WORLDWIDE

wwPDB

PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:09 AM GMT

PDB ID	:	2ZRZ
Title	:	Crystal structure of Sulfolobus shibatae isopentenyl diphosphate isomerase in complex with reduced FMN and DMAPP
Authors	:	Unno, H.; Yamashita, S.; Ikeda, Y.; Sekiguchi, S.; Yoshida, N.; Yoshimura, T.; Kusunoki, M.; Nakayama, T.; Nishino, T.; Hemmi, H.
Deposited on	:	2008-09-01
Resolution	:	2.90 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

http://wwpdb.org/validation/2016/XrayValidationReportHelp

with specific help available everywhere you see the ⓘ symbol.

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

|		
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865
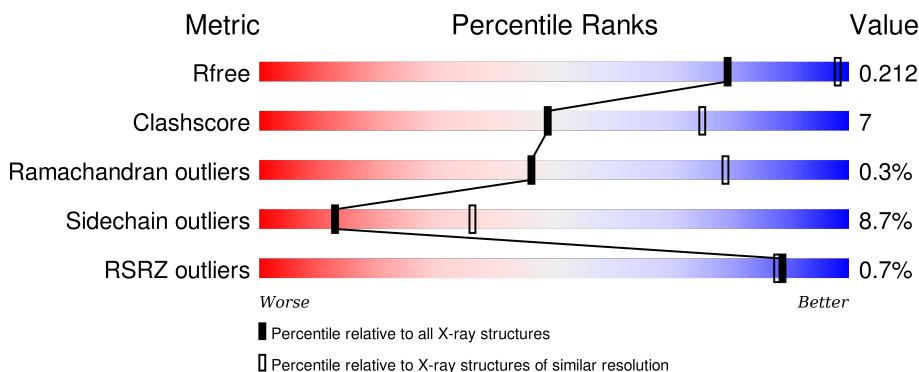
1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION
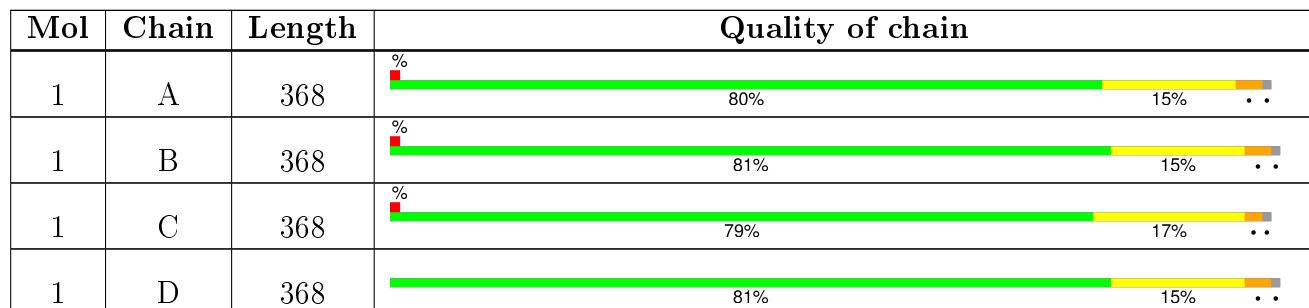
The reported resolution of this entry is 2.90 Å.

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}	91344	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (2.90-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	
1	B	368	
1	C	368	
1	D	368	

2 Entry composition (i)
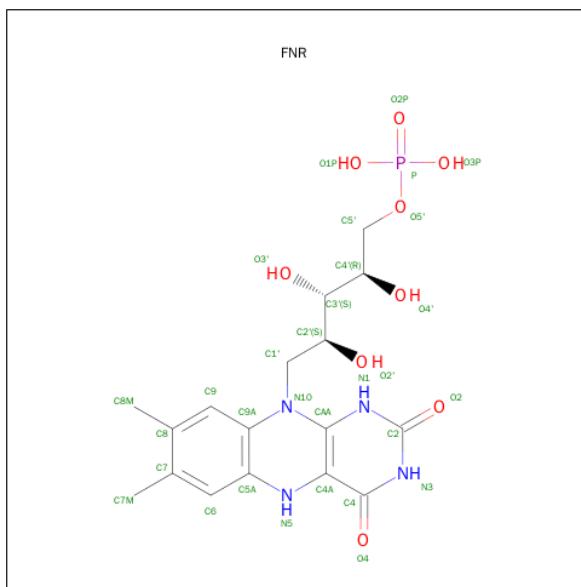
There are 5 unique types of molecules in this entry. The entry contains 11588 atoms, of which 0 are hydrogens and 0 are deuteriums.

