



Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 04:16 am BST

PDB ID : 3B06
Title : Crystal structure of Sulfolobus shibatae isopentenyl diphosphate isomerase in complex with reduced FMN and DMAPP.
Authors : Unno, H.; Nagai, T.; Hemmi, H.
Deposited on : 2011-06-03
Resolution : 2.29 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 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

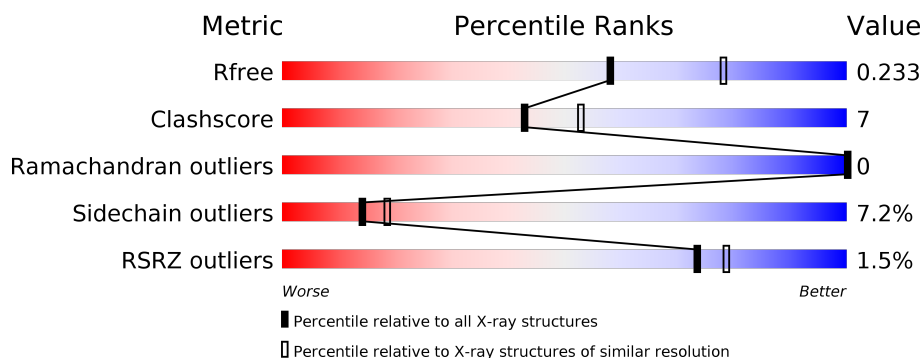
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.29 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 ≥ 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	368	<div> <div>2%</div> <div> <div></div> <div>82%</div> <div>14%</div> <div>• •</div> </div> </div>
1	B	368	<div> <div>2%</div> <div> <div></div> <div>80%</div> <div>15%</div> <div>• •</div> </div> </div>
1	C	368	<div> <div>%</div> <div> <div></div> <div>80%</div> <div>15%</div> <div>• •</div> </div> </div>
1	D	368	<div> <div>%</div> <div> <div></div> <div>82%</div> <div>14%</div> <div>• •</div> </div> </div>

2 Entry composition [i](#)

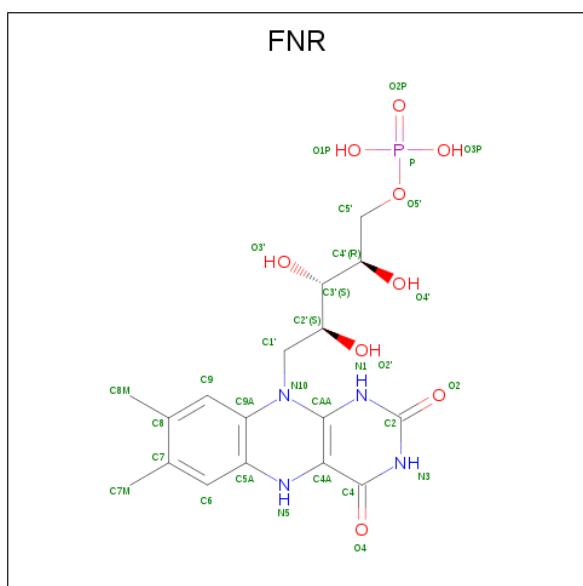
There are 5 unique types of molecules in this entry. The entry contains 11710 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Isopentenyl-diphosphate delta-isomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	364	Total	C	N	O	S	0	0	0
			2808	1799	475	523	11			
1	B	364	Total	C	N	O	S	0	0	0
			2808	1799	475	523	11			
1	C	364	Total	C	N	O	S	0	0	0
			2808	1799	475	523	11			
1	D	364	Total	C	N	O	S	0	0	0
			2808	1799	475	523	11			

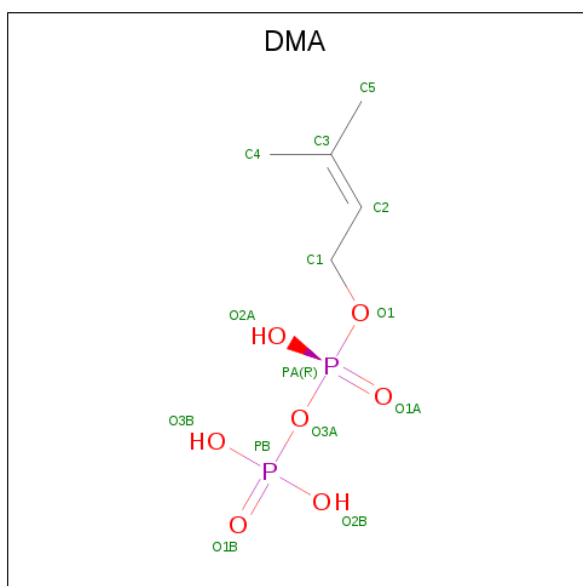
- Molecule 2 is 1-DEOXY-1-(7,8-DIMETHYL-2,4-DIOXO-3,4-DIHYDRO-2H-BENZO[G]P TERIDIN-1-ID-10(5H)-YL)-5-O-PHOSPHONATO-D-RIBITOL (three-letter code: FNR) (formula: $C_{17}H_{23}N_4O_9P$).



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

- Molecule 3 is DIMETHYLALLYL DIPHOSPHATE (three-letter code: DMA) (formula: $C_5H_{12}O_7P_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			14	5	7	2		
3	B	1	Total	C	O	P	0	0
			14	5	7	2		
3	C	1	Total	C	O	P	0	0
			14	5	7	2		
3	D	1	Total	C	O	P	0	0
			14	5	7	2		

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mg	0	0
			1	1		
4	A	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	1	Total 1	Mg 1	0	0
4	C	1	Total 1	Mg 1	0	0

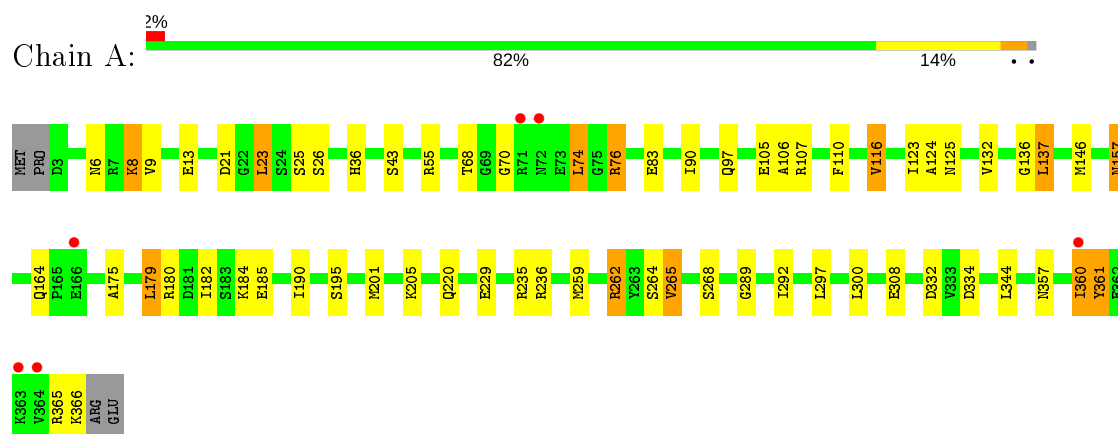
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	73	Total 73	O 73	0	0
5	B	63	Total 63	O 63	0	0
5	C	86	Total 86	O 86	0	0
5	D	72	Total 72	O 72	0	0

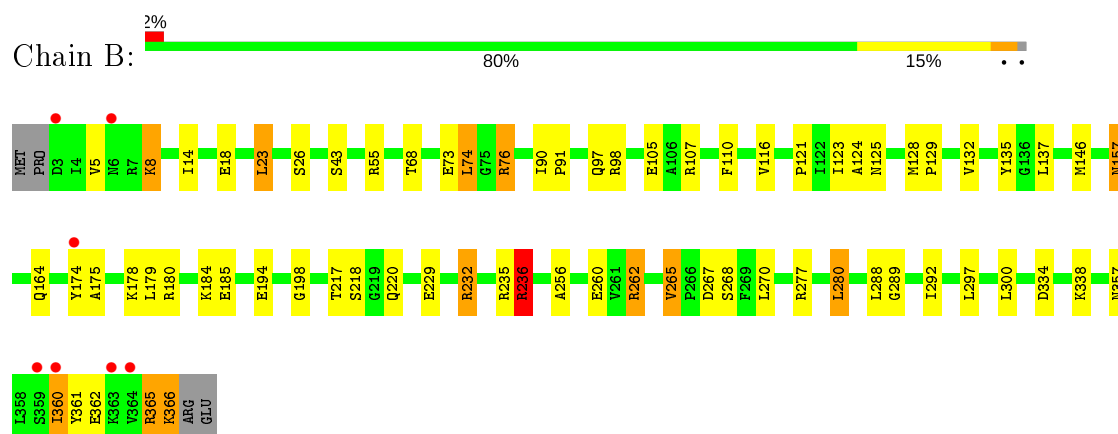
3 Residue-property plots [i](#)

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.

