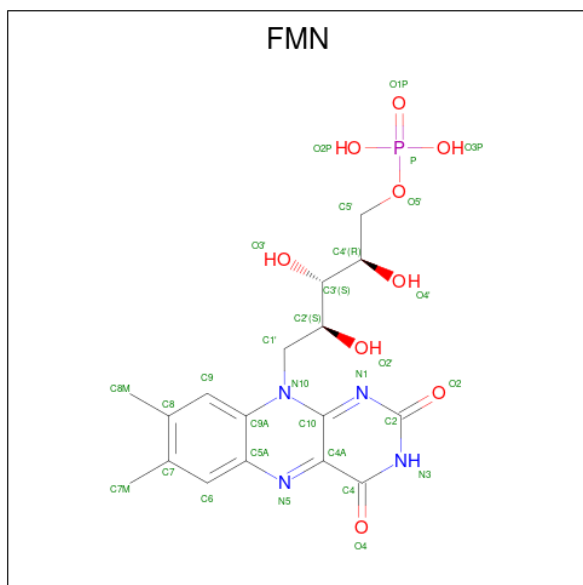
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	6	3	3	0	0
3	A	1	6	3	3	0	0
3	A	1	6	3	3	0	0
3	A	1	6	3	3	0	0
3	A	1	6	3	3	0	0
3	A	1	6	3	3	0	0
3	A	1	6	3	3	0	0
3	A	1	6	3	3	0	0
3	B	1	6	3	3	0	0
3	B	1	6	3	3	0	0
3	B	1	6	3	3	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	1
			12	6	6		

- Molecule 4 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



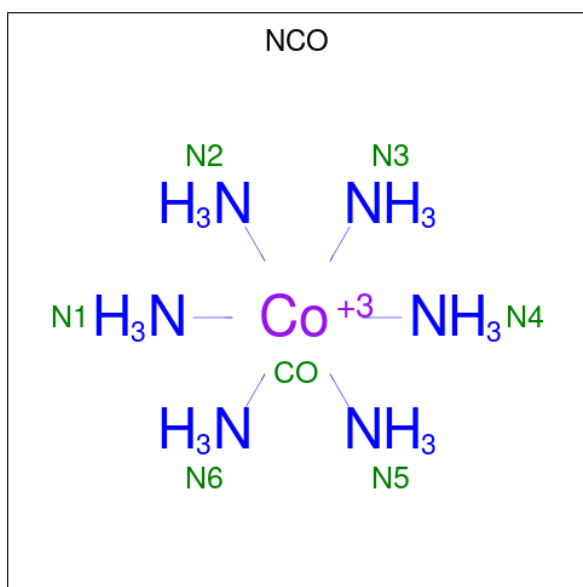
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
4	B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0

- Molecule 6 is COBALT HEXAMMINE(III) (CCD ID: NCO) (formula: $\text{CoH}_{18}\text{N}_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	Co	N	0	0
			7	1	6		
6	B	1	Total	Co	N	0	1
			14	2	12		

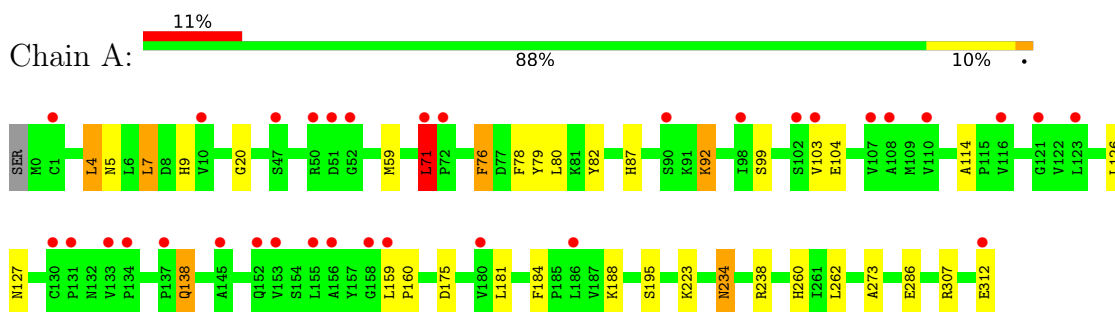
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	255	Total	O	0	0
			255	255		
7	B	268	Total	O	0	0
			268	268		

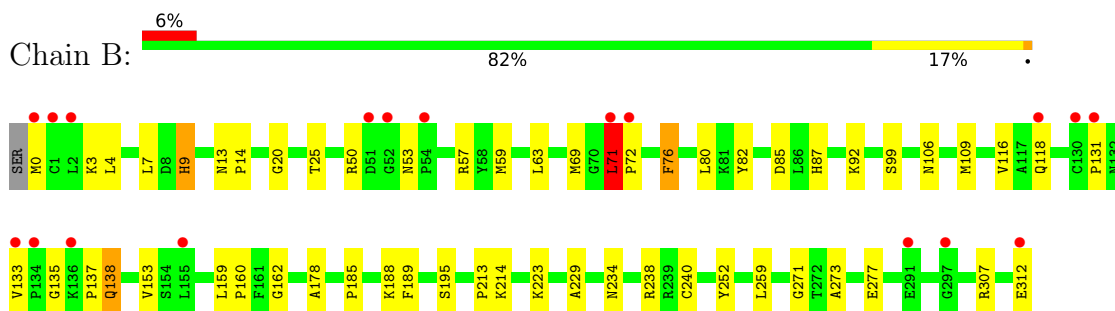
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Dihydroorotate dehydrogenase (fumarate)



- Molecule 1: Dihydroorotate dehydrogenase (fumarate)