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: $C_{17}H_{23}N_4O_9P$).
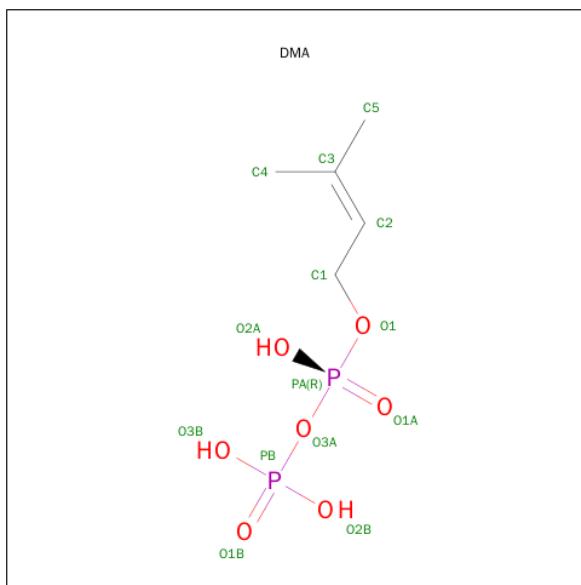

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

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 (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		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	1	Total 1	Mg 1	0	0
4	C	1	Total 1	Mg 1	0	0
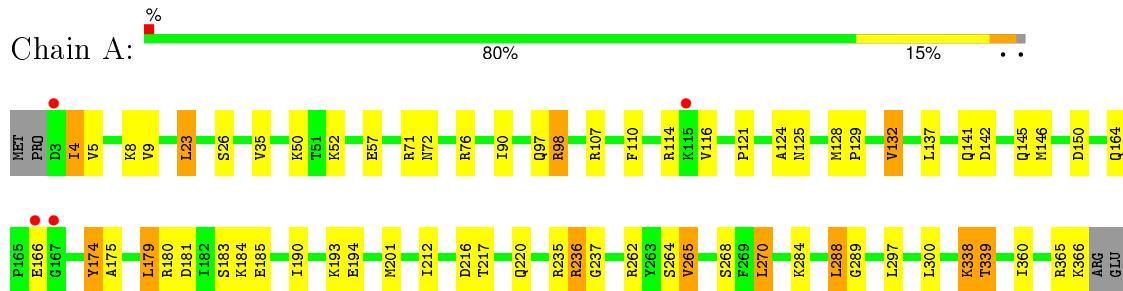
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	44	Total 44	O 44	0	0
5	B	47	Total 47	O 47	0	0
5	C	41	Total 41	O 41	0	0
5	D	40	Total 40	O 40	0	0
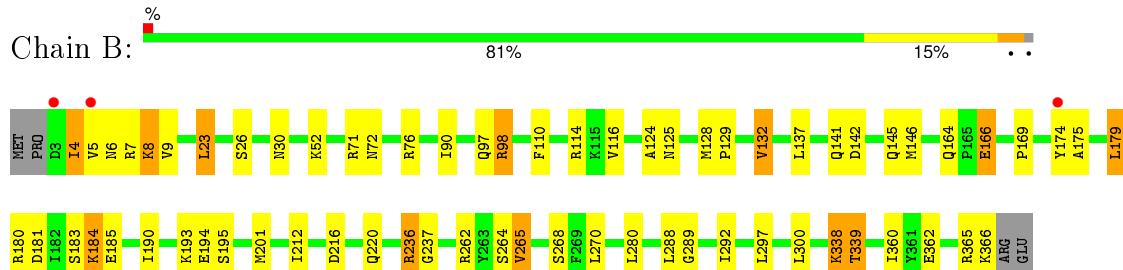
3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.
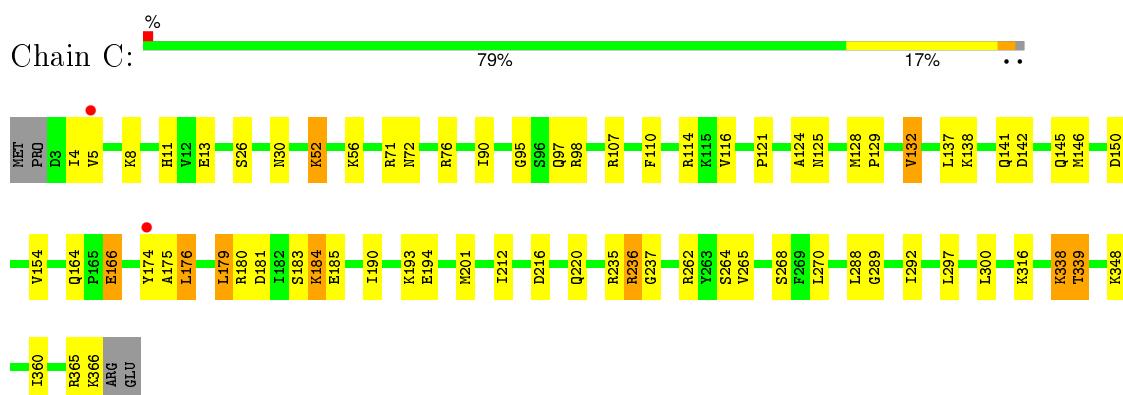
- Molecule 1: Isopentenyl-diphosphate delta-isomerase

