



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:14 PM UTC

PDB ID : 3B06 / pdb_00003b06
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 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)
Xtriage (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

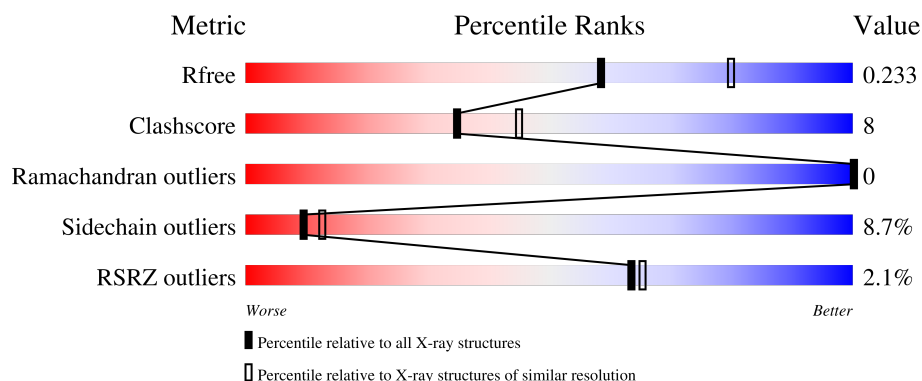
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

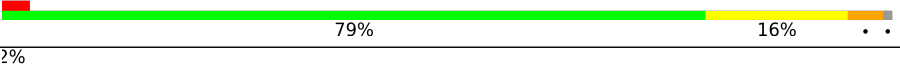
The reported resolution of this entry is 2.29 Å.

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}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (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 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	368	 81% 14% . .
1	B	368	 79% 16% . .
1	C	368	 77% 17% 5% .
1	D	368	 80% 15% . .

2 Entry composition [i](#)

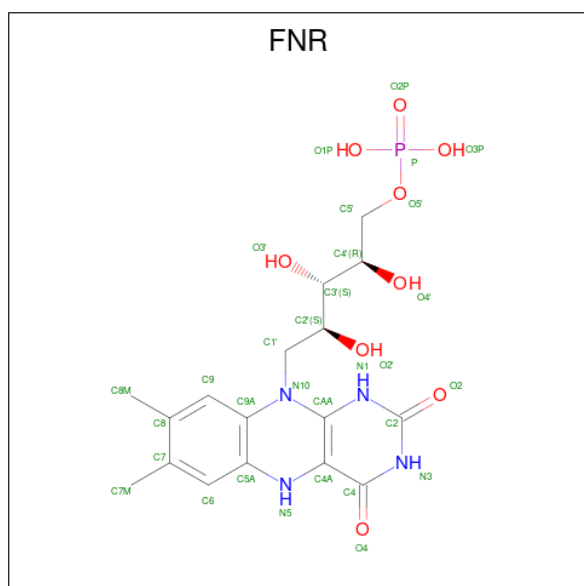
There are 5 unique types of molecules in this entry. The entry contains 11710 atoms, of which 0 are hydrogens and 0 are deuteriums.

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]PT ERIDIN-1-ID-10(5H)-YL)-5-O-PHOSPHONATO-D-RIBITOL (CCD ID: FNR) (formula: $C_{17}H_{23}N_4O_9P$).



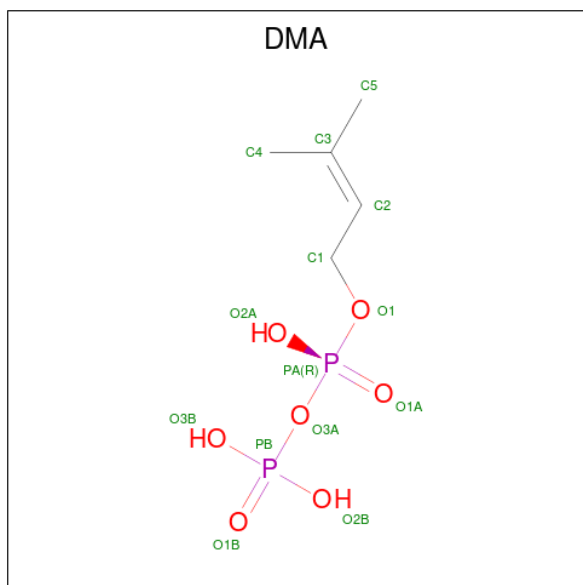
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

Continued on next page...

Continued from previous page...

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 (CCD ID: 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 (CCD ID: MG) (formula: Mg).

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

Continued on next page...

Continued from previous page...

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

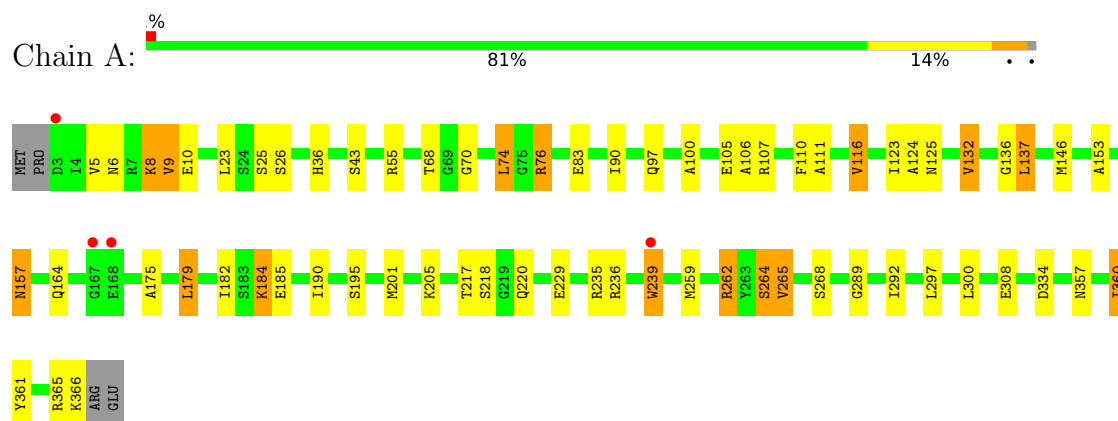
- Molecule 5 is water.

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

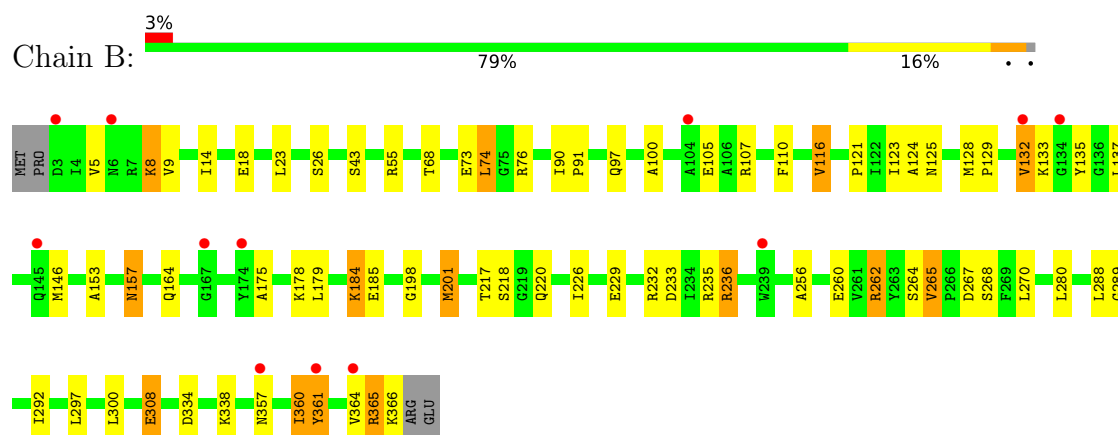
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, 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.