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	68.28Å 71.86Å 124.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.71 50.00 – 1.71	Depositor EDS
% Data completeness (in resolution range)	99.7 (50.00-1.71) 99.7 (50.00-1.71)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.11 (at 1.71Å)	Xtrriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.179 , 0.221 (Not available) , 0.220	Depositor DCC
R_{free} test set	3333 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	14.0	Xtrriage
Anisotropy	0.065	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 41.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.000 for k,h,-l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5574	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 83.16 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.3275e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: FMN, 5LM, NCO, GOL, EDO

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	1.52	13/2452 (0.5%)	1.29	8/3321 (0.2%)
1	B	1.50	12/2473 (0.5%)	1.29	8/3348 (0.2%)
All	All	1.51	25/4925 (0.5%)	1.29	16/6669 (0.2%)

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	71	LEU	C-N	8.54	1.41	1.33
1	B	71	LEU	CA-C	8.13	1.63	1.52
1	A	71	LEU	CA-C	7.44	1.62	1.52
1	A	126	LEU	N-CA	-7.36	1.37	1.46
1	B	153	VAL	C-O	-6.87	1.16	1.24
1	A	114	ALA	N-CA	6.68	1.52	1.46
1	A	159	LEU	CA-C	6.33	1.58	1.52
1	A	79	TYR	N-CA	6.27	1.54	1.46
1	A	159	LEU	C-O	-6.14	1.17	1.24
1	A	7	LEU	CA-C	5.96	1.60	1.52
1	A	184	PHE	N-CA	-5.93	1.40	1.46
1	B	118	GLN	C-O	-5.93	1.17	1.24
1	B	9	HIS	CA-C	-5.92	1.45	1.52
1	A	286	GLU	N-CA	5.71	1.53	1.46
1	B	133	VAL	N-CA	5.56	1.50	1.46
1	B	178	ALA	CA-C	5.45	1.59	1.52
1	A	262	LEU	CA-C	-5.41	1.45	1.52
1	B	259	LEU	N-CA	-5.37	1.39	1.46
1	B	106	ASN	C-O	-5.34	1.17	1.24
1	B	240	CYS	CA-CB	5.34	1.59	1.53
1	A	4	LEU	CA-C	-5.33	1.46	1.52
1	A	92	LYS	N-CA	-5.32	1.40	1.46
1	B	76	PHE	C-O	-5.26	1.18	1.24
1	A	175	ASP	N-CA	5.21	1.52	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	229	ALA	N-CA	5.08	1.52	1.46

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	3	LYS	CA-C-O	-7.64	112.69	121.47
1	B	72	PRO	CB-CA-C	-7.37	104.69	111.40
1	B	71	LEU	N-CA-C	6.84	124.93	109.81
1	A	71	LEU	CA-C-N	-6.60	111.59	119.84
1	A	71	LEU	C-N-CA	-6.60	111.59	119.84
1	B	72	PRO	N-CA-C	6.55	120.95	110.21
1	A	71	LEU	N-CA-C	6.01	123.09	109.81
1	A	260	HIS	O-C-N	5.81	128.28	122.12
1	A	234	ASN	N-CA-C	5.69	117.48	111.28
1	B	271	GLY	O-C-N	5.64	125.01	121.85
1	A	181	LEU	N-CA-C	5.43	117.91	111.33
1	A	5	ASN	CB-CA-C	5.34	118.41	110.62
1	B	3	LYS	CA-C-N	5.28	130.89	121.75
1	B	3	LYS	C-N-CA	5.28	130.89	121.75
1	A	76	PHE	N-CA-C	5.10	117.50	111.33
1	B	85	ASP	N-CA-C	5.04	120.08	113.88

There are no chirality outliers.

There are no planarity outliers.

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	2397	0	2399	21	0
1	B	2409	0	2423	36	0
2	A	17	0	0	2	0
2	B	17	0	0	2	0
3	A	42	0	56	0	0
3	B	42	0	56	3	0
4	A	31	0	19	1	0
4	B	31	0	19	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	20	0	30	5	0
5	B	24	0	36	5	0
6	B	21	0	0	0	0
7	A	255	0	0	4	0
7	B	268	0	0	4	0
All	All	5574	0	5038	57	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 6.