- Molecule 1: Isopentenyl-diphosphate delta-isomerase
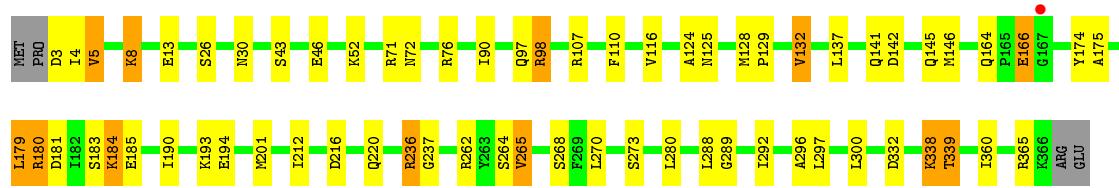
- Molecule 1: Isopentenyl-diphosphate delta-isomerase

- Molecule 1: Isopentenyl-diphosphate delta-isomerase

4 Data and refinement statistics (i)

| Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	100.88Å　　100.88Å　　334.86Å 90.00°　　　90.00°　　　90.00°	Depositor
Resolution (Å)	48.85　–　2.90 48.83　–　2.90	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.85-2.90) 99.5 (48.83-2.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	2.52 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.192　,　0.213 0.192　,　0.212	Depositor DCC
R_{free} test set	1969 reflections (5.27%)	DCC
Wilson B-factor (Å^2)	52.7	Xtriage
Anisotropy	0.050	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 35.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$<|L|> = 0.50, <L^2> = 0.34$	Xtriage
Outliers	2 of 39344 reflections (0.005%)	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	11588	wwPDB-VP
Average B, all atoms (Å^2)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.07% of the height of the origin peak. No significant pseudotranslation is detected.*

---

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $<|L|>$, $<L^2>$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: 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	0.57	0/2855	0.85	10/3846 (0.3%)
1	B	0.59	0/2855	0.89	12/3846 (0.3%)
1	C	0.58	0/2855	1.16	16/3846 (0.4%)
1	D	0.55	0/2855	0.88	9/3846 (0.2%)
All	All	0.57	0/11420	0.95	47/15384 (0.3%)

There are no bond length outliers.

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	180	ARG	NE-CZ-NH1	-24.96	107.82	120.30
1	C	98	ARG	NE-CZ-NH1	-23.95	108.32	120.30
1	C	180	ARG	NE-CZ-NH2	22.55	131.57	120.30
1	C	98	ARG	NE-CZ-NH2	22.36	131.48	120.30
1	B	236	ARG	NE-CZ-NH1	-18.67	110.97	120.30
1	D	236	ARG	NE-CZ-NH2	17.95	129.27	120.30
1	B	236	ARG	NE-CZ-NH2	17.84	129.22	120.30
1	D	236	ARG	NE-CZ-NH1	-17.44	111.58	120.30
1	A	236	ARG	NE-CZ-NH2	-16.53	112.04	120.30
1	C	236	ARG	NE-CZ-NH2	-16.30	112.15	120.30
1	C	236	ARG	NE-CZ-NH1	15.58	128.09	120.30
1	A	236	ARG	NE-CZ-NH1	15.48	128.04	120.30
1	C	98	ARG	CD-NE-CZ	12.76	141.47	123.60
1	C	180	ARG	CD-NE-CZ	10.84	138.78	123.60
1	A	236	ARG	CD-NE-CZ	10.13	137.79	123.60
1	C	236	ARG	CD-NE-CZ	10.08	137.71	123.60
1	D	236	ARG	CD-NE-CZ	9.67	137.14	123.60
1	B	236	ARG	CD-NE-CZ	9.35	136.69	123.60
1	D	98	ARG	NE-CZ-NH1	8.90	124.75	120.30
1	B	98	ARG	NE-CZ-NH2	-8.84	115.88	120.30