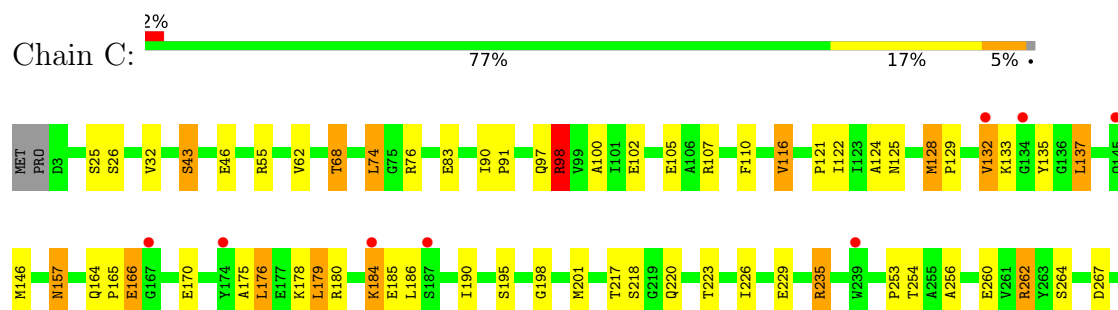
- Molecule 1: Isopentenyl-diphosphate delta-isomerase



- Molecule 1: Isopentenyl-diphosphate delta-isomerase

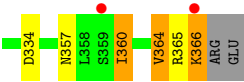
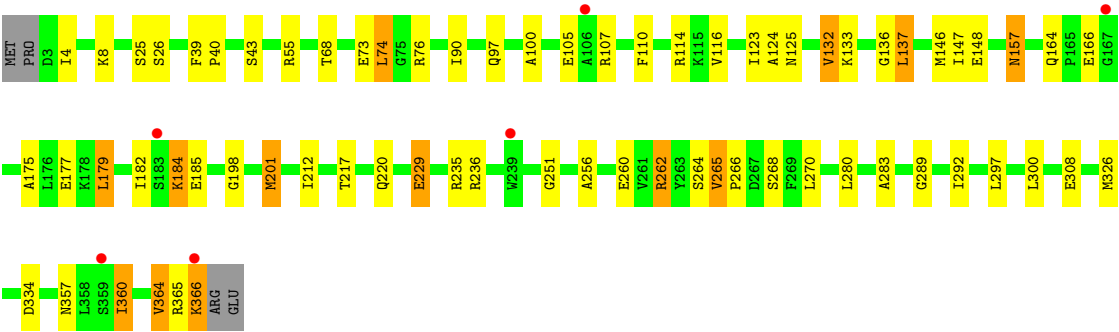
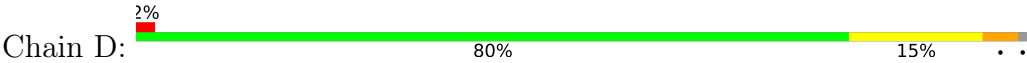


- Molecule 1: Isopentenyl-diphosphate delta-isomerase





● 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 (4.73%)	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)	0.31 , 23.0	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, FNR, MG

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	1.28	4/2855 (0.1%)	1.23	7/3846 (0.2%)
1	B	1.29	3/2855 (0.1%)	1.23	11/3846 (0.3%)
1	C	1.27	4/2855 (0.1%)	1.31	21/3846 (0.5%)
1	D	1.27	3/2855 (0.1%)	1.19	7/3846 (0.2%)
All	All	1.28	14/11420 (0.1%)	1.24	46/15384 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	1	0

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	9	VAL	CA-CB	7.01	1.63	1.54
1	D	364	VAL	CA-CB	6.23	1.61	1.54
1	B	364	VAL	CA-C	5.93	1.60	1.52
1	A	239	TRP	CA-C	5.58	1.60	1.52
1	C	128	MET	C-O	-5.49	1.19	1.24
1	D	229	GLU	C-O	-5.41	1.17	1.24
1	B	233	ASP	CA-C	5.32	1.59	1.52
1	B	153	ALA	CA-CB	5.31	1.61	1.53
1	A	153	ALA	CA-CB	5.31	1.61	1.53
1	A	111	ALA	CA-CB	5.26	1.61	1.53
1	C	336	LEU	N-CA	5.24	1.52	1.46
1	C	122	ILE	C-O	-5.23	1.18	1.24
1	D	283	ALA	C-O	5.13	1.30	1.24
1	C	317	ILE	CA-CB	5.09	1.60	1.54

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	165	PRO	CA-C-N	15.16	148.99	121.70
1	C	165	PRO	C-N-CA	15.16	148.99	121.70
1	A	76	ARG	NE-CZ-NH2	11.06	129.16	119.20
1	C	98	ARG	NE-CZ-NH2	10.03	128.23	119.20
1	A	76	ARG	NE-CZ-NH1	-9.77	111.73	121.50
1	C	165	PRO	O-C-N	-8.56	111.09	122.64
1	A	76	ARG	CD-NE-CZ	8.54	136.36	124.40
1	C	98	ARG	NE-CZ-NH1	-8.27	113.23	121.50
1	B	133	LYS	CA-C-N	-7.67	114.32	123.44
1	B	133	LYS	C-N-CA	-7.67	114.32	123.44
1	C	180	ARG	NE-CZ-NH2	7.50	125.95	119.20
1	D	262	ARG	NE-CZ-NH1	-7.00	114.50	121.50
1	C	262	ARG	NE-CZ-NH1	-6.91	114.59	121.50
1	C	180	ARG	NE-CZ-NH1	-6.26	115.24	121.50
1	C	262	ARG	NE-CZ-NH2	6.20	124.78	119.20
1	B	262	ARG	NE-CZ-NH1	-6.05	115.45	121.50
1	A	365	ARG	N-CA-C	-5.89	105.35	112.54
1	B	116	VAL	CB-CA-C	5.86	117.26	110.88
1	B	201	MET	N-CA-C	5.75	117.55	111.28
1	D	364	VAL	N-CA-C	5.74	115.93	110.42
1	D	4	ILE	N-CA-C	-5.65	104.85	110.62
1	B	226	ILE	N-CA-C	-5.60	105.06	110.72
1	C	306	GLY	N-CA-C	5.55	117.73	111.85
1	D	133	LYS	CA-C-N	-5.54	116.85	123.44
1	D	133	LYS	C-N-CA	-5.54	116.85	123.44
1	A	262	ARG	NE-CZ-NH1	-5.46	116.03	121.50
1	C	328	THR	N-CA-C	-5.42	106.04	113.30
1	A	264	SER	N-CA-C	-5.41	106.52	113.23
1	C	133	LYS	CA-C-N	-5.40	115.80	123.08
1	C	133	LYS	C-N-CA	-5.40	115.80	123.08
1	C	226	ILE	N-CA-C	-5.39	105.27	110.72
1	B	364	VAL	N-CA-C	5.35	116.08	110.62
1	B	116	VAL	N-CA-CB	-5.32	105.00	112.35
1	C	297	LEU	CA-C-N	-5.32	114.18	119.56
1	C	297	LEU	C-N-CA	-5.32	114.18	119.56
1	B	116	VAL	N-CA-C	-5.31	107.21	113.42
1	D	201	MET	N-CA-C	5.27	117.02	111.28
1	B	365	ARG	N-CA-C	-5.22	105.76	111.82
1	A	76	ARG	CG-CD-NE	-5.19	100.59	112.00
1	B	361	TYR	N-CA-C	5.13	117.28	111.02
1	C	98	ARG	CD-NE-CZ	5.12	131.57	124.40
1	C	235	ARG	CA-C-N	-5.12	114.50	122.73

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	235	ARG	C-N-CA	-5.12	114.50	122.73
1	D	262	ARG	NE-CZ-NH2	5.11	123.80	119.20
1	C	68	THR	N-CA-C	5.05	115.98	108.86
1	C	166	GLU	CB-CA-C	5.03	119.65	110.10

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	40	0
1	B	2808	0	2890	41	0
1	C	2808	0	2890	49	0
1	D	2808	0	2890	44	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	11684	174	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 8.