All (57) 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:76:PHE:CD1	1:B:109[B]:MET:HE3	1.92	1.05
1:A:234:ASN:HD21	1:A:238:ARG:HE	1.24	0.84
1:B:234:ASN:HD21	1:B:238:ARG:HE	1.26	0.83
1:B:99:SER:HB3	2:B:401:5LM:SAN	2.22	0.79
1:B:138:GLN:HE21	1:B:138:GLN:H	1.27	0.79
1:B:76:PHE:CG	1:B:109[B]:MET:HE3	2.19	0.78
1:B:76:PHE:CD1	1:B:109[B]:MET:CE	2.66	0.78
1:B:50:ARG:HD3	1:B:71:LEU:HD13	1.66	0.77
1:A:138:GLN:HE21	1:A:138:GLN:H	1.34	0.74
1:B:273:ALA:HB1	5:B:412:EDO:H11	1.74	0.69
1:A:59:MET:HE3	7:A:602:HOH:O	1.93	0.68
1:A:99:SER:HB3	2:A:401:5LM:SAN	2.35	0.67
1:A:234:ASN:ND2	1:A:238:ARG:HE	1.94	0.66
1:B:80:LEU:HD11	1:B:116:VAL:HG21	1.80	0.62
1:A:82:TYR:OH	1:A:87:HIS:HD2	1.84	0.61
1:A:273:ALA:HB1	5:A:412:EDO:H11	1.83	0.60
1:B:135:GLY:HA2	3:B:405:GOL:H2	1.84	0.60
1:B:137:PRO:HD3	3:B:405:GOL:H32	1.85	0.57
1:B:25:THR:HG22	5:B:415:EDO:H12	1.87	0.56
1:A:223:LYS:HD2	5:A:410:EDO:H11	1.87	0.56
1:B:234:ASN:ND2	1:B:238:ARG:HE	1.99	0.56
1:B:87:HIS:HE1	1:B:92:LYS:O	1.89	0.55
1:A:104:GLU:OE1	7:A:501:HOH:O	2.18	0.55
1:B:138:GLN:HE21	1:B:138:GLN:N	2.03	0.53
1:A:78:PHE:N	5:A:411:EDO:H11	2.24	0.53
1:A:160:PRO:HB3	1:A:188:LYS:HG3	1.91	0.52
1:A:7:LEU:O	1:A:9:HIS:HD2	1.93	0.52
1:B:82:TYR:OH	1:B:87:HIS:HD2	1.93	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:GLY:HA3	4:A:409:FMN:N5	2.26	0.50
1:B:20:GLY:HA3	4:B:408:FMN:N5	2.27	0.50
1:B:13:ASN:HB2	1:B:14:PRO:HD2	1.95	0.48
1:B:273:ALA:CB	5:B:412:EDO:H11	2.40	0.48
1:B:59:MET:HE3	7:B:613:HOH:O	2.12	0.48
1:A:234:ASN:HD21	1:A:238:ARG:NE	2.03	0.46
1:B:135:GLY:CA	3:B:405:GOL:H2	2.45	0.46
1:A:195[A]:SER:OG	2:A:401:5LM:OAH	2.30	0.46
1:B:57:ARG:HG3	1:B:69:MET:SD	2.57	0.45
1:A:87:HIS:HE1	1:A:92:LYS:O	2.00	0.45
1:B:131:PRO:HB2	7:B:590:HOH:O	2.17	0.44
5:A:410:EDO:H12	1:B:63:LEU:HD21	1.99	0.44
1:B:53:ASN:HB3	1:B:213:PRO:HG3	1.99	0.44
1:B:71:LEU:HA	2:B:401:5LM:CAQ	2.47	0.44
1:A:273:ALA:CB	5:A:412:EDO:H11	2.47	0.43
1:B:162:GLY:HA3	1:B:189:PHE:CZ	2.52	0.43
1:A:103:VAL:HG12	7:A:551:HOH:O	2.18	0.43
1:B:185:PRO:O	1:B:188:LYS:NZ	2.44	0.43
1:B:223:LYS:HG2	1:B:252:TYR:CE1	2.54	0.43
1:B:277:GLU:HB2	5:B:412:EDO:H12	2.01	0.43
1:B:87:HIS:HA	5:B:416:EDO:H11	2.02	0.42
1:A:76:PHE:CE2	1:A:80:LEU:HD22	2.54	0.42
1:B:7:LEU:O	1:B:9:HIS:HD2	2.02	0.42
1:B:50:ARG:HD3	1:B:71:LEU:CD1	2.44	0.42
1:B:195[A]:SER:HB3	7:B:526:HOH:O	2.19	0.42
1:A:195[B]:SER:HB3	7:A:522:HOH:O	2.20	0.41
1:B:9:HIS:HE1	7:B:622:HOH:O	2.04	0.41
1:B:159:LEU:HB3	1:B:160:PRO:HD2	2.03	0.40
1:A:99:SER:HB2	1:A:127:ASN:HB3	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	313/314 (100%)	302 (96%)	10 (3%)	1 (0%)	36	24
1	B	315/314 (100%)	304 (96%)	10 (3%)	1 (0%)	36	24
All	All	628/628 (100%)	606 (96%)	20 (3%)	2 (0%)	36	24

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	71	LEU
1	A	71	LEU

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	260/259 (100%)	255 (98%)	5 (2%)	50	27
1	B	262/259 (101%)	256 (98%)	6 (2%)	44	21
All	All	522/518 (101%)	511 (98%)	11 (2%)	47	23

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	A	71	LEU
1	A	138	GLN
1	A	307	ARG
1	A	312	GLU
1	B	0	MET
1	B	4	LEU
1	B	138	GLN
1	B	214	LYS
1	B	307	ARG
1	B	312	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	HIS
1	A	87	HIS
1	A	138	GLN
1	A	215	GLN
1	A	234	ASN
1	A	275	GLN
1	B	9	HIS
1	B	87	HIS
1	B	138	GLN
1	B	234	ASN
1	B	275	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

32 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	$\# Z > 2$
5	EDO	A	411	-	3,3,3	0.40	0	2,2,2	1.33	0
5	EDO	B	411	-	3,3,3	0.62	0	2,2,2	0.31	0
4	FMN	B	408	-	33,33,33	1.42	3 (9%)	48,50,50	1.31	5 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	5LM	A	401	1	18,18,18	2.24	7 (38%)	24,24,24	2.39	9 (37%)
4	FMN	A	409	-	33,33,33	1.41	4 (12%)	48,50,50	1.32	4 (8%)
5	EDO	B	414	-	3,3,3	0.58	0	2,2,2	0.36	0
6	NCO	B	410[A]	-	6,6,6	1.18	0	-		
3	GOL	B	402	-	5,5,5	0.63	0	5,5,5	0.76	0
3	GOL	A	403	-	5,5,5	0.96	0	5,5,5	0.94	0
5	EDO	B	416	-	3,3,3	0.47	0	2,2,2	0.20	0
5	EDO	B	413	-	3,3,3	0.51	0	2,2,2	0.40	0
3	GOL	A	408	-	5,5,5	1.44	1 (20%)	5,5,5	1.86	1 (20%)
3	GOL	B	403	-	5,5,5	1.02	0	5,5,5	2.18	1 (20%)
3	GOL	B	407[A]	-	5,5,5	0.63	0	5,5,5	0.52	0
6	NCO	B	410[B]	-	6,6,6	0.98	0	-		
3	GOL	A	402	-	5,5,5	0.56	0	5,5,5	0.48	0
3	GOL	B	405	-	5,5,5	0.56	0	5,5,5	1.59	2 (40%)
3	GOL	B	407[B]	-	5,5,5	0.70	0	5,5,5	0.81	0
5	EDO	B	415	-	3,3,3	0.28	0	2,2,2	0.45	0
5	EDO	A	414	-	3,3,3	2.42	2 (66%)	2,2,2	3.16	2 (100%)
6	NCO	B	409	-	6,6,6	3.31	6 (100%)	-		
5	EDO	A	412	-	3,3,3	0.48	0	2,2,2	0.97	0
3	GOL	A	407	-	5,5,5	0.48	0	5,5,5	0.33	0
5	EDO	B	412	-	3,3,3	0.49	0	2,2,2	1.16	0
3	GOL	A	406	-	5,5,5	0.65	0	5,5,5	1.30	1 (20%)
3	GOL	A	405	-	5,5,5	0.46	0	5,5,5	0.90	0
5	EDO	A	413	-	3,3,3	0.38	0	2,2,2	0.59	0
5	EDO	A	410	-	3,3,3	0.42	0	2,2,2	0.64	0
3	GOL	A	404	-	5,5,5	0.22	0	5,5,5	0.65	0
3	GOL	B	404	-	5,5,5	0.52	0	5,5,5	0.81	0
3	GOL	B	406	-	5,5,5	0.17	0	5,5,5	0.64	0
2	5LM	B	401	1	18,18,18	2.43	8 (44%)	24,24,24	2.32	10 (41%)