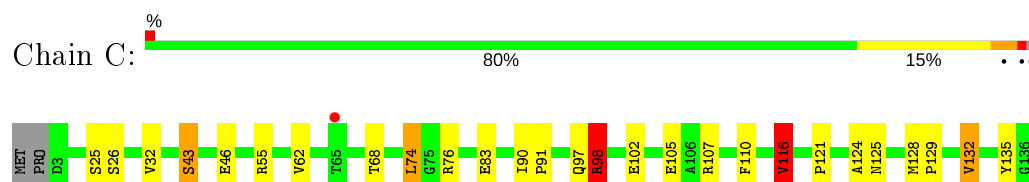
- Molecule 1: Isopentenyl-diphosphate delta-isomerase

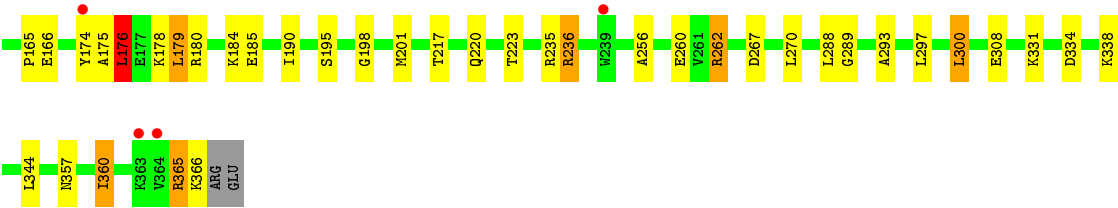


- Molecule 1: Isopentenyl-diphosphate delta-isomerase

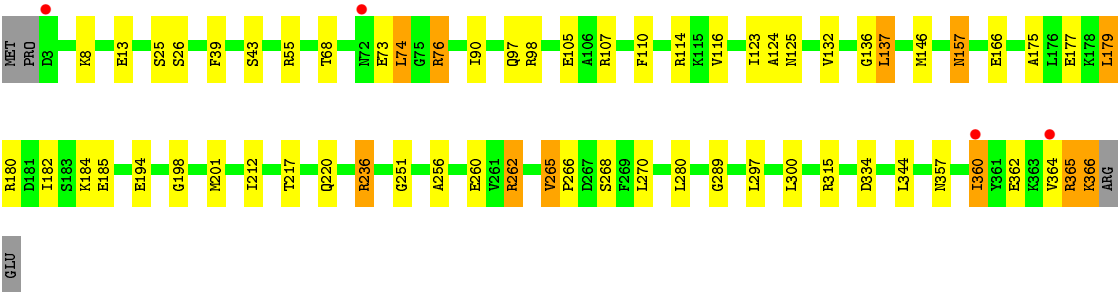
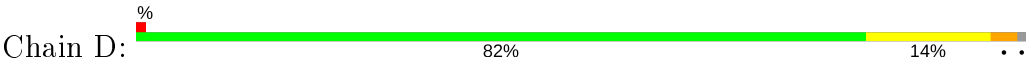


- Molecule 1: Isopentenyl-diphosphate delta-isomerase





● Molecule 1: Isopentenyl-diphosphate delta-isomerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	100.84Å 100.84Å 334.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.39 – 2.29 37.39 – 2.29	Depositor EDS
% Data completeness (in resolution range)	93.5 (37.39-2.29) 93.4 (37.39-2.29)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.53 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.204 , 0.239 0.199 , 0.233	Depositor DCC
R_{free} test set	3699 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	44.6	Xtriage
Anisotropy	0.065	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 35.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11710	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.23% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: DMA, MG, FNR

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	1.05	2/2855 (0.1%)	1.10	19/3846 (0.5%)
1	B	1.09	4/2855 (0.1%)	1.02	16/3846 (0.4%)
1	C	1.06	2/2855 (0.1%)	1.13	21/3846 (0.5%)
1	D	1.04	1/2855 (0.0%)	1.00	14/3846 (0.4%)
All	All	1.06	9/11420 (0.1%)	1.06	70/15384 (0.5%)

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	C	1	0

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	362	GLU	CG-CD	6.67	1.61	1.51
1	C	174	TYR	CD1-CE1	5.95	1.48	1.39
1	C	174	TYR	CE1-CZ	5.94	1.46	1.38
1	B	362	GLU	CB-CG	5.79	1.63	1.52
1	A	308	GLU	CG-CD	5.76	1.60	1.51
1	B	174	TYR	CD1-CE1	5.52	1.47	1.39
1	D	13	GLU	CD-OE2	5.25	1.31	1.25
1	A	13	GLU	CD-OE1	5.15	1.31	1.25
1	B	174	TYR	CE1-CZ	5.06	1.45	1.38

All (70) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	76	ARG	NE-CZ-NH2	17.71	129.16	120.30
1	A	76	ARG	NE-CZ-NH1	-17.13	111.73	120.30
1	C	98	ARG	NE-CZ-NH2	15.86	128.23	120.30
1	C	98	ARG	NE-CZ-NH1	-14.14	113.23	120.30
1	D	262	ARG	NE-CZ-NH1	-11.60	114.50	120.30
1	C	262	ARG	NE-CZ-NH1	-11.42	114.59	120.30
1	C	180	ARG	NE-CZ-NH2	11.29	125.95	120.30
1	A	365	ARG	NE-CZ-NH2	-11.15	114.72	120.30
1	A	236	ARG	NE-CZ-NH2	-10.95	114.82	120.30
1	C	165	PRO	C-N-CA	10.92	148.99	121.70
1	C	236	ARG	NE-CZ-NH2	-10.75	114.92	120.30
1	A	236	ARG	NE-CZ-NH1	10.64	125.62	120.30
1	C	180	ARG	NE-CZ-NH1	-10.12	115.24	120.30
1	D	180	ARG	NE-CZ-NH1	9.91	125.26	120.30
1	B	262	ARG	NE-CZ-NH1	-9.69	115.45	120.30
1	A	365	ARG	NE-CZ-NH1	9.55	125.08	120.30
1	C	236	ARG	NE-CZ-NH1	9.36	124.98	120.30
1	A	76	ARG	CD-NE-CZ	9.12	136.36	123.60
1	C	262	ARG	NE-CZ-NH2	8.97	124.78	120.30
1	B	235	ARG	NE-CZ-NH2	-8.87	115.86	120.30
1	A	262	ARG	NE-CZ-NH1	-8.53	116.03	120.30
1	D	180	ARG	NE-CZ-NH2	-8.00	116.30	120.30
1	B	180	ARG	NE-CZ-NH1	7.96	124.28	120.30
1	C	165	PRO	CA-C-N	7.39	133.46	117.20
1	C	165	PRO	O-C-N	-7.26	111.09	122.70
1	D	262	ARG	NE-CZ-NH2	7.00	123.80	120.30
1	B	180	ARG	NE-CZ-NH2	-6.90	116.85	120.30
1	B	76	ARG	NE-CZ-NH1	6.66	123.63	120.30
1	D	236	ARG	NE-CZ-NH2	6.62	123.61	120.30
1	B	236	ARG	NE-CZ-NH2	6.46	123.53	120.30
1	B	98	ARG	NE-CZ-NH2	-6.40	117.10	120.30
1	D	76	ARG	NE-CZ-NH1	6.39	123.50	120.30
1	A	180	ARG	NE-CZ-NH1	6.32	123.46	120.30
1	B	277	ARG	NE-CZ-NH2	6.26	123.43	120.30
1	B	236	ARG	NE-CZ-NH1	-6.16	117.22	120.30
1	B	365	ARG	NE-CZ-NH1	6.07	123.34	120.30
1	B	98	ARG	NE-CZ-NH1	6.06	123.33	120.30
1	D	344	LEU	CA-CB-CG	6.04	129.19	115.30
1	B	23	LEU	CB-CG-CD2	5.99	121.18	111.00
1	C	201	MET	CA-CB-CG	5.92	123.37	113.30
1	C	235	ARG	NE-CZ-NH1	5.92	123.26	120.30
1	A	361	TYR	CB-CG-CD2	-5.88	117.47	121.00
1	C	98	ARG	CD-NE-CZ	5.69	131.57	123.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	344	LEU	CA-CB-CG	5.66	128.31	115.30
1	D	236	ARG	NE-CZ-NH1	-5.65	117.47	120.30
1	A	201	MET	CA-CB-CG	5.63	122.87	113.30
1	A	262	ARG	NE-CZ-NH2	5.63	123.11	120.30
1	D	365	ARG	NE-CZ-NH2	-5.51	117.54	120.30
1	B	235	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	D	201	MET	CA-CB-CG	5.45	122.56	113.30
1	A	344	LEU	CA-CB-CG	5.37	127.65	115.30
1	C	365	ARG	NE-CZ-NH2	-5.34	117.63	120.30
1	A	236	ARG	CD-NE-CZ	5.34	131.08	123.60
1	A	76	ARG	CG-CD-NE	-5.34	100.59	111.80
1	A	23	LEU	CB-CG-CD2	5.31	120.03	111.00
1	D	362	GLU	OE1-CD-OE2	-5.28	116.96	123.30
1	D	98	ARG	NE-CZ-NH2	-5.27	117.66	120.30
1	A	332	ASP	CB-CG-OD2	5.27	123.04	118.30
1	D	315	ARG	NE-CZ-NH1	5.16	122.88	120.30
1	B	232	ARG	NE-CZ-NH2	-5.16	117.72	120.30
1	C	176	LEU	CB-CG-CD1	5.15	119.76	111.00
1	A	235	ARG	NE-CZ-NH2	-5.14	117.73	120.30
1	B	76	ARG	NE-CZ-NH2	-5.11	117.75	120.30
1	C	236	ARG	CD-NE-CZ	5.05	130.67	123.60
1	C	300	LEU	CA-CB-CG	5.03	126.87	115.30
1	A	21	ASP	CB-CG-OD1	5.03	122.83	118.30
1	B	280	LEU	CB-CG-CD2	5.03	119.55	111.00
1	C	235	ARG	NE-CZ-NH2	-5.03	117.79	120.30
1	C	116	VAL	CG1-CB-CG2	5.01	118.92	110.90
1	D	98	ARG	NE-CZ-NH1	5.00	122.80	120.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	C	166	GLU	CA