All (174) 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:HA	1:C:184:LYS:HE2	1.33	1.10
1:A:184:LYS:HA	1:A:184:LYS:HE2	1.33	1.09
1:B:184:LYS:HA	1:B:184:LYS:HE2	1.37	1.04
1:D:110:PHE:HB2	1:D:146:MET:HE2	1.41	1.02
1:C:132:VAL:HG12	1:C:175:ALA:HB2	1.43	1.00
1:D:184:LYS:HE2	1:D:184:LYS:HA	1.39	0.99
1:A:110:PHE:HB2	1:A:146:MET:HE2	1.47	0.96
1:A:265:VAL:HG22	1:A:268:SER:HB3	1.49	0.93
1:B:110:PHE:HB2	1:B:146:MET:HE2	1.52	0.91
1:C:110:PHE:HB2	1:C:146:MET:HE2	1.51	0.90
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:A:184:LYS:HE2	1:A:184:LYS:CA	2.11	0.81
1:D:107:ARG:HA	1:D:146:MET:HE3	1.67	0.77
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:C:107:ARG:HA	1:C:146:MET:HE3	1.70	0.73
1:A:137:LEU:HD11	1:A:185:GLU:HG2	1.71	0.72
1:D:184:LYS:HE2	1:D:184:LYS:CA	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:A:201:MET:HE3	1:A:264:SER:HB3	1.76	0.68
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:110:PHE:CB	1:D:146:MET:HE2	2.24	0.65
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:A:107:ARG:HA	1:A:146:MET:HE3	1.80	0.62
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

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:97:GLN:HE21	1:D:125:ASN:H	1.47	0.62
1:C:107:ARG:HA	1:C:146:MET:CE	2.30	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:B:107:ARG:HA	1:B:146:MET:HE3	1.83	0.59
1:C:201:MET:HE3	1:C:264:SER:HB3	1.84	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:B:107:ARG:HA	1:B:146:MET:CE	2.34	0.58
1:B:201:MET:HE3	1:B:264:SER:HB3	1.85	0.58
1:A:107:ARG:HA	1:A:146:MET:CE	2.34	0.57
1:C:25:SER:HB2	1:C:220:GLN:NE2	2.19	0.57
1:D:107:ARG:HA	1:D:146:MET:CE	2.33	0.57
1:B:157:ASN:HD22	1:B:157:ASN:H	1.52	0.56
1:C:100:ALA:CB	1:C:146:MET:HE1	2.35	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:C:365:ARG:O	1:C:366:LYS:HB2	2.05	0.55
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:H6	2:A:669:FNR:H9	1.89	0.55
1:B:157:ASN:HD22	1:B:157:ASN:N	2.06	0.54
1:D:136:GLY:HA2	1:D:182:ILE:HD11	1.90	0.54
1:D:100:ALA:CB	1:D:146:MET:HE1	2.38	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:D:107:ARG:CA	1:D:146:MET:HE3	2.38	0.52
1:B:68:THR:OG1	1:B:74:LEU:HG	2.10	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:HE2	1:C:184:LYS:CA	2.19	0.51
1:A:164:GLN:HG3	1:A:229:GLU:CD	2.36	0.50
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:C:107:ARG:CA	1:C:146:MET:HE3	2.41	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:B:100:ALA:CB	1:B:146:MET:HE1	2.42	0.49
1:A:97:GLN:NE2	1:A:124:ALA:HB1	2.28	0.49
1:B:164:GLN:HG3	1:B:229:GLU:CD	2.38	0.49
1:C:157:ASN:H	1:C:157:ASN:HD22	1.61	0.49
1:A:157:ASN:HD22	1:A:157:ASN:N	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
1:D:201:MET:HE3	1:D:264:SER:HB3	1.94	0.48
1:D:266:PRO:HB3	1:D:364:VAL:HG13	1.96	0.48
1:A:100:ALA:CB	1:A:146:MET:HE1	2.44	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:C:357:ASN:CG	1:C:360:ILE:HG23	2.39	0.48
1:A:107:ARG:CA	1:A:146:MET:HE3	2.44	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:B:217:THR:O	1:B:218:SER:C	2.57	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:308:GLU:H	1:C:308:GLU:CD	2.24	0.46
1:C:135:TYR:O	1:C:178:LYS:CE	2.63	0.45
1:A:110:PHE:CB	1:A:146:MET:HE2	2.31	0.45
1:D:157:ASN:HD22	1:D:157:ASN:H	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:C:110:PHE:CB	1:C:146:MET:HE2	2.35	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:B:308:GLU:H	1:B:308:GLU:CD	2.26	0.44
1:D:366:LYS:HA	1:D:366:LYS:HD3	1.85	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:C:164:GLN:HG3	1:C:229:GLU:CD	2.43	0.43
1:A:136:GLY:HA2	1:A:182:ILE:HD11	2.00	0.43
1:A:70:GLY:HA2	1:A:106:ALA:HB1	2.00	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:OD1	1:B:267:ASP:N	2.43	0.43
1:D:166:GLU:HG2	1:D:166:GLU:O	2.19	0.43
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:C:217:THR:O	1:C:218:SER:C	2.63	0.42
1:C:253:PRO:O	1:C:254:THR:C	2.62	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:A:217:THR:O	1:A:218:SER:C	2.62	0.41
1:D:123:ILE:HD12	1:D:123:ILE:N	2.36	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:107:ARG:CA	1:B:146:MET:HE3	2.49	0.41
1:B:288:LEU:O	1:B:361:TYR:OH	2.21	0.41
1:D:114:ARG:HA	1:D:114:ARG:HD3	1.95	0.41
1:A:259:MET:HA	1:A:361:TYR:OH	2.21	0.41
1:D:40:PRO:HG2	1:D:326:MET:HE3	2.03	0.41
1:D:164:GLN:HG3	1:D:229:GLU:CD	2.46	0.41
1:A:36:HIS:HB2	1:D:251:GLY:HA2	2.02	0.40
1:D:184:LYS:CA	1:D:184:LYS:CE	2.96	0.40
1:A:10:GLU:CD	1:A:236:ARG:HH22	2.29	0.40
1:D:110:PHE:CD1	1:D:146:MET:HE2	2.57	0.40
1:A:239:TRP:H	1:A:239:TRP:CD1	2.40	0.40
1:B:198:GLY:HA2	1:B:217:THR:O	2.22	0.40
1:D:147:ILE:O	1:D:148:GLU:C	2.65	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 [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	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
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%)	272 (91%)	26 (9%)	9	12
1	B	298/302 (99%)	271 (91%)	27 (9%)	9	11
1	C	298/302 (99%)	273 (92%)	25 (8%)	10	14
1	D	298/302 (99%)	272 (91%)	26 (9%)	9	12
All	All	1192/1208 (99%)	1088 (91%)	104 (9%)	9	12