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	EDO	A	411	-	-	1/1/1/1	-
5	EDO	B	411	-	-	0/1/1/1	-
4	FMN	B	408	-	-	1/18/18/18	0/3/3/3
2	5LM	A	401	1	-	3/6/22/22	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	FMN	A	409	-	-	1/18/18/18	0/3/3/3
5	EDO	B	414	-	-	0/1/1/1	-
3	GOL	B	402	-	-	3/4/4/4	-
3	GOL	A	403	-	-	0/4/4/4	-
5	EDO	B	416	-	-	1/1/1/1	-
5	EDO	B	413	-	-	0/1/1/1	-
3	GOL	A	408	-	-	4/4/4/4	-
3	GOL	B	403	-	-	0/4/4/4	-
3	GOL	B	407[A]	-	-	0/4/4/4	-
3	GOL	A	402	-	-	0/4/4/4	-
3	GOL	B	405	-	-	2/4/4/4	-
3	GOL	B	407[B]	-	-	0/4/4/4	-
5	EDO	B	415	-	-	1/1/1/1	-
5	EDO	A	414	-	-	1/1/1/1	-
5	EDO	A	412	-	-	1/1/1/1	-
3	GOL	A	407	-	-	4/4/4/4	-
5	EDO	B	412	-	-	1/1/1/1	-
3	GOL	A	406	-	-	2/4/4/4	-
3	GOL	A	405	-	-	1/4/4/4	-
5	EDO	A	413	-	-	1/1/1/1	-
5	EDO	A	410	-	-	1/1/1/1	-
3	GOL	A	404	-	-	0/4/4/4	-
3	GOL	B	404	-	-	0/4/4/4	-
3	GOL	B	406	-	-	2/4/4/4	-
2	5LM	B	401	1	-	3/6/22/22	0/2/2/2

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	5LM	CAJ-CAE	5.38	1.51	1.37
2	B	401	5LM	CAJ-CAE	5.36	1.51	1.37
2	B	401	5LM	OAI-CAD	5.34	1.33	1.23
2	A	401	5LM	OAI-CAD	4.51	1.32	1.23
6	B	409	NCO	CO-N6	3.91	2.09	1.96
6	B	409	NCO	CO-N1	3.85	2.09	1.96
6	B	409	NCO	CO-N4	3.65	2.08	1.96
4	A	409	FMN	C1'-C2'	-3.56	1.47	1.52
4	B	408	FMN	C9-C8	-3.56	1.34	1.39
2	B	401	5LM	CAF-NAA	-3.41	1.32	1.38
4	B	408	FMN	C4-N3	-3.20	1.32	1.38
6	B	409	NCO	CO-N2	3.17	2.06	1.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	409	FMN	C5'-C4'	3.15	1.56	1.51
5	A	414	EDO	O1-C1	2.88	1.56	1.42
2	B	401	5LM	CAM-SAN	-2.86	1.64	1.72
4	A	409	FMN	C9A-C5A	2.80	1.45	1.41
2	A	401	5LM	OAG-CAF	2.71	1.28	1.23
6	B	409	NCO	CO-N5	2.65	2.05	1.96
2	B	401	5LM	CAE-CAD	2.60	1.49	1.45
3	A	408	GOL	C1-C2	-2.57	1.42	1.51
2	A	401	5LM	CAF-NAA	-2.56	1.34	1.38
2	A	401	5LM	CAM-SAN	-2.53	1.65	1.72
2	A	401	5LM	CAD-NAC	-2.52	1.34	1.38
4	A	409	FMN	C4-N3	-2.51	1.34	1.38
2	A	401	5LM	CAE-CAD	2.40	1.49	1.45
5	A	414	EDO	O2-C2	2.36	1.54	1.42
2	B	401	5LM	CAB-NAC	-2.28	1.33	1.37
6	B	409	NCO	CO-N3	2.26	2.04	1.96
2	B	401	5LM	CAD-NAC	-2.19	1.34	1.38
2	B	401	5LM	OAG-CAF	2.07	1.27	1.23
4	B	408	FMN	P-O5'	2.06	1.66	1.60