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	2808	0	2890	36	0
1	B	2808	0	2890	39	0
1	C	2808	0	2889	45	0
1	D	2808	0	2890	38	0
2	A	31	0	22	1	0
2	B	31	0	22	0	0
2	C	31	0	22	1	0
2	D	31	0	22	0	0
3	A	14	0	9	2	0
3	B	14	0	9	1	0
3	C	14	0	9	1	0
3	D	14	0	9	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	73	0	0	0	0
5	B	63	0	0	1	0
5	C	86	0	0	1	0
5	D	72	0	0	2	0
All	All	11710	0	11683	158	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.

All (158) 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:184:LYS:HE2	1:C:184:LYS:HA	1.33	1.10
1:A:184:LYS:HA	1:A:184:LYS:HE2	1.33	1.09
1:B:184:LYS:HE2	1:B:184:LYS:HA	1.37	1.04
1:C:132:VAL:HG12	1:C:175:ALA:HB2	1.43	1.00
1:D:184:LYS:HA	1:D:184:LYS:HE2	1.39	0.99
1:A:265:VAL:HG22	1:A:268:SER:HB3	1.49	0.93
1:C:137:LEU:HD11	1:C:185:GLU:HG2	1.54	0.90
1:D:265:VAL:HG22	1:D:268:SER:HB3	1.56	0.88
1:B:265:VAL:HG22	1:B:268:SER:HB3	1.60	0.82
1:C:107:ARG:HA	1:C:146:MET:HE3	1.61	0.82
1:A:184:LYS:HE2	1:A:184:LYS:CA	2.11	0.81
1:D:107:ARG:HA	1:D:146:MET:HE3	1.60	0.80
1:A:107:ARG:HA	1:A:146:MET:HE3	1.62	0.80
1:D:110:PHE:CD1	1:D:146:MET:HE1	2.20	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:357:ASN:OD1	1:D:360:ILE:HG23	1.87	0.75
1:C:357:ASN:OD1	1:C:360:ILE:HG23	1.87	0.74
1:B:107:ARG:HA	1:B:146:MET:HE3	1.67	0.74
1:A:137:LEU:HD11	1:A:185:GLU:HG2	1.71	0.72
1:B:110:PHE:CD1	1:B:146:MET:HE1	2.25	0.72
1:D:184:LYS:CA	1:D:184:LYS:HE2	2.17	0.70
1:B:184:LYS:HG3	5:B:415:HOH:O	1.90	0.70
1:A:26:SER:H	1:A:220:GLN:HE21	1.37	0.70
1:B:97:GLN:HE21	1:B:125:ASN:H	1.42	0.68
1:C:110:PHE:CD1	1:C:146:MET:HE1	2.29	0.68
1:A:110:PHE:CD1	1:A:146:MET:HE1	2.29	0.67
1:A:262:ARG:HD2	1:A:289:GLY:O	1.94	0.67
1:C:135:TYR:O	1:C:178:LYS:HE2	1.95	0.67
1:C:184:LYS:HA	1:C:184:LYS:CE	2.19	0.66
1:B:26:SER:H	1:B:220:GLN:HE21	1.43	0.66
1:D:366:LYS:O	5:D:437:HOH:O	2.13	0.65
1:C:262:ARG:HD2	1:C:289:GLY:O	1.97	0.65
1:C:97:GLN:HE21	1:C:125:ASN:H	1.43	0.64
1:A:97:GLN:HE22	1:A:124:ALA:HB1	1.61	0.64
1:D:262:ARG:HD2	1:D:289:GLY:O	1.99	0.63
1:D:137:LEU:HD11	1:D:185:GLU:HG2	1.80	0.62
1:B:357:ASN:OD1	1:B:360:ILE:HG23	2.00	0.62
1:D:97:GLN:HE21	1:D:125:ASN:H	1.47	0.62
1:A:132:VAL:HG12	1:A:175:ALA:HB2	1.81	0.61
1:B:338:LYS:HG2	1:B:366:LYS:HB3	1.81	0.61
1:A:357:ASN:OD1	1:A:360:ILE:HG23	2.01	0.61
1:B:365:ARG:O	1:B:366:LYS:HB2	2.01	0.60
1:B:184:LYS:HE2	1:B:184:LYS:CA	2.19	0.60
1:A:26:SER:H	1:A:220:GLN:NE2	1.99	0.60
1:D:132:VAL:HG12	1:D:175:ALA:HB2	1.84	0.59
1:C:107:ARG:HA	1:C:146:MET:CE	2.30	0.59
1:C:26:SER:H	1:C:220:GLN:HE21	1.51	0.58
1:D:26:SER:H	1:D:220:GLN:HE21	1.51	0.58
1:D:110:PHE:HB2	1:D:146:MET:HE2	1.85	0.57
1:C:25:SER:HB2	1:C:220:GLN:NE2	2.19	0.57
1:B:107:ARG:HA	1:B:146:MET:CE	2.34	0.56
1:B:157:ASN:H	1:B:157:ASN:HD22	1.52	0.56
1:C:365:ARG:O	1:C:366:LYS:HB2	2.05	0.56
1:B:26:SER:H	1:B:220:GLN:NE2	2.03	0.56
1:B:135:TYR:O	1:B:178:LYS:HE2	2.05	0.56
1:D:107:ARG:HA	1:D:146:MET:CE	2.33	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:198:GLY:HA2	1:D:217:THR:O	2.06	0.55
1:A:97:GLN:HE21	1:A:125:ASN:H	1.53	0.55
1:B:137:LEU:CD2	1:B:185:GLU:HG2	2.37	0.55
1:C:25:SER:HB2	1:C:220:GLN:HE21	1.71	0.55
2:A:669:FNR:H9	2:A:669:FNR:H6	1.89	0.55
1:A:110:PHE:HB2	1:A:146:MET:HE2	1.87	0.55
1:A:107:ARG:HA	1:A:146:MET:CE	2.34	0.55
1:B:157:ASN:HD22	1:B:157:ASN:N	2.06	0.54
1:D:110:PHE:HB2	1:D:146:MET:CE	2.37	0.54
1:D:136:GLY:HA2	1:D:182:ILE:HD11	1.90	0.54
1:A:123:ILE:HD12	1:A:123:ILE:N	2.23	0.53
1:D:132:VAL:CG1	1:D:175:ALA:HB2	2.39	0.53
1:D:26:SER:H	1:D:220:GLN:NE2	2.07	0.53
1:D:97:GLN:HE22	1:D:124:ALA:HB1	1.75	0.52
1:A:132:VAL:CG1	1:A:175:ALA:HB2	2.40	0.52
1:B:97:GLN:HE22	1:B:124:ALA:HB1	1.74	0.52
1:A:8:LYS:NZ	3:A:701:DMA:O1B	2.43	0.52
1:A:157:ASN:HD22	1:A:157:ASN:H	1.58	0.52
1:C:110:PHE:HB2	1:C:146:MET:HE2	1.92	0.52
1:B:68:THR:OG1	1:B:74:LEU:HG	2.10	0.52
1:B:14:ILE:HG23	1:B:18:GLU:HG3	1.92	0.51
1:C:137:LEU:CD1	1:C:185:GLU:HG2	2.36	0.51
1:C:26:SER:H	1:C:220:GLN:NE2	2.08	0.51
1:B:262:ARG:HD2	1:B:289:GLY:O	2.11	0.51
1:C:184:LYS:CA	1:C:184:LYS:HE2	2.19	0.51
1:C:331:LYS:HE2	5:C:448:HOH:O	2.11	0.50
1:B:137:LEU:HD22	1:B:185:GLU:HG2	1.93	0.50
1:D:68:THR:OG1	1:D:74:LEU:HG	2.11	0.50
1:C:98:ARG:HD2	1:C:102:GLU:OE2	2.12	0.50
1:A:195:SER:HB2	3:A:701:DMA:H51	1.92	0.50
1:A:25:SER:HB2	1:A:220:GLN:NE2	2.27	0.50
1:C:176:LEU:HD13	1:D:39:PHE:CE1	2.46	0.50
1:B:232:ARG:O	1:B:236:ARG:HD3	2.11	0.50
1:A:83:GLU:HB3	1:A:116:VAL:HG13	1.93	0.49
1:B:8:LYS:NZ	3:B:701:DMA:O1B	2.46	0.49
1:A:110:PHE:HB2	1:A:146:MET:CE	2.43	0.49
1:A:97:GLN:NE2	1:A:124:ALA:HB1	2.28	0.49
1:C:157:ASN:HD22	1:C:157:ASN:H	1.61	0.49
1:A:157:ASN:N	1:A:157:ASN:HD22	2.10	0.48
1:B:97:GLN:NE2	1:B:125:ASN:H	2.10	0.48
1:C:338:LYS:HG2	1:C:366:LYS:HB3	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:266:PRO:HB3	1:D:364:VAL:HG13	1.96	0.48
1:C:32:VAL:HG21	1:C:288:LEU:HD11	1.95	0.48
1:C:97:GLN:NE2	1:C:125:ASN:H	2.10	0.48
1:D:177:GLU:OE2	5:D:426:HOH:O	2.20	0.48
1:C:195:SER:HB2	3:C:701:DMA:H41	1.96	0.47
1:C:62:VAL:HA	1:C:293:ALA:O	2.15	0.47
1:B:123:ILE:HD12	1:B:123:ILE:N	2.30	0.47
1:B:256:ALA:O	1:B:260:GLU:HG3	2.15	0.47
1:C:97:GLN:HE22	1:C:124:ALA:HB1	1.78	0.47
1:C:198:GLY:HA2	1:C:217:THR:O	2.15	0.47
1:D:360:ILE:O	1:D:364:VAL:HG23	2.14	0.47
1:C:157:ASN:HD22	1:C:157:ASN:N	2.13	0.46
1:A:164:GLN:HG3	1:A:229:GLU:CD	2.36	0.46
1:B:91:PRO:HB3	1:B:121:PRO:HB2	1.98	0.46
1:C:179:LEU:HD22	1:C:190:ILE:HD13	1.97	0.46
1:C:135:TYR:O	1:C:178:LYS:CE	2.63	0.45
1:D:157:ASN:H	1:D:157:ASN:HD22	1.65	0.45
2:C:669:FNR:H6	2:C:669:FNR:H9	1.98	0.45
1:A:68:THR:OG1	1:A:74:LEU:HG	2.17	0.45
1:D:157:ASN:HD22	1:D:157:ASN:N	2.14	0.45
1:C:83:GLU:HB3	1:C:116:VAL:HG13	1.99	0.45
1:A:265:VAL:CG2	1:A:268:SER:HB3	2.36	0.45
1:C:68:THR:OG1	1:C:74:LEU:HG	2.18	0.44
1:D:366:LYS:HA	1:D:366:LYS:HD3	1.85	0.44
1:B:164:GLN:HG3	1:B:229:GLU:CD	2.38	0.44
1:C:110:PHE:HB2	1:C:146:MET:CE	2.47	0.44
1:B:132:VAL:CG2	1:B:175:ALA:HB2	2.47	0.44
1:C:223:THR:OG1	1:C:297:LEU:HB2	2.18	0.44
1:D:179:LEU:HD13	1:D:212:ILE:HD11	1.98	0.44
1:C:128:MET:N	1:C:129:PRO:CD	2.81	0.44
1:A:205:LYS:HE3	1:A:264:SER:HB2	2.00	0.44
1:D:256:ALA:O	1:D:260:GLU:HG3	2.18	0.44
1:C:43:SER:O	1:C:46:GLU:HG2	2.18	0.43
1:A:136:GLY:HA2	1:A:182:ILE:HD11	2.00	0.43
1:C:357:ASN:CG	1:C:360:ILE:HG23	2.39	0.43
1:A:70:GLY:HA2	1:A:106:ALA:HB1	2.00	0.43
1:B:110:PHE:HB2	1:B:146:MET:CE	2.49	0.43
1:B:132:VAL:HG23	1:B:175:ALA:HB2	1.99	0.43
1:C:267:ASP:N	1:C:267:ASP:OD1	2.48	0.43
1:A:25:SER:HB2	1:A:220:GLN:HE21	1.83	0.43
1:B:267:ASP:N	1:B:267:ASP:OD1	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:110:PHE:HD1	1:B:146:MET:HE1	1.81	0.43
1:D:166:GLU:HG2	1:D:166:GLU:O	2.19	0.43
1:B:217:THR:O	1:B:218:SER:C	2.57	0.42
1:C:256:ALA:O	1:C:260:GLU:HG3	2.19	0.42
1:D:25:SER:HB2	1:D:220:GLN:NE2	2.34	0.42
1:C:91:PRO:HB3	1:C:121:PRO:HB2	2.00	0.42
1:D:25:SER:HB2	1:D:220:GLN:HE21	1.85	0.41
1:B:137:LEU:HD21	1:B:185:GLU:HG2	2.02	0.41
1:B:128:MET:N	1:B:129:PRO:CD	2.84	0.41
1:A:179:LEU:HD22	1:A:190:ILE:HD13	2.03	0.41
1:C:110:PHE:HD1	1:C:146:MET:HE1	1.83	0.41
1:D:123:ILE:HD12	1:D:123:ILE:N	2.36	0.41
1:B:288:LEU:O	1:B:361:TYR:OH	2.21	0.41
1:C:308:GLU:H	1:C:308:GLU:CD	2.24	0.41
1:D:114:ARG:HA	1:D:114:ARG:HD3	1.95	0.41
1:A:107:ARG:CA	1:A:146:MET:HE3	2.44	0.41
1:A:259:MET:HA	1:A:361:TYR:OH	2.21	0.41
1:D:184:LYS:CA	1:D:184:LYS:CE	2.96	0.40
1:A:36:HIS:HB2	1:D:251:GLY:HA2	2.02	0.40
1:B:198:GLY:HA2	1:B:217:THR:O	2.22	0.40
1:D:365:ARG:HG3	1:D:366:LYS:N	2.37	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	362/368 (98%)	351 (97%)	11 (3%)	0	100	100
1	B	362/368 (98%)	347 (96%)	15 (4%)	0	100	100
1	C	362/368 (98%)	349 (96%)	13 (4%)	0	100	100
1	D	362/368 (98%)	349 (96%)	13 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1448/1472 (98%)	1396 (96%)	52 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	298/302 (99%)	277 (93%)	21 (7%)	15	19
1	B	298/302 (99%)	274 (92%)	24 (8%)	11	15
1	C	298/302 (99%)	279 (94%)	19 (6%)	17	23
1	D	298/302 (99%)	276 (93%)	22 (7%)	13	17
All	All	1192/1208 (99%)	1106 (93%)	86 (7%)	14	18