All (104) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	VAL
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	132	VAL
1	A	137	LEU
1	A	157	ASN
1	A	179	LEU
1	A	184	LYS
1	A	235	ARG
1	A	265	VAL
1	A	292	ILE
1	A	297	LEU
1	A	300	LEU
1	A	308	GLU
1	A	334	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	360	ILE
1	A	366	LYS
1	B	5	VAL
1	B	8	LYS
1	B	9	VAL
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	132	VAL
1	B	157	ASN
1	B	179	LEU
1	B	184	LYS
1	B	235	ARG
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	308	GLU
1	B	334	ASP
1	B	360	ILE
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	170	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	176	LEU
1	C	179	LEU
1	C	184	LYS
1	C	186	LEU
1	C	235	ARG
1	C	270	LEU
1	C	292	ILE
1	C	300	LEU
1	C	308	GLU
1	C	334	ASP
1	C	360	ILE
1	C	366	LYS
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	132	VAL
1	D	137	LEU
1	D	157	ASN
1	D	179	LEU
1	D	184	LYS
1	D	235	ARG
1	D	236	ARG
1	D	265	VAL
1	D	270	LEU
1	D	280	LEU
1	D	292	ILE
1	D	297	LEU
1	D	300	LEU
1	D	308	GLU
1	D	334	ASP
1	D	360	ILE
1	D	366	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	97	GLN
1	A	157	ASN
1	A	164	GLN
1	A	220	GLN
1	A	246	ASN
1	B	6	ASN
1	B	11	HIS
1	B	97	GLN
1	B	157	ASN
1	B	164	GLN
1	B	197	ASN
1	B	220	GLN
1	B	246	ASN
1	C	6	ASN
1	C	97	GLN
1	C	157	ASN
1	C	164	GLN
1	C	220	GLN
1	C	246	ASN
1	D	97	GLN
1	D	157	ASN
1	D	164	GLN
1	D	197	ASN
1	D	220	GLN
1	D	246	ASN

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](#)

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$
2	FNR	C	669	-	32,33,33	1.34	6 (18%)	41,50,50	1.80	8 (19%)
2	FNR	D	669	-	32,33,33	1.08	2 (6%)	41,50,50	1.36	8 (19%)
2	FNR	A	669	-	32,33,33	1.42	7 (21%)	41,50,50	1.51	4 (9%)
3	DMA	B	701	4	12,13,13	1.56	1 (8%)	15,19,19	1.65	3 (20%)
3	DMA	D	701	4	12,13,13	0.98	0	15,19,19	1.63	3 (20%)
3	DMA	C	701	4	12,13,13	1.48	1 (8%)	15,19,19	1.45	3 (20%)
2	FNR	B	669	-	32,33,33	1.09	2 (6%)	41,50,50	1.55	6 (14%)
3	DMA	A	701	4	12,13,13	1.10	1 (8%)	15,19,19	1.27	1 (6%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FNR	C	669	-	-	5/18/18/18	0/3/3/3
2	FNR	D	669	-	-	4/18/18/18	0/3/3/3
2	FNR	A	669	-	-	5/18/18/18	0/3/3/3
3	DMA	B	701	4	-	3/13/13/13	-
3	DMA	D	701	4	-	3/13/13/13	-
3	DMA	C	701	4	-	2/13/13/13	-
2	FNR	B	669	-	-	5/18/18/18	0/3/3/3
3	DMA	A	701	4	-	3/13/13/13	-

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	701	DMA	PA-O3A	4.97	1.64	1.59
3	C	701	DMA	PA-O3A	4.62	1.64	1.59
2	A	669	FNR	C9A-N10	3.70	1.47	1.41
2	C	669	FNR	C6-C7	3.35	1.44	1.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	669	FNR	C4A-C4	2.70	1.49	1.41
2	A	669	FNR	C6-C5A	2.56	1.43	1.39
2	C	669	FNR	CAA-N10	2.50	1.42	1.38
2	A	669	FNR	C5A-N5	-2.44	1.35	1.39
2	D	669	FNR	C4A-C4	2.42	1.49	1.41
3	A	701	DMA	PA-O3A	2.29	1.62	1.59
2	A	669	FNR	CAA-N10	2.29	1.42	1.38
2	A	669	FNR	C5A-C9A	2.27	1.43	1.40
2	A	669	FNR	C4A-C4	2.22	1.48	1.41
2	D	669	FNR	C6-C5A	2.22	1.43	1.39
2	A	669	FNR	C2-N1	-2.22	1.33	1.37
2	B	669	FNR	C5'-C4'	2.21	1.54	1.51
2	C	669	FNR	C6-C5A	2.20	1.43	1.39
2	C	669	FNR	C4A-C4	2.18	1.48	1.41
2	C	669	FNR	CAA-N1	-2.08	1.33	1.37
2	C	669	FNR	O2-C2	2.08	1.27	1.23

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	669	FNR	C4-N3-C2	-5.33	119.03	126.37
2	C	669	FNR	O4-C4-C4A	-4.78	115.73	127.26
2	B	669	FNR	N3-C2-N1	4.56	122.90	115.74
2	B	669	FNR	O2-C2-N1	-4.08	114.61	121.86
2	A	669	FNR	O4-C4-C4A	-4.05	117.50	127.26
3	B	701	DMA	C5-C3-C4	3.98	123.75	114.59
3	D	701	DMA	O3B-PB-O2B	3.59	121.27	107.80
2	D	669	FNR	N3-C2-N1	3.55	121.32	115.74
2	C	669	FNR	C4A-C4-N3	3.30	121.20	112.13
2	A	669	FNR	N3-C2-N1	3.29	120.91	115.74
2	B	669	FNR	C4-C4A-N5	3.22	124.61	116.37
2	C	669	FNR	N3-C2-N1	3.12	120.64	115.74
3	D	701	DMA	C5-C3-C4	3.08	121.68	114.59
2	B	669	FNR	C4-N3-C2	-3.04	122.19	126.37
3	C	701	DMA	C5-C3-C4	2.94	121.35	114.59
3	B	701	DMA	C1-C2-C3	-2.83	122.19	126.76
2	B	669	FNR	O4-C4-C4A	-2.73	120.67	127.26
3	D	701	DMA	C4-C3-C2	-2.73	114.47	122.66
2	D	669	FNR	O4-C4-C4A	-2.72	120.71	127.26
3	C	701	DMA	C1-C2-C3	-2.63	122.51	126.76
2	D	669	FNR	C4-N3-C2	-2.62	122.75	126.37
2	C	669	FNR	O1P-P-O5'	-2.62	99.84	106.67

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	701	DMA	C5-C3-C4	2.62	120.61	114.59
3	C	701	DMA	O3B-PB-O2B	2.55	117.36	107.80
3	B	701	DMA	C5-C3-C2	-2.53	115.06	122.66
2	C	669	FNR	O3P-P-O1P	2.50	117.18	107.80
2	D	669	FNR	O2-C2-N3	-2.50	117.42	121.86
2	C	669	FNR	C5A-C9A-N10	2.50	120.83	118.01
2	D	669	FNR	C4A-C4-N3	2.48	118.95	112.13
2	A	669	FNR	C1'-N10-C9A	2.47	125.44	120.63
2	D	669	FNR	C4-C4A-N5	2.30	122.26	116.37
2	C	669	FNR	C6-C5A-C9A	-2.30	117.28	119.80
2	A	669	FNR	C9-C9A-C5A	-2.22	116.85	119.95
2	D	669	FNR	C5A-C9A-N10	2.13	120.42	118.01
2	D	669	FNR	C9-C9A-N10	-2.08	119.05	121.85
2	B	669	FNR	C1'-N10-C9A	2.04	124.59	120.63

There are no chirality outliers.