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	5LM	CAJ-CAK-CAL	-6.24	105.11	123.20
2	A	401	5LM	CAJ-CAK-CAL	-5.30	107.84	123.20
2	A	401	5LM	CAD-NAC-CAB	-5.01	119.47	126.37
2	A	401	5LM	NAC-CAB-NAA	4.55	122.89	115.74
2	B	401	5LM	CAD-NAC-CAB	-4.20	120.59	126.37
2	B	401	5LM	NAC-CAB-NAA	4.06	122.13	115.74
4	B	408	FMN	O2-C2-N1	-3.88	115.36	121.80
3	B	403	GOL	O1-C1-C2	3.50	126.14	110.38
2	A	401	5LM	CAF-NAA-CAB	-3.46	121.61	126.37
3	A	408	GOL	O1-C1-C2	3.41	125.75	110.38
4	A	409	FMN	O2-C2-N1	-3.35	116.23	121.80
4	A	409	FMN	O4-C4-N3	3.24	126.21	120.11
5	A	414	EDO	O2-C2-C1	3.24	137.06	112.39
4	A	409	FMN	O4-C4-C4A	-3.23	118.00	126.53
2	A	401	5LM	CAE-CAD-NAC	3.08	119.84	114.45
5	A	414	EDO	O1-C1-C2	3.08	135.82	112.39
4	B	408	FMN	C5A-C9A-N10	2.97	120.65	117.97
4	B	408	FMN	O4-C4-N3	2.83	125.44	120.11
2	A	401	5LM	CAE-CAF-NAA	2.74	119.24	114.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	5LM	OAG-CAF-NAA	-2.73	114.99	120.11
2	B	401	5LM	CAF-NAA-CAB	-2.70	122.65	126.37
2	A	401	5LM	CAD-CAE-CAF	-2.66	116.56	119.56
2	B	401	5LM	CAD-CAE-CAF	-2.65	116.58	119.56
4	B	408	FMN	O4-C4-C4A	-2.60	119.66	126.53
3	B	405	GOL	O3-C3-C2	2.58	121.98	110.38
2	B	401	5LM	CAE-CAF-NAA	2.57	118.94	114.45
3	A	406	GOL	O1-C1-C2	2.50	121.64	110.38
2	B	401	5LM	CAE-CAD-NAC	2.49	118.81	114.45
4	B	408	FMN	C9A-N10-C10	-2.43	117.04	120.75
2	A	401	5LM	OAH-CAB-NAA	-2.42	117.56	121.86
3	B	405	GOL	C3-C2-C1	2.36	120.45	111.80
4	A	409	FMN	C5A-C9A-N10	2.29	120.04	117.97
2	B	401	5LM	OAH-CAB-NAA	-2.15	118.03	121.86
2	B	401	5LM	CAQ-CAM-SAN	2.10	115.07	110.86
2	A	401	5LM	OAI-CAD-CAE	-2.08	121.40	125.98

There are no chirality outliers.

All (34) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	5LM	CAF-CAE-CAJ-CAK
2	A	401	5LM	CAD-CAE-CAJ-CAK
2	B	401	5LM	CAF-CAE-CAJ-CAK
2	B	401	5LM	CAD-CAE-CAJ-CAK
3	A	406	GOL	C1-C2-C3-O3
3	A	407	GOL	O1-C1-C2-C3
3	A	408	GOL	C1-C2-C3-O3
3	B	402	GOL	C1-C2-C3-O3
3	B	405	GOL	C1-C2-C3-O3
2	A	401	5LM	CAE-CAJ-CAK-CAL
2	B	401	5LM	CAE-CAJ-CAK-CAL
3	A	407	GOL	C1-C2-C3-O3
3	A	408	GOL	O1-C1-C2-C3
3	A	407	GOL	O1-C1-C2-O2
3	A	408	GOL	O1-C1-C2-O2
3	A	408	GOL	O2-C2-C3-O3
3	B	402	GOL	O2-C2-C3-O3
5	A	413	EDO	O1-C1-C2-O2
5	B	412	EDO	O1-C1-C2-O2
3	B	405	GOL	O2-C2-C3-O3
3	A	405	GOL	O2-C2-C3-O3