All (86) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	ASN
1	A	8	LYS
1	A	9	VAL
1	A	23	LEU
1	A	43	SER
1	A	55	ARG
1	A	74	LEU
1	A	76	ARG
1	A	90	ILE
1	A	105	GLU
1	A	116	VAL
1	A	137	LEU
1	A	157	ASN
1	A	179	LEU
1	A	265	VAL
1	A	292	ILE
1	A	297	LEU

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Mol	Chain	Res	Type
1	A	300	LEU
1	A	334	ASP
1	A	360	ILE
1	A	366	LYS
1	B	5	VAL
1	B	8	LYS
1	B	23	LEU
1	B	43	SER
1	B	55	ARG
1	B	73	GLU
1	B	74	LEU
1	B	76	ARG
1	B	90	ILE
1	B	105	GLU
1	B	116	VAL
1	B	157	ASN
1	B	179	LEU
1	B	194	GLU
1	B	236	ARG
1	B	265	VAL
1	B	270	LEU
1	B	280	LEU
1	B	292	ILE
1	B	297	LEU
1	B	300	LEU
1	B	334	ASP
1	B	360	ILE
1	B	366	LYS
1	C	43	SER
1	C	55	ARG
1	C	74	LEU
1	C	76	ARG
1	C	90	ILE
1	C	98	ARG
1	C	105	GLU
1	C	116	VAL
1	C	132	VAL
1	C	137	LEU
1	C	157	ASN
1	C	166	GLU
1	C	176	LEU
1	C	179	LEU

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Mol	Chain	Res	Type
1	C	236	ARG
1	C	270	LEU
1	C	300	LEU
1	C	334	ASP
1	C	360	ILE
1	D	8	LYS
1	D	43	SER
1	D	55	ARG
1	D	73	GLU
1	D	74	LEU
1	D	76	ARG
1	D	90	ILE
1	D	105	GLU
1	D	116	VAL
1	D	137	LEU
1	D	157	ASN
1	D	179	LEU
1	D	194	GLU
1	D	236	ARG
1	D	265	VAL
1	D	270	LEU
1	D	280	LEU
1	D	297	LEU
1	D	300	LEU
1	D	334	ASP
1	D	360	ILE
1	D	366	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	97	GLN
1	A	157	ASN
1	A	220	GLN
1	A	246	ASN
1	B	6	ASN
1	B	97	GLN
1	B	157	ASN
1	B	164	GLN
1	B	197	ASN
1	B	220	GLN
1	B	246	ASN