All (30) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	701	DMA	C1-O1-PA-O1A
3	A	701	DMA	C1-O1-PA-O2A
3	B	701	DMA	C1-O1-PA-O1A
3	B	701	DMA	C1-O1-PA-O2A
3	C	701	DMA	C1-O1-PA-O3A
3	D	701	DMA	C1-O1-PA-O2A
2	A	669	FNR	C2'-C3'-C4'-O4'
2	C	669	FNR	C2'-C3'-C4'-O4'
2	D	669	FNR	C2'-C3'-C4'-O4'
2	D	669	FNR	O3'-C3'-C4'-O4'
2	C	669	FNR	O3'-C3'-C4'-C5'
2	C	669	FNR	O3'-C3'-C4'-O4'
2	D	669	FNR	O3'-C3'-C4'-C5'
2	B	669	FNR	C2'-C3'-C4'-O4'
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	C2'-C3'-C4'-C5'
3	A	701	DMA	C1-O1-PA-O3A
3	B	701	DMA	C1-O1-PA-O3A
3	C	701	DMA	C1-O1-PA-O1A
3	D	701	DMA	C1-O1-PA-O1A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
3	D	701	DMA	C1-O1-PA-O3A
2	B	669	FNR	C2'-C3'-C4'-C5'
2	B	669	FNR	O3'-C3'-C4'-C5'
2	A	669	FNR	C2'-C3'-C4'-C5'
2	A	669	FNR	O3'-C3'-C4'-C5'
2	A	669	FNR	O3'-C3'-C4'-O4'
2	B	669	FNR	O3'-C3'-C4'-O4'

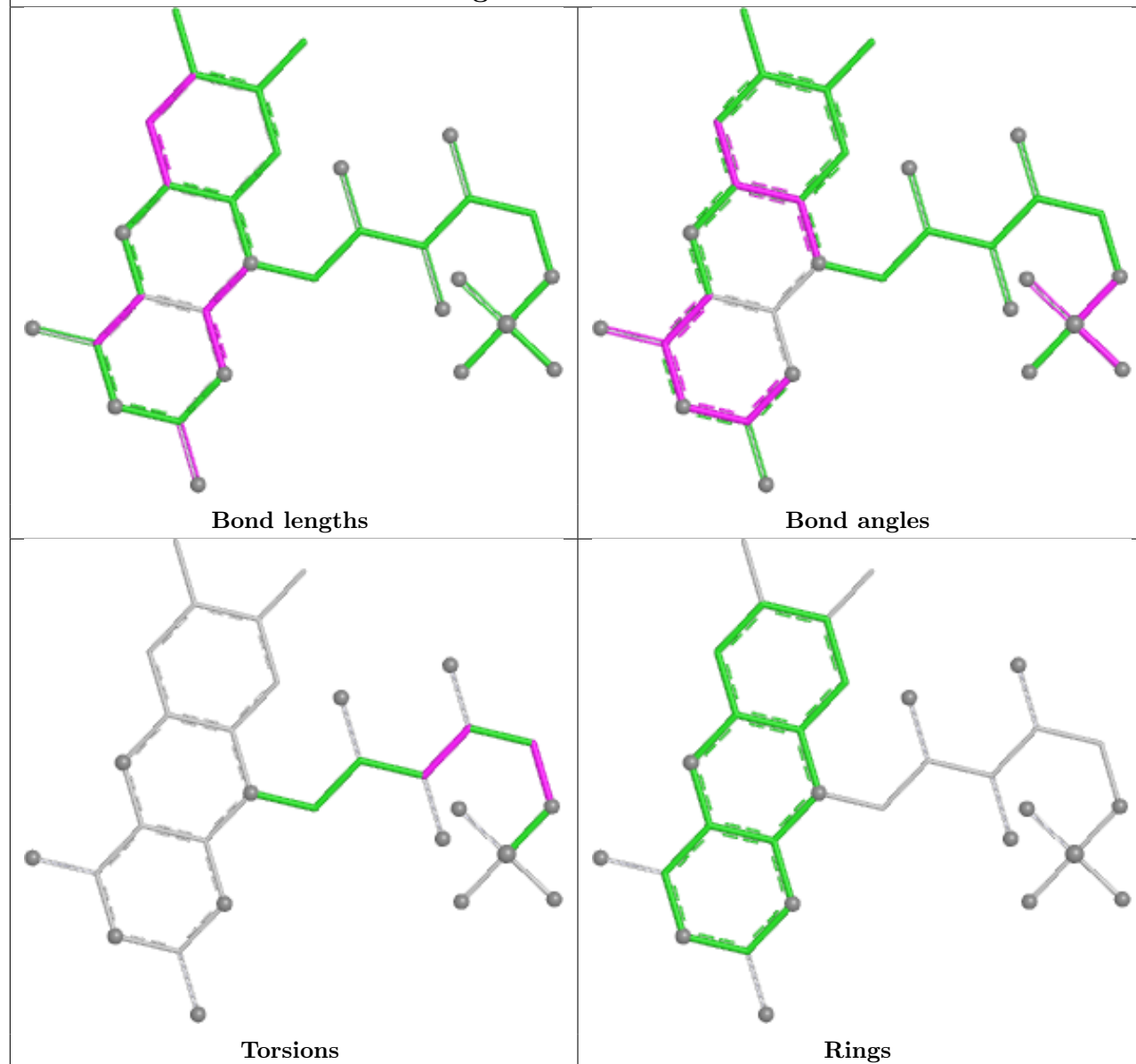
There are no ring outliers.

5 monomers are involved in 6 short contacts:

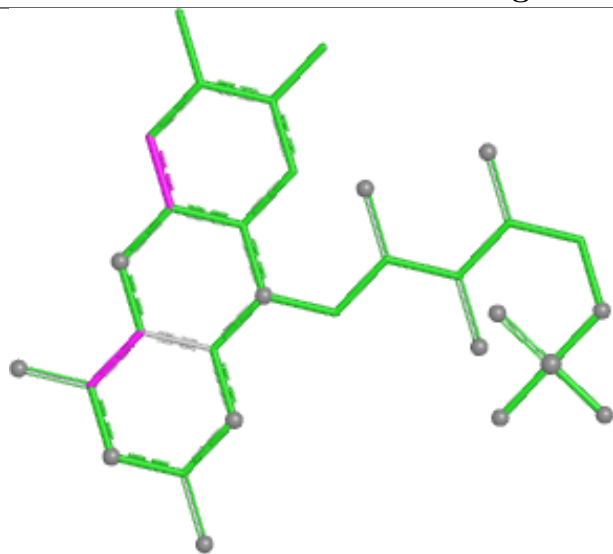
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	669	FNR	1	0
2	A	669	FNR	1	0
3	B	701	DMA	1	0
3	C	701	DMA	1	0
3	A	701	DMA	2	0

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.