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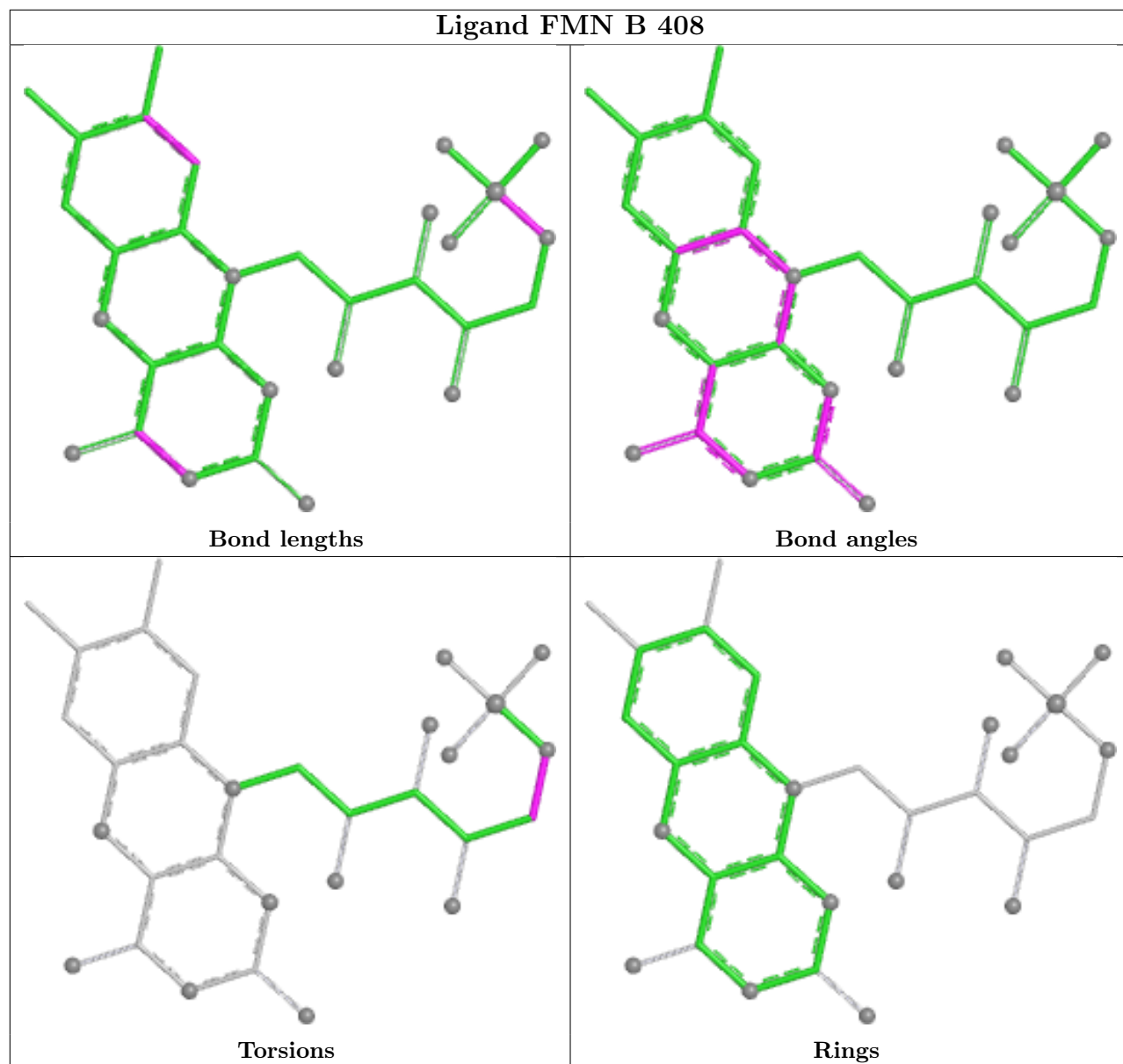
Mol	Chain	Res	Type	Atoms
3	B	402	GOL	O1-C1-C2-O2
3	B	406	GOL	O1-C1-C2-O2
5	B	416	EDO	O1-C1-C2-O2
3	B	406	GOL	O1-C1-C2-C3
4	B	408	FMN	C4'-C5'-O5'-P
5	A	412	EDO	O1-C1-C2-O2
4	A	409	FMN	C4'-C5'-O5'-P
3	A	407	GOL	O2-C2-C3-O3
5	A	411	EDO	O1-C1-C2-O2
3	A	406	GOL	O2-C2-C3-O3
5	A	410	EDO	O1-C1-C2-O2
5	B	415	EDO	O1-C1-C2-O2
5	A	414	EDO	O1-C1-C2-O2

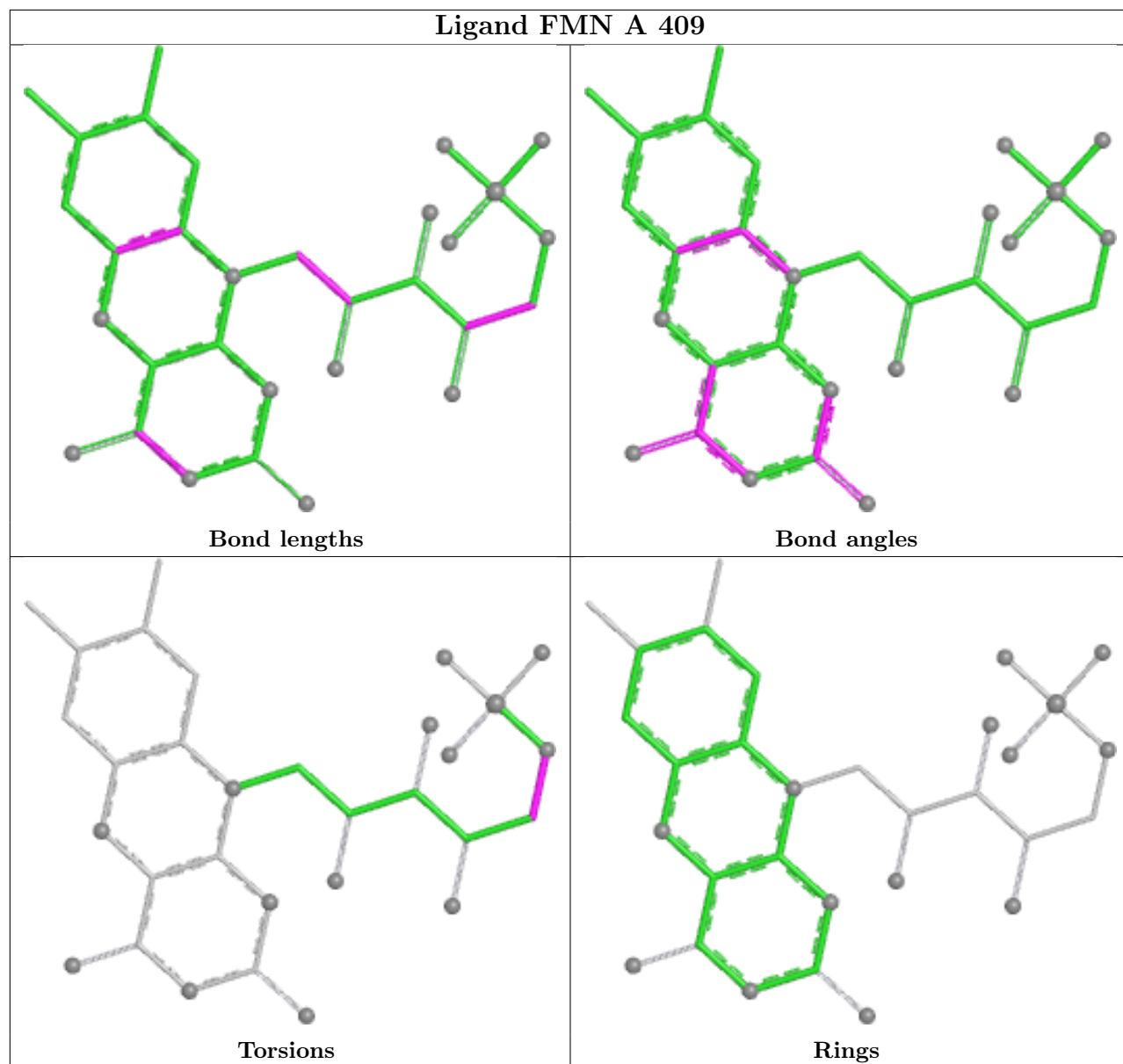
There are no ring outliers.