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Mol	Chain	Res	Type
1	C	6	ASN
1	C	97	GLN
1	C	157	ASN
1	C	164	GLN
1	C	197	ASN
1	C	220	GLN
1	C	246	ASN
1	C	312	GLN
1	D	97	GLN
1	D	157	ASN
1	D	197	ASN
1	D	220	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](#)

Of 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 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	DMA	D	701	4	11,13,13	0.95	0	15,19,19	1.86	4 (26%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	DMA	B	701	4	11,13,13	0.61	0	15,19,19	1.83	4 (26%)
3	DMA	A	701	4	11,13,13	0.89	0	15,19,19	1.39	2 (13%)
2	FNR	C	669	-	31,33,33	2.23	6 (19%)	40,50,50	2.50	13 (32%)
3	DMA	C	701	4	11,13,13	0.68	0	15,19,19	1.64	4 (26%)
2	FNR	A	669	-	31,33,33	2.79	6 (19%)	40,50,50	3.13	9 (22%)
2	FNR	B	669	-	31,33,33	2.25	6 (19%)	40,50,50	2.72	10 (25%)
2	FNR	D	669	-	31,33,33	2.33	3 (9%)	40,50,50	2.76	9 (22%)

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	DMA	D	701	4	-	3/13/13/13	-
3	DMA	B	701	4	-	3/13/13/13	-
3	DMA	A	701	4	-	3/13/13/13	-
2	FNR	C	669	-	-	5/18/18/18	0/3/3/3
3	DMA	C	701	4	-	2/13/13/13	-
2	FNR	A	669	-	-	4/18/18/18	0/3/3/3
2	FNR	B	669	-	-	4/18/18/18	0/3/3/3
2	FNR	D	669	-	-	4/18/18/18	0/3/3/3

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	669	FNR	C4A-CAA	12.08	1.50	1.38
2	D	669	FNR	C4A-CAA	10.61	1.49	1.38
2	B	669	FNR	C4A-CAA	9.41	1.48	1.38
2	C	669	FNR	C4A-CAA	9.30	1.48	1.38
2	A	669	FNR	C9A-N10	6.70	1.47	1.38
2	B	669	FNR	C4-C4A	4.97	1.49	1.41
2	D	669	FNR	C4-C4A	4.50	1.49	1.41
2	A	669	FNR	C4-C4A	4.15	1.48	1.41
2	C	669	FNR	C4-C4A	4.08	1.48	1.41
2	B	669	FNR	C9A-N10	4.00	1.43	1.38
2	C	669	FNR	C9A-N10	3.55	1.43	1.38
2	A	669	FNR	CAA-N1	2.99	1.37	1.33
2	D	669	FNR	C9A-N10	2.97	1.42	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	669	FNR	C4A-N5	2.71	1.37	1.33
2	C	669	FNR	C4-N3	2.65	1.37	1.33
2	C	669	FNR	C6-C7	2.54	1.44	1.37
2	B	669	FNR	C1'-N10	-2.45	1.45	1.48
2	A	669	FNR	C2-N1	-2.19	1.33	1.38
2	B	669	FNR	C5'-C4'	2.13	1.54	1.51
2	B	669	FNR	C4-N3	2.03	1.36	1.33
2	A	669	FNR	C4-N3	2.03	1.36	1.33

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	669	FNR	C4-N3-C2	10.25	123.80	115.14
2	A	669	FNR	C1'-N10-C9A	9.08	125.44	118.29
2	D	669	FNR	C4-N3-C2	9.02	122.75	115.14
2	C	669	FNR	C4-C4A-CAA	-8.98	114.00	119.95
2	D	669	FNR	C4-C4A-CAA	-8.39	114.40	119.95
2	B	669	FNR	C4-N3-C2	8.34	122.19	115.14
2	B	669	FNR	C1'-N10-C9A	8.00	124.59	118.29
2	A	669	FNR	C4-C4A-CAA	-7.55	114.95	119.95
2	D	669	FNR	C1'-N10-C9A	7.37	124.10	118.29
2	A	669	FNR	C4A-N5-C5A	6.22	122.99	116.77
2	C	669	FNR	C4A-N5-C5A	5.51	122.27	116.77
2	B	669	FNR	C4-C4A-N5	5.26	124.61	118.60
2	B	669	FNR	C4A-N5-C5A	4.97	121.74	116.77
2	B	669	FNR	C4A-C4-N3	-4.95	116.66	123.43
2	D	669	FNR	C4A-N5-C5A	4.84	121.60	116.77
2	A	669	FNR	C4A-C4-N3	-4.72	116.98	123.43
2	B	669	FNR	CAA-C4A-N5	-4.67	118.03	121.26
2	C	669	FNR	C4-N3-C2	4.60	119.03	115.14
2	C	669	FNR	C1'-N10-C9A	4.34	121.71	118.29
2	C	669	FNR	C5A-C9A-N10	4.30	120.83	117.72
3	B	701	DMA	C5-C3-C4	4.14	123.75	114.60
2	B	669	FNR	C4-C4A-CAA	-3.91	117.36	119.95
2	D	669	FNR	CAA-C4A-N5	-3.77	118.65	121.26
2	A	669	FNR	C7-C6-C5A	-3.76	115.89	121.22
2	D	669	FNR	C5A-C9A-N10	3.73	120.42	117.72
3	D	701	DMA	O3B-PB-O2B	3.57	121.27	107.64
2	A	669	FNR	C4A-CAA-N10	-3.49	116.71	120.30
2	A	669	FNR	C5A-C9A-N10	3.41	120.19	117.72
2	B	669	FNR	P-O5'-C5'	3.39	127.62	118.30
2	D	669	FNR	C4A-C4-N3	-3.28	118.95	123.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	669	FNR	C9A-N10-CAA	-3.23	117.67	121.91
3	D	701	DMA	C5-C3-C4	3.21	121.68	114.60
2	D	669	FNR	C4-C4A-N5	3.20	122.26	118.60
2	A	669	FNR	C9A-N10-CAA	-3.17	117.75	121.91
3	C	701	DMA	C5-C3-C4	3.06	121.35	114.60
3	D	701	DMA	PA-O3A-PB	-3.05	122.36	132.83
2	C	669	FNR	C9A-N10-CAA	-3.00	117.99	121.91
2	C	669	FNR	C4A-CAA-N10	-2.98	117.24	120.30
3	C	701	DMA	PA-O3A-PB	-2.88	122.93	132.83
3	D	701	DMA	C4-C3-C2	-2.83	114.47	122.65
3	B	701	DMA	C1-C2-C3	-2.82	122.19	126.75
2	B	669	FNR	C9A-N10-CAA	-2.78	118.27	121.91
3	A	701	DMA	C5-C3-C4	2.72	120.61	114.60
2	C	669	FNR	CAA-C4A-N5	-2.70	119.39	121.26
3	B	701	DMA	C5-C3-C2	-2.63	115.06	122.65
3	C	701	DMA	C1-C2-C3	-2.62	122.51	126.75
2	C	669	FNR	O1P-P-O5'	-2.59	99.84	106.73
3	C	701	DMA	O3B-PB-O2B	2.55	117.36	107.64
2	C	669	FNR	C6-C5A-N5	2.52	121.83	119.05
2	C	669	FNR	O3P-P-O1P	2.50	117.18	107.64
2	C	669	FNR	C4-C4A-N5	2.49	121.45	118.60
3	B	701	DMA	PA-O3A-PB	-2.49	124.28	132.83
2	B	669	FNR	C7-C6-C5A	-2.44	117.77	121.22
2	C	669	FNR	C1'-N10-CAA	2.07	120.26	118.41
3	A	701	DMA	C5-C3-C2	-2.06	116.69	122.65

There are no chirality outliers.

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	701	DMA	C1-O1-PA-O2A
3	D	701	DMA	C1-O1-PA-O3A
3	B	701	DMA	C1-O1-PA-O1A
3	B	701	DMA	C1-O1-PA-O2A
3	B	701	DMA	C1-O1-PA-O3A
3	A	701	DMA	C1-O1-PA-O1A
3	A	701	DMA	C1-O1-PA-O2A
3	A	701	DMA	C1-O1-PA-O3A
3	C	701	DMA	C1-O1-PA-O3A
2	D	669	FNR	O3'-C3'-C4'-O4'
2	C	669	FNR	C2'-C3'-C4'-O4'
2	A	669	FNR	C2'-C3'-C4'-O4'

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Mol	Chain	Res	Type	Atoms
2	D	669	FNR	C2'-C3'-C4'-O4'
2	C	669	FNR	O3'-C3'-C4'-C5'
2	C	669	FNR	C4'-C5'-O5'-P
2	A	669	FNR	C4'-C5'-O5'-P
2	B	669	FNR	C4'-C5'-O5'-P
2	D	669	FNR	C4'-C5'-O5'-P
2	C	669	FNR	O3'-C3'-C4'-O4'
3	D	701	DMA	C1-O1-PA-O1A
3	C	701	DMA	C1-O1-PA-O1A
2	D	669	FNR	O3'-C3'-C4'-C5'
2	B	669	FNR	C2'-C3'-C4'-O4'
2	C	669	FNR	C2'-C3'-C4'-C5'
2	B	669	FNR	C2'-C3'-C4'-C5'
2	A	669	FNR	C2'-C3'-C4'-C5'
2	B	669	FNR	O3'-C3'-C4'-C5'
2	A	669	FNR	O3'-C3'-C4'-C5'