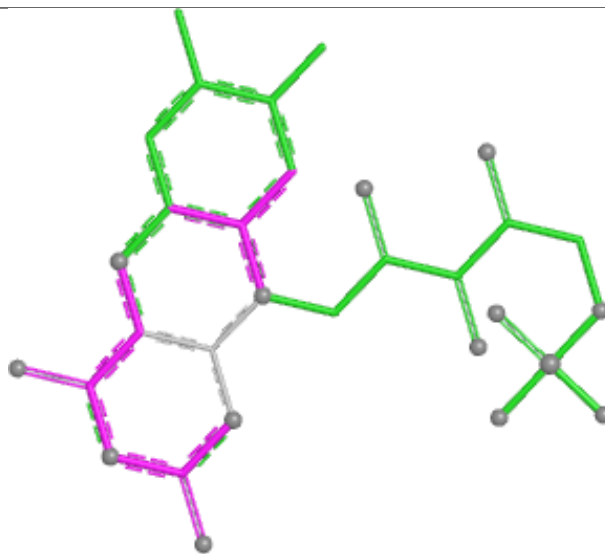
Ligand FNR C 669



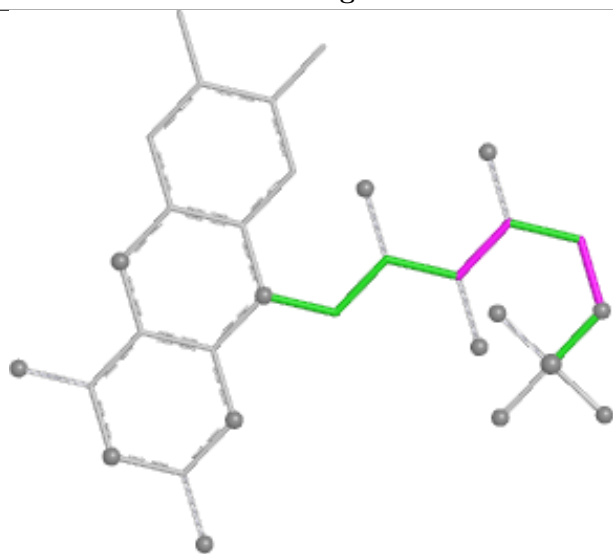
Ligand FNR D 669



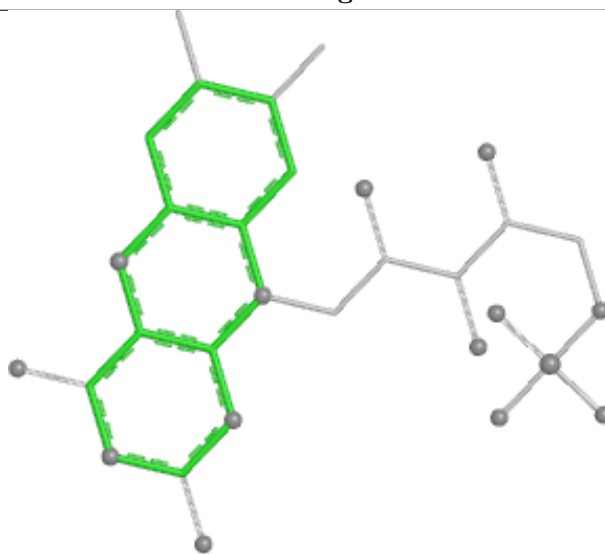
Bond lengths



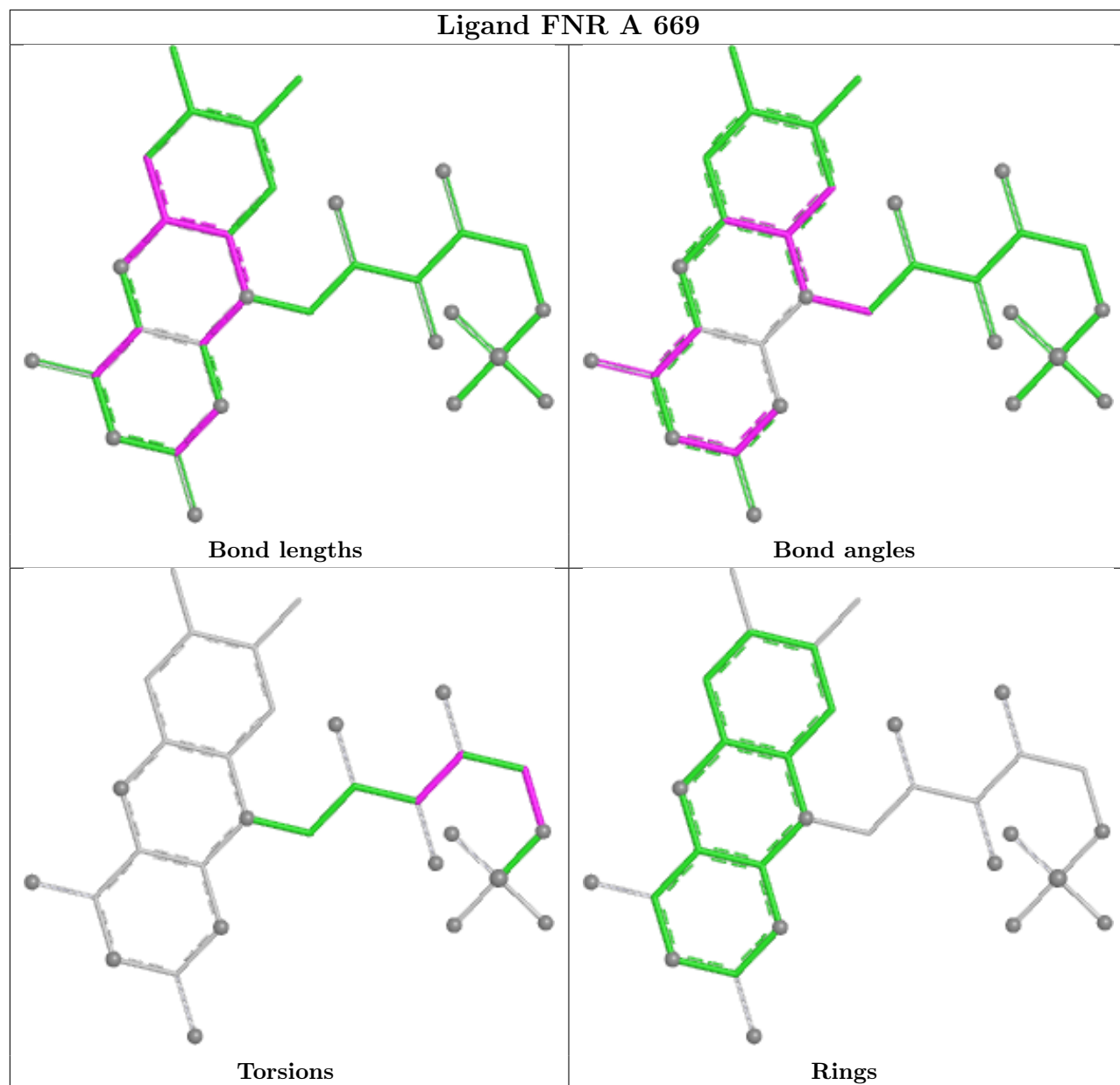
Bond angles

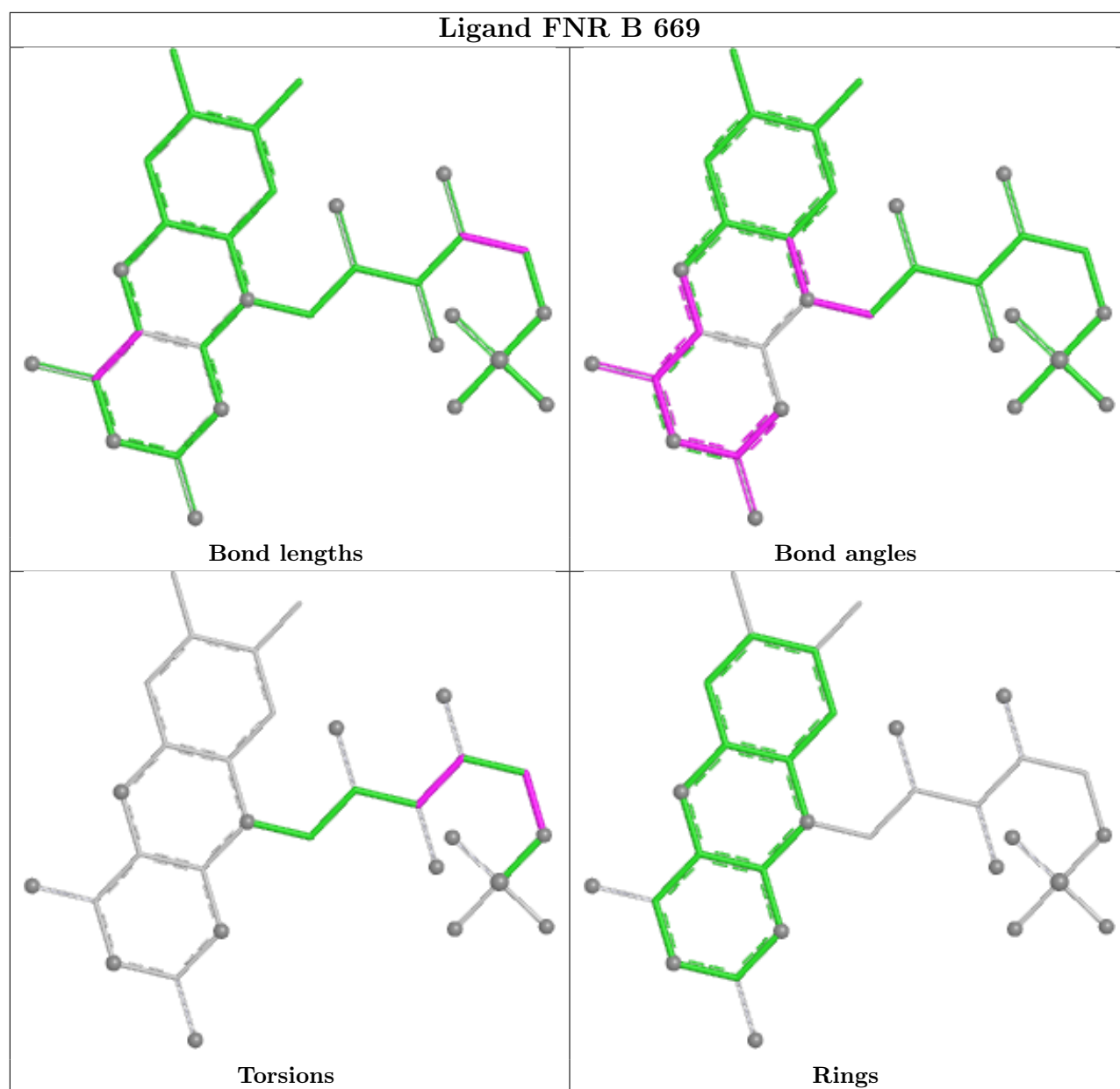


Torsions



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%)	0.03	4 (1%) 78 79	33, 43, 64, 76	0
1	B	364/368 (98%)	0.06	12 (3%) 49 51	33, 43, 64, 78	0
1	C	364/368 (98%)	0.05	9 (2%) 58 60	32, 43, 63, 74	0
1	D	364/368 (98%)	0.01	6 (1%) 70 72	32, 43, 64, 74	0
All	All	1456/1472 (98%)	0.04	31 (2%) 63 65	32, 43, 64, 78	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	174	TYR	5.0
1	B	167	GLY	4.2
1	A	167	GLY	4.2
1	C	134	GLY	3.8
1	B	134	GLY	3.6
1	C	239	TRP	3.3
1	D	183	SER	3.2
1	B	174	TYR	3.0
1	C	145	GLN	3.0
1	C	132	VAL	2.9
1	C	366	LYS	2.9
1	A	168	GLU	2.8
1	D	239	TRP	2.8
1	A	239	TRP	2.8
1	B	104	ALA	2.7
1	B	132	VAL	2.6
1	B	3	ASP	2.6
1	B	6	ASN	2.6
1	B	239	TRP	2.5
1	B	364	VAL	2.4