11 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	411	EDO	1	0
4	B	408	FMN	1	0
2	A	401	5LM	2	0
4	A	409	FMN	1	0
5	B	416	EDO	1	0
3	B	405	GOL	3	0
5	B	415	EDO	1	0
5	A	412	EDO	2	0
5	B	412	EDO	3	0
5	A	410	EDO	2	0
2	B	401	5LM	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, 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	313/314 (99%)	0.47	33 (10%) 11 16	5, 16, 37, 50	2 (0%)
1	B	313/314 (99%)	0.36	18 (5%) 29 35	5, 15, 36, 65	4 (1%)
All	All	626/628 (99%)	0.41	51 (8%) 18 23	5, 16, 37, 65	6 (0%)

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	52	GLY	5.9
1	B	0	MET	5.4
1	A	52	GLY	4.9
1	B	71	LEU	4.8
1	A	155	LEU	4.5
1	A	108	ALA	4.4
1	A	133	VAL	4.3
1	B	133	VAL	4.3
1	A	134	PRO	3.7
1	B	134	PRO	3.7
1	A	156	ALA	3.5
1	A	71	LEU	3.3
1	B	1	CYS	3.3
1	B	51	ASP	3.2
1	B	72	PRO	3.1
1	A	51	ASP	3.0
1	A	131	PRO	3.0
1	B	2	LEU	2.9
1	A	130	CYS	2.9
1	A	153	VAL	2.9
1	A	312	GLU	2.9
1	B	54	PRO	2.7
1	A	72	PRO	2.6
1	B	312	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	130	CYS	2.5
1	A	50	ARG	2.5
1	A	102	SER	2.5
1	A	159	LEU	2.5
1	B	131	PRO	2.4
1	A	116	VAL	2.4
1	A	186	LEU	2.4
1	B	136	LYS	2.3
1	A	10	VAL	2.3
1	A	152	GLN	2.3
1	A	158	GLY	2.3
1	A	145	ALA	2.3
1	B	291	GLU	2.3
1	A	103	VAL	2.3
1	A	90	SER	2.2
1	A	121	GLY	2.2
1	A	98	ILE	2.2
1	A	107	VAL	2.2
1	A	47	SER	2.2
1	A	123	LEU	2.2
1	A	1	CYS	2.2
1	A	110	VAL	2.1
1	B	155	LEU	2.1
1	B	118	GLN	2.1
1	B	297	GLY	2.1
1	A	137	PRO	2.1
1	A	180	VAL	2.0

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 oligosaccharides 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,

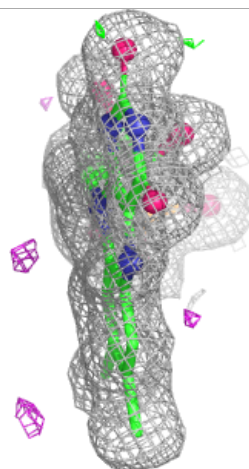
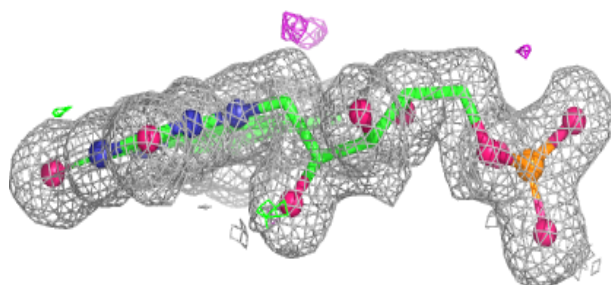
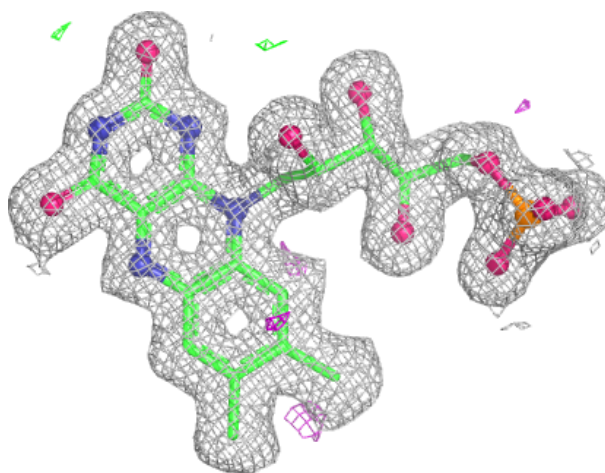
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