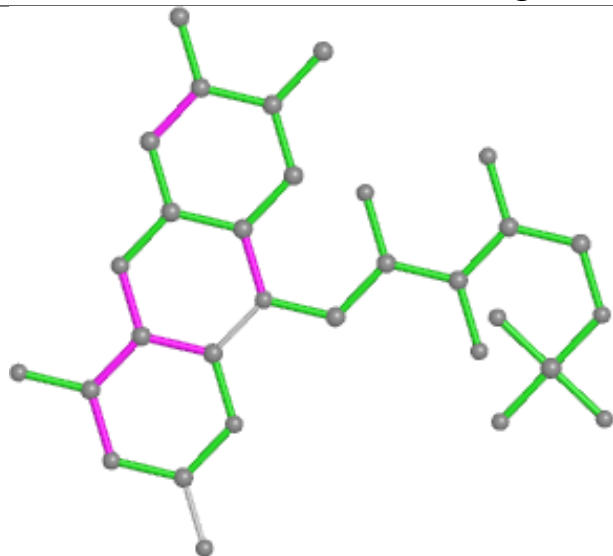
There are no ring outliers.

5 monomers are involved in 6 short contacts:

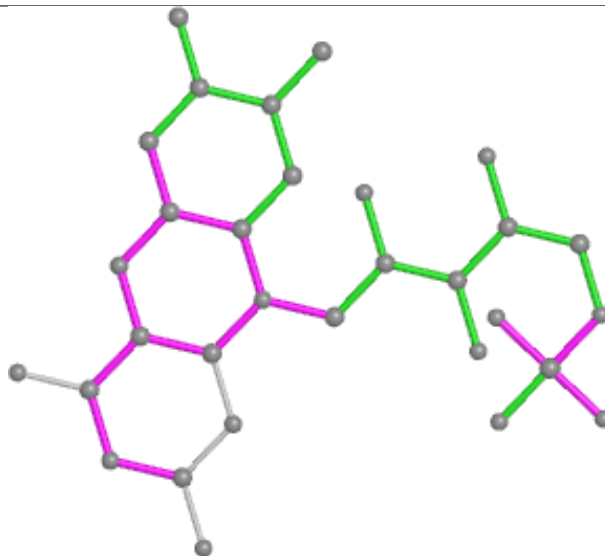
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	701	DMA	1	0
3	A	701	DMA	2	0
2	C	669	FNR	1	0
3	C	701	DMA	1	0
2	A	669	FNR	1	0

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.

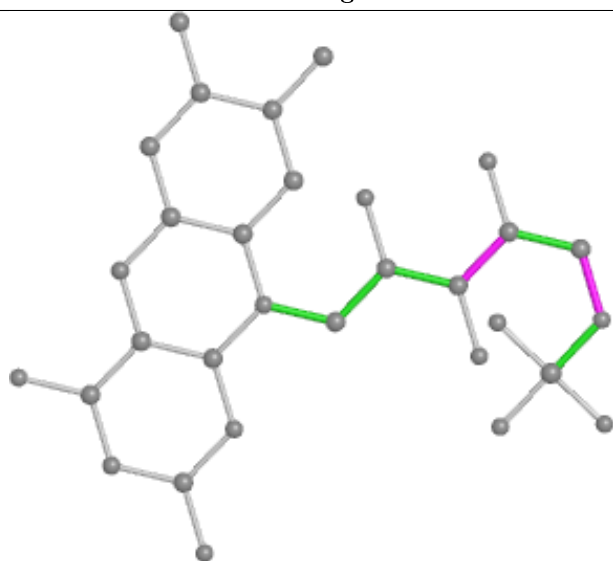
Ligand FNR C 669



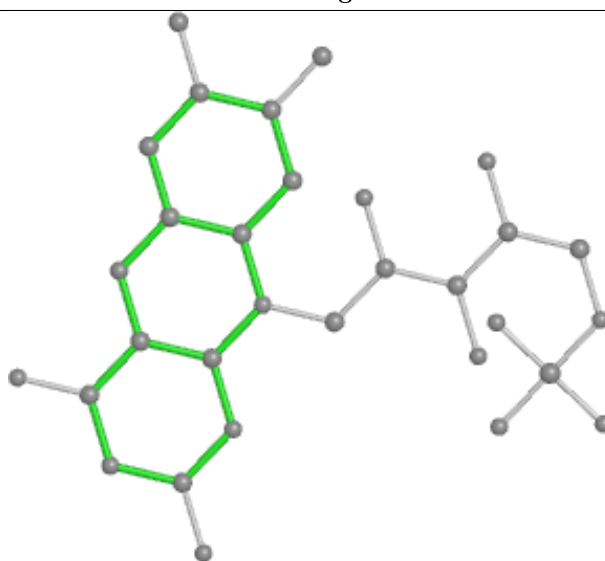
Bond lengths



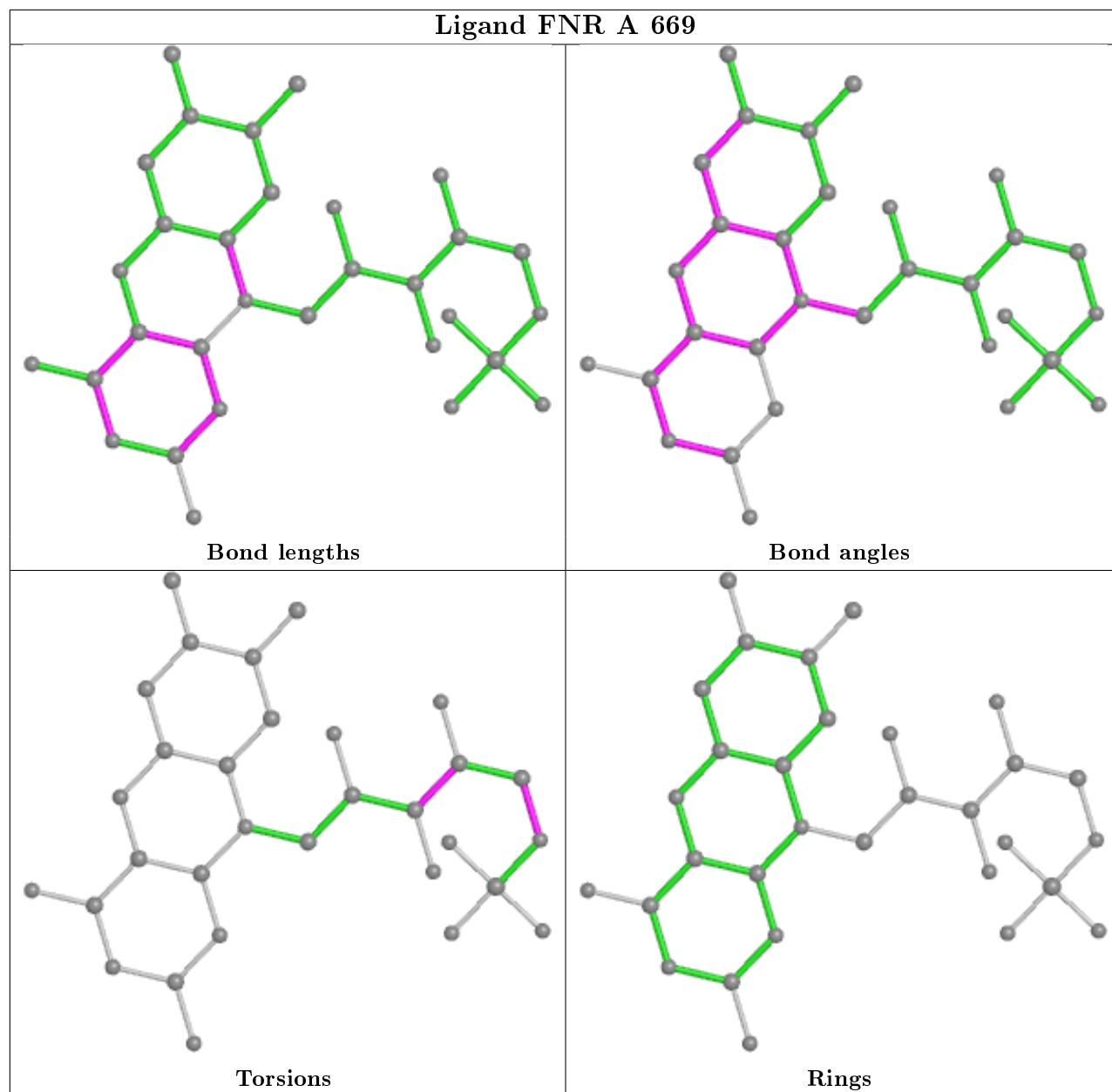
Bond angles

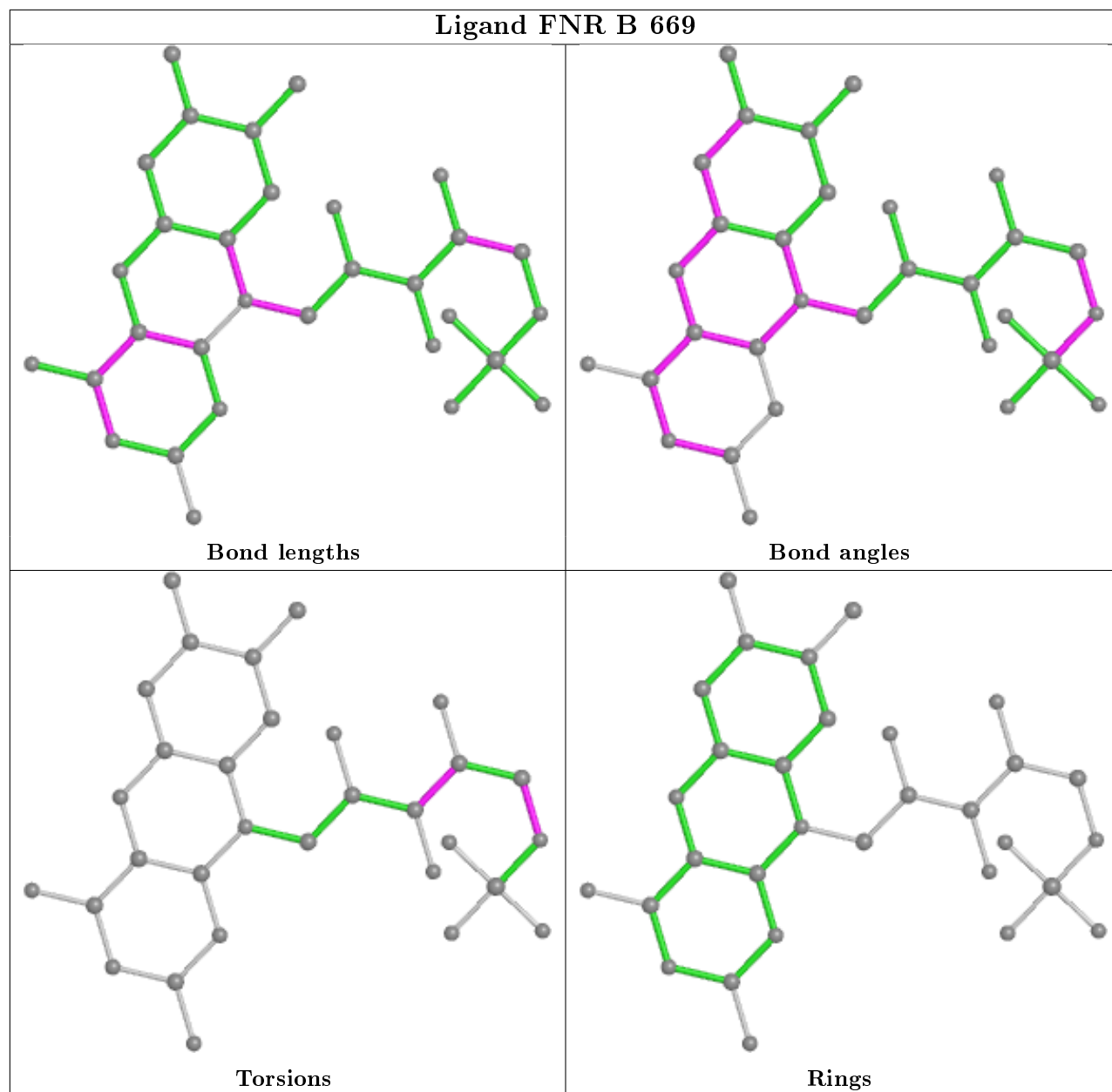


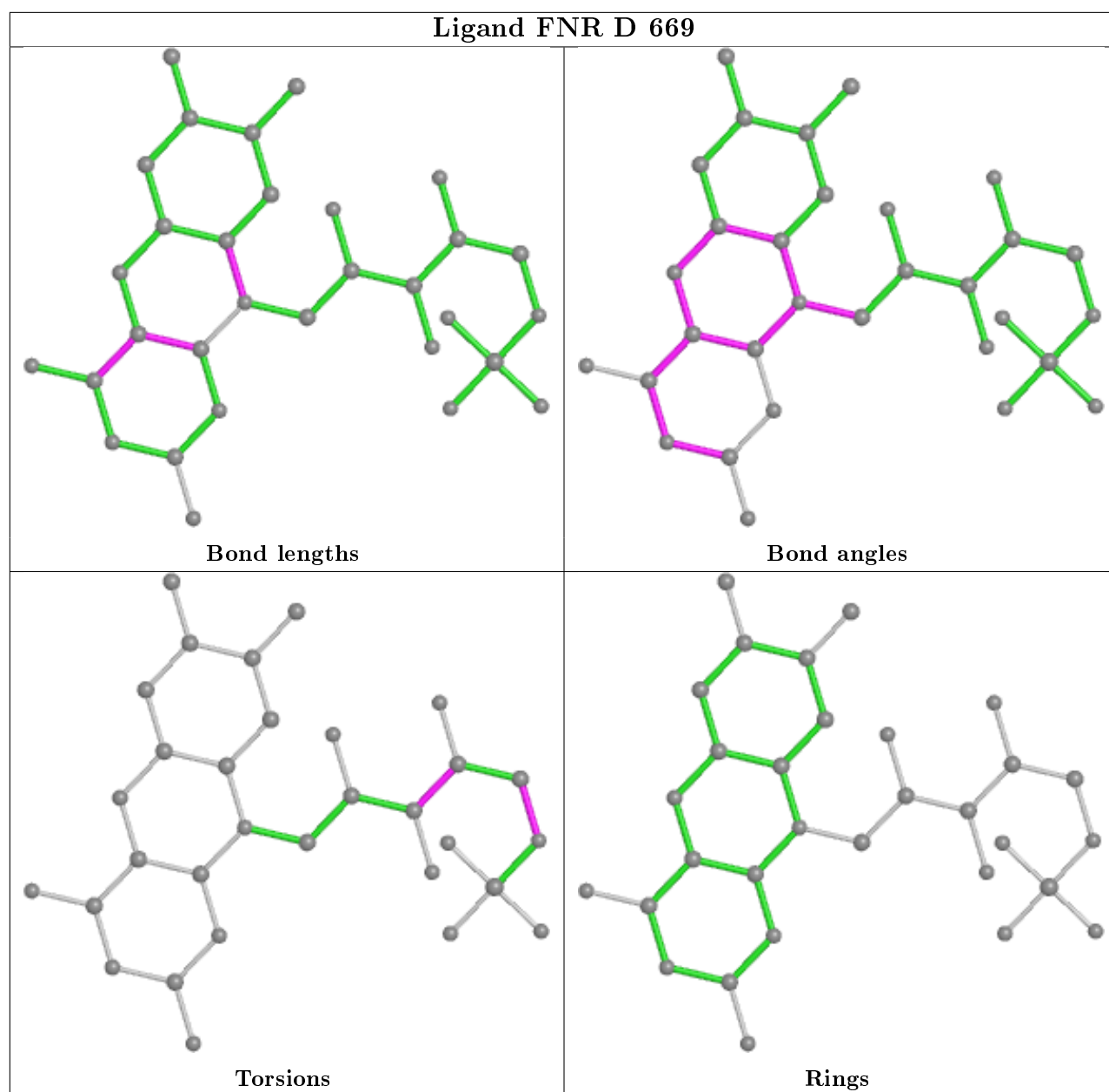
Torsions



Rings







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	364/368 (98%)	-0.22	6 (1%) 72 77	33, 43, 64, 76	0
1	B	364/368 (98%)	-0.23	7 (1%) 66 73	33, 43, 64, 78	0
1	C	364/368 (98%)	-0.22	5 (1%) 75 80	33, 43, 63, 74	0
1	D	364/368 (98%)	-0.28	4 (1%) 80 85	32, 43, 64, 74	0
All	All	1456/1472 (98%)	-0.24	22 (1%) 73 79	32, 43, 64, 78	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	364	VAL	4.2
1	C	174	TYR	3.9
1	A	360	ILE	3.5
1	D	72	ASN	3.0
1	D	360	ILE	2.9
1	B	174	TYR	2.9
1	B	3	ASP	2.7
1	B	363	LYS	2.6
1	C	364	VAL	2.6
1	A	363	LYS	2.6
1	A	72	ASN	2.6
1	B	6	ASN	2.6
1	D	3	ASP	2.2
1	B	359	SER	2.2
1	A	166	GLU	2.2
1	A	71	ARG	2.2
1	C	363	LYS	2.1
1	C	65	THR	2.1
1	A	364	VAL	2.1
1	D	364	VAL	2.1
1	C	239	TRP	2.1
1	B	360	ILE	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 carbohydrates in this entry.

6.4 Ligands [i](#)

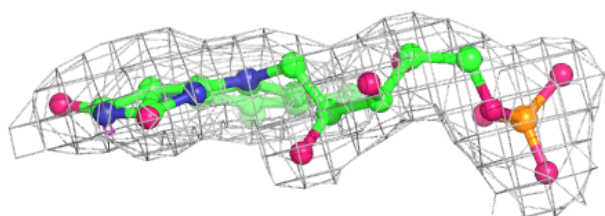
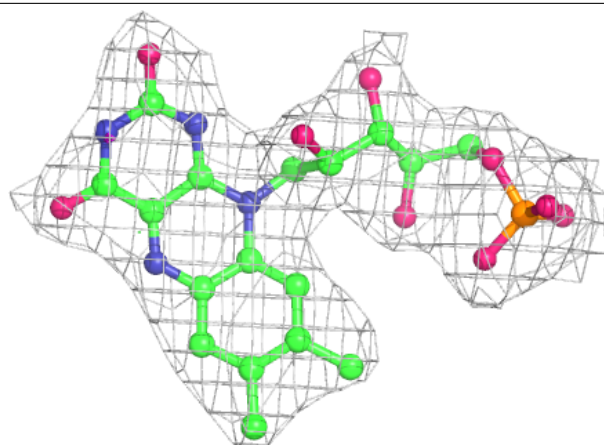
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	MG	C	1001	1/1	0.81	0.18	66,66,66,66	0
4	MG	D	1001	1/1	0.91	0.25	62,62,62,62	0
4	MG	A	1001	1/1	0.92	0.14	73,73,73,73	0
4	MG	B	1001	1/1	0.94	0.15	71,71,71,71	0
2	FNR	A	669	31/31	0.97	0.14	30,40,47,48	0
2	FNR	D	669	31/31	0.97	0.12	37,42,45,47	0
3	DMA	C	701	14/14	0.98	0.08	49,53,57,59	0
3	DMA	D	701	14/14	0.98	0.09	45,52,55,56	0
2	FNR	B	669	31/31	0.98	0.12	33,41,45,46	0
3	DMA	B	701	14/14	0.98	0.08	53,57,61,62	0
3	DMA	A	701	14/14	0.98	0.09	53,56,60,60	0
2	FNR	C	669	31/31	0.98	0.12	36,39,42,43	0

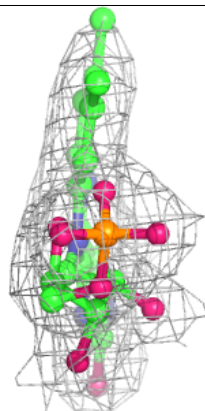
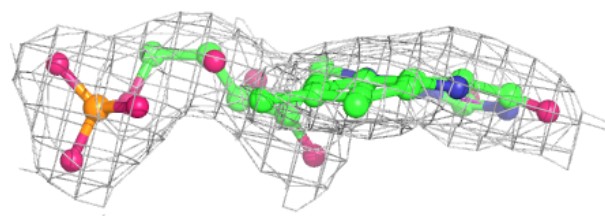
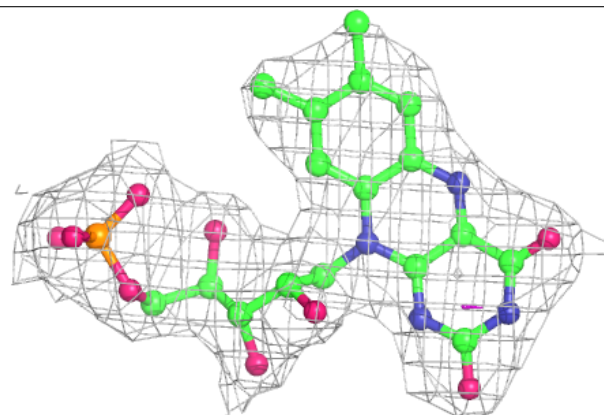
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around FNR A 669:

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

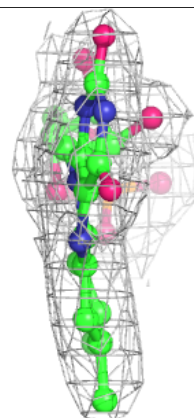
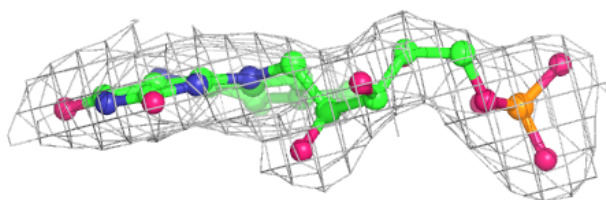
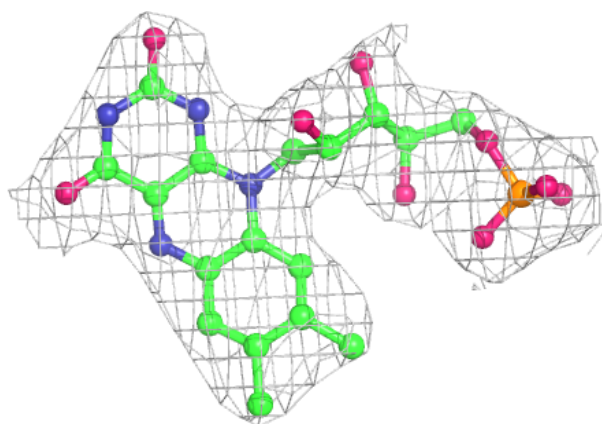
**Electron density around FNR D 669:**

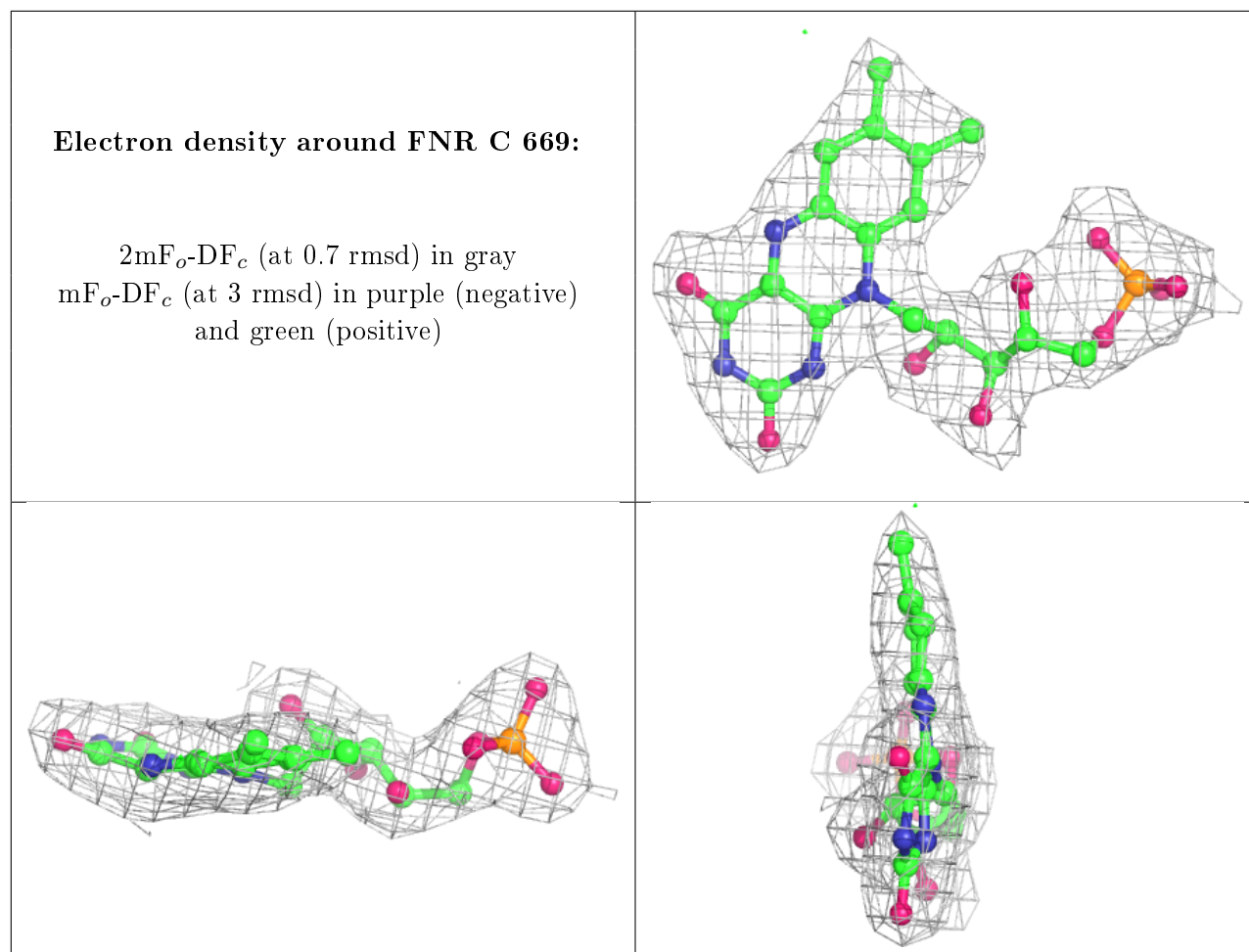
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around FNR B 669:

$2mF_o-DF_c$ (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.