1	D	366	LYS	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	184	LYS	2.3
1	C	167	GLY	2.2
1	B	145	GLN	2.2
1	A	3	ASP	2.2
1	D	359	SER	2.2
1	C	187	SER	2.1
1	B	361	TYR	2.1
1	D	106	ALA	2.1
1	D	167	GLY	2.1
1	B	357	ASN	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](#)

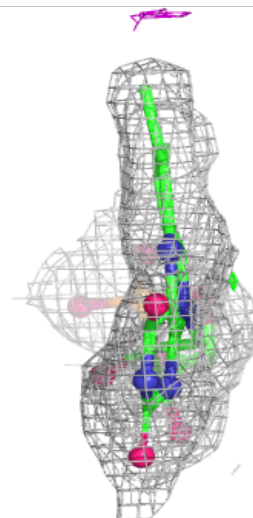
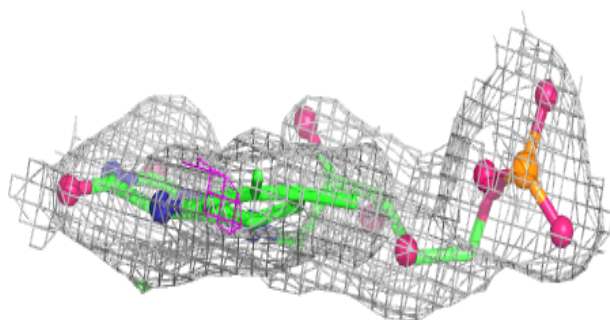
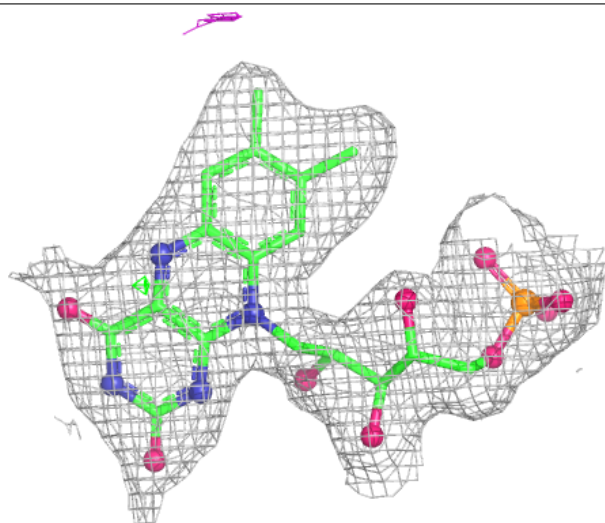
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	MG	D	1001	1/1	0.63	0.20	62,62,62,62	0
4	MG	C	1001	1/1	0.68	0.20	66,66,66,66	0
4	MG	B	1001	1/1	0.71	0.15	71,71,71,71	0
4	MG	A	1001	1/1	0.78	0.15	73,73,73,73	0
3	DMA	B	701	14/14	0.95	0.09	53,57,61,62	0
3	DMA	C	701	14/14	0.95	0.09	49,53,57,59	0
3	DMA	A	701	14/14	0.95	0.09	53,56,60,60	0
3	DMA	D	701	14/14	0.96	0.09	45,52,55,56	0
2	FNR	A	669	31/31	0.97	0.06	30,40,47,48	0
2	FNR	D	669	31/31	0.97	0.06	37,42,45,47	0
2	FNR	C	669	31/31	0.98	0.05	36,39,42,43	0
2	FNR	B	669	31/31	0.98	0.06	33,41,45,46	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.