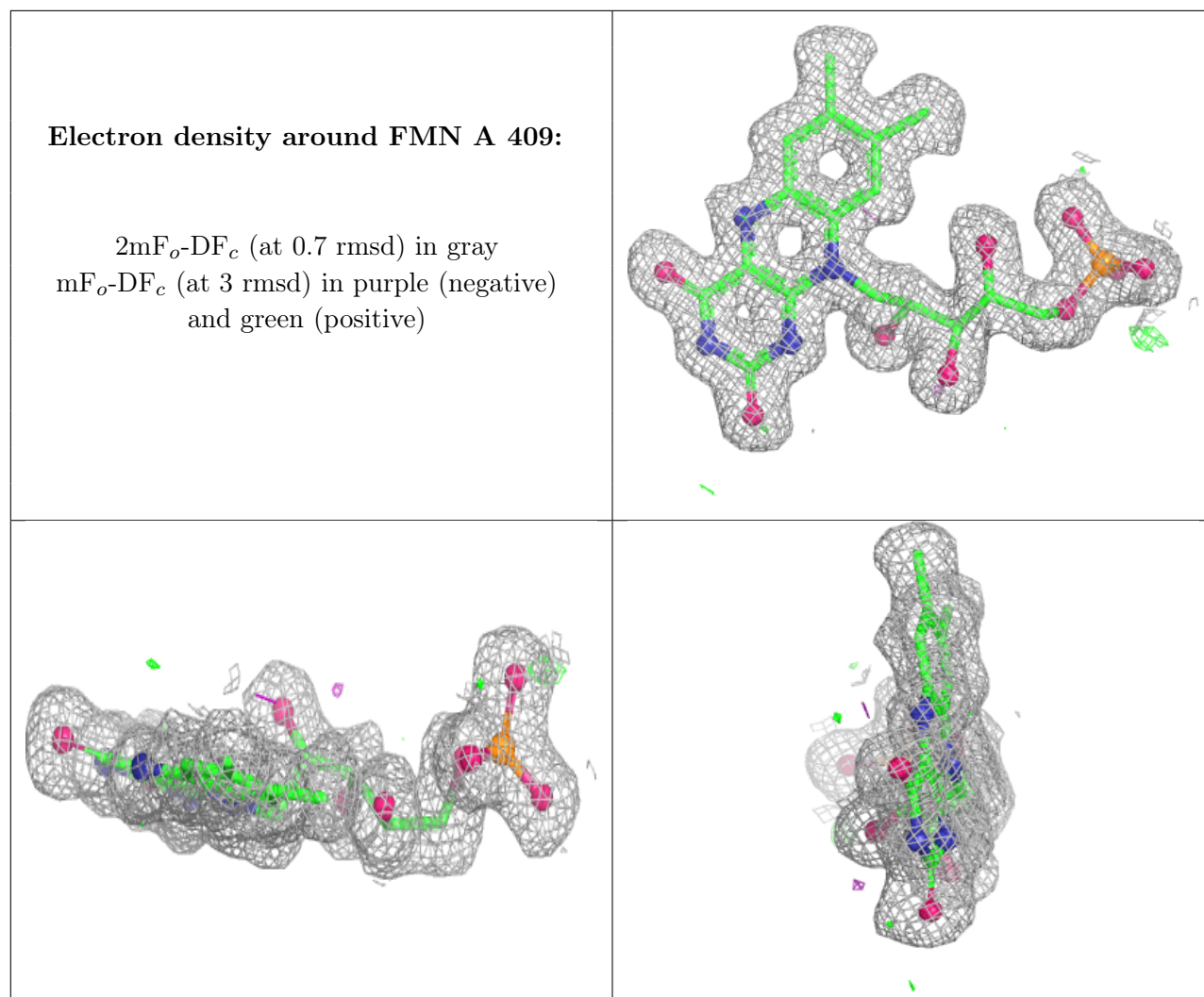
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	EDO	B	413	4/4	0.67	0.15	40,42,46,48	0
5	EDO	A	410	4/4	0.72	0.15	41,42,44,48	0
5	EDO	B	411	4/4	0.73	0.16	41,41,44,45	0
5	EDO	A	411	4/4	0.73	0.18	31,33,37,43	0
3	GOL	A	407	6/6	0.74	0.18	41,54,57,67	0
3	GOL	A	406	6/6	0.75	0.16	36,39,43,44	0
3	GOL	A	404	6/6	0.78	0.15	38,40,44,46	0
3	GOL	A	408	6/6	0.78	0.24	20,26,32,34	0
3	GOL	B	402	6/6	0.81	0.14	29,32,33,40	0
3	GOL	B	406	6/6	0.81	0.13	36,37,41,42	0
3	GOL	B	405	6/6	0.84	0.12	29,38,42,42	0
5	EDO	B	416	4/4	0.84	0.15	37,38,41,41	0
3	GOL	A	403	6/6	0.85	0.14	25,31,33,35	0
3	GOL	B	403	6/6	0.85	0.15	17,30,35,39	0
5	EDO	A	413	4/4	0.85	0.17	29,34,36,37	0
3	GOL	B	404	6/6	0.87	0.11	30,36,37,38	0
5	EDO	B	412	4/4	0.88	0.19	25,27,27,27	0
5	EDO	A	414	4/4	0.89	0.12	16,17,17,18	0
2	5LM	B	401	17/17	0.90	0.14	14,23,53,62	0
2	5LM	A	401	17/17	0.91	0.13	13,25,56,65	0
3	GOL	A	405	6/6	0.91	0.10	22,29,31,32	0
5	EDO	B	415	4/4	0.92	0.15	25,28,30,31	0
5	EDO	B	414	4/4	0.92	0.09	24,25,27,28	0
6	NCO	B	410[A]	7/7	0.92	0.17	21,22,23,24	7
6	NCO	B	410[B]	7/7	0.92	0.17	22,22,23,24	7
3	GOL	B	407[B]	6/6	0.93	0.07	12,13,15,15	6
5	EDO	A	412	4/4	0.93	0.15	25,25,25,27	0
3	GOL	B	407[A]	6/6	0.93	0.07	18,20,21,21	6
3	GOL	A	402	6/6	0.95	0.09	19,24,26,28	0
4	FMN	B	408	31/31	0.98	0.04	5,7,9,12	0
4	FMN	A	409	31/31	0.98	0.05	5,8,10,11	0
6	NCO	B	409	7/7	1.00	0.06	10,10,11,11	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 FMN B 408:

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





6.5 Other polymers [i](#)

There are no such residues in this entry.