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	98	ARG	NE-CZ-NH1	8.67	124.63	120.30
1	D	98	ARG	NE-CZ-NH2	-8.56	116.02	120.30
1	A	98	ARG	NE-CZ-NH1	8.51	124.55	120.30
1	D	180	ARG	NE-CZ-NH2	-8.24	116.18	120.30
1	D	180	ARG	NE-CZ-NH1	8.22	124.41	120.30
1	A	180	ARG	NE-CZ-NH2	-7.94	116.33	120.30
1	C	297	LEU	CB-CG-CD1	7.82	124.30	111.00
1	B	180	ARG	NE-CZ-NH2	-7.62	116.49	120.30
1	A	98	ARG	NE-CZ-NH2	-7.61	116.50	120.30
1	B	132	VAL	CG1-CB-CG2	7.49	122.88	110.90
1	A	180	ARG	NE-CZ-NH1	7.17	123.88	120.30
1	C	176	LEU	CB-CG-CD1	6.60	122.23	111.00
1	B	180	ARG	NE-CZ-NH1	6.59	123.59	120.30
1	C	154	VAL	CG1-CB-CG2	6.53	121.35	110.90
1	C	265	VAL	CG1-CB-CG2	6.42	121.16	110.90
1	D	5	VAL	CG1-CB-CG2	6.40	121.14	110.90
1	A	270	LEU	CB-CG-CD1	6.26	121.64	111.00
1	C	180	ARG	CG-CD-NE	5.98	124.36	111.80
1	C	154	VAL	CA-CB-CG2	5.74	119.50	110.90
1	B	23	LEU	CB-CG-CD2	5.48	120.31	111.00
1	A	23	LEU	CB-CG-CD2	5.30	120.02	111.00
1	A	9	VAL	CG1-CB-CG2	5.24	119.28	110.90
1	B	137	LEU	CB-CG-CD2	5.17	119.78	111.00
1	B	132	VAL	CA-CB-CG1	5.16	118.64	110.90
1	B	9	VAL	CG1-CB-CG2	5.10	119.06	110.90
1	D	5	VAL	CA-CB-CG1	5.10	118.54	110.90
1	C	154	VAL	CA-CB-CG1	5.04	118.46	110.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2808	0	2890	46	0
1	B	2808	0	2890	40	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2808	0	2890	43	0
1	D	2808	0	2890	38	0
2	A	31	0	22	0	0
2	B	31	0	22	0	0
2	C	31	0	22	0	0
2	D	31	0	22	1	0
3	A	14	0	9	0	0
3	B	14	0	9	3	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	44	0	0	10	0
5	B	47	0	0	8	0
5	C	41	0	0	7	0
5	D	40	0	0	8	0
All	All	11588	0	11684	167	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 (167) 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:30:ASN:HB2	5:C:733:HOH:O	1.38	1.21
1:D:30:ASN:HB2	5:D:751:HOH:O	1.58	1.03
1:A:57:GLU:HG3	5:A:739:HOH:O	1.59	1.03
1:A:174:TYR:CE2	5:A:742:HOH:O	2.11	1.00
1:B:30:ASN:HB2	5:B:738:HOH:O	1.60	1.00
1:D:184:LYS:HA	1:D:184:LYS:HE2	1.51	0.93
5:B:722:HOH:O	1:C:348:LYS:HD3	1.68	0.92
1:C:184:LYS:HE2	1:C:184:LYS:HA	1.55	0.88
1:D:184:LYS:CA	1:D:184:LYS:HE2	2.05	0.87
1:B:184:LYS:HA	1:B:184:LYS:HE2	1.57	0.87
1:A:184:LYS:HE2	1:A:184:LYS:HA	1.59	0.85
1:C:184:LYS:CA	1:C:184:LYS:HE2	2.08	0.83
1:D:265:VAL:HG22	1:D:268:SER:HB3	1.61	0.82
1:B:184:LYS:HE2	1:B:184:LYS:CA	2.09	0.82
5:B:733:HOH:O	1:C:316:LYS:HE3	1.77	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:184:LYS:CA	1:A:184:LYS:HE2	2.09	0.81
1:D:3:ASP:HA	5:D:761:HOH:O	1.81	0.80
1:B:265:VAL:HG22	1:B:268:SER:HB3	1.63	0.80
1:A:265:VAL:HG22	1:A:268:SER:HB3	1.63	0.79
1:A:235:ARG:HD2	5:A:714:HOH:O	1.83	0.78
1:D:13:GLU:OE2	5:D:757:HOH:O	2.05	0.74
1:D:110:PHE:HB2	1:D:146:MET:CE	2.18	0.74
1:A:110:PHE:HB2	1:A:146:MET:CE	2.18	0.74
1:C:110:PHE:HB2	1:C:146:MET:CE	2.19	0.72
1:B:110:PHE:HB2	1:B:146:MET:CE	2.19	0.72
1:B:110:PHE:HB2	1:B:146:MET:HE2	1.72	0.70
1:C:164:GLN:HG2	1:C:166:GLU:HG3	1.75	0.69
1:D:184:LYS:CE	1:D:184:LYS:HA	2