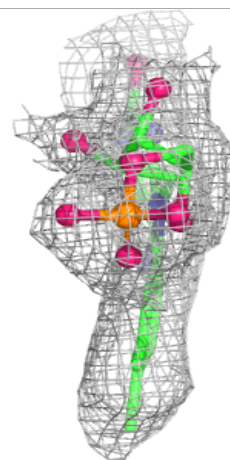
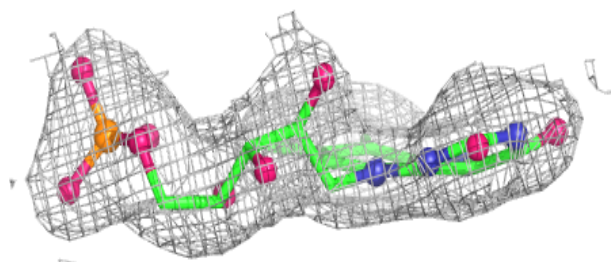
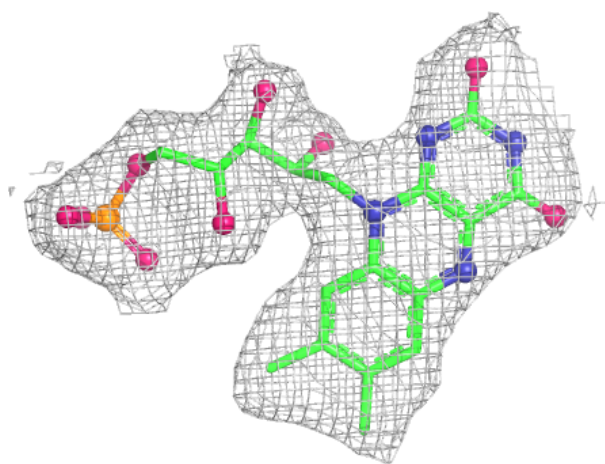
Electron density around FNR A 669:

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



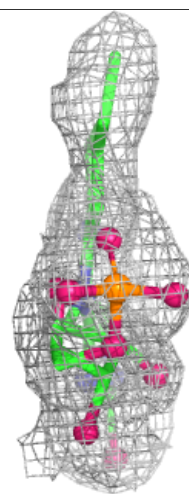
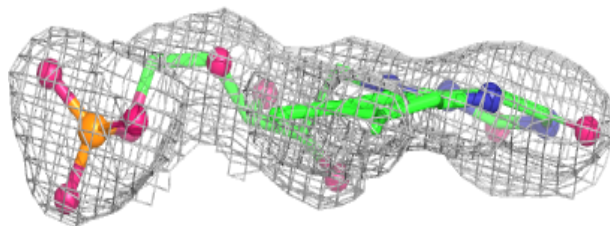
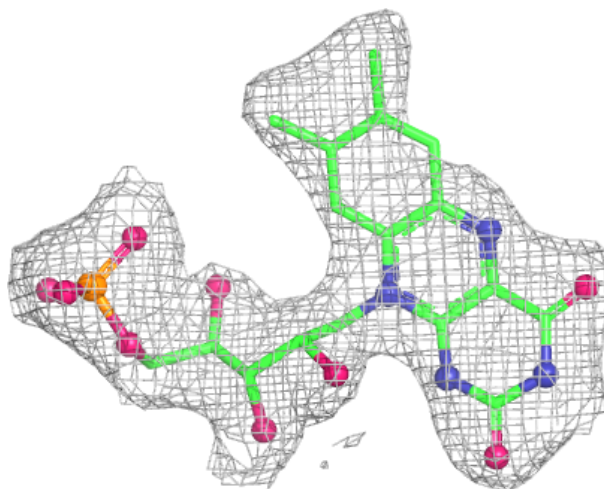
Electron density around FNR D 669:

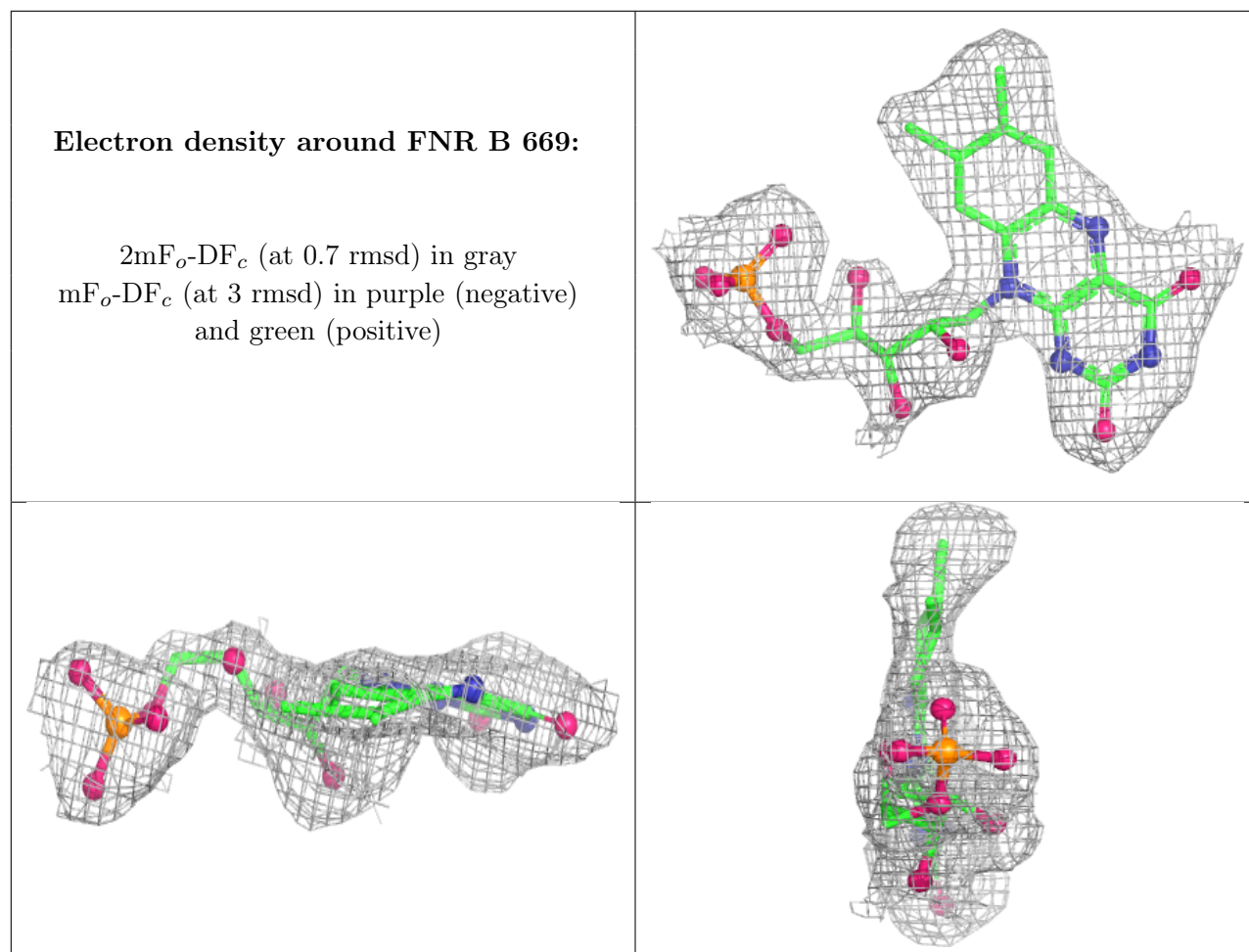
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around FNR C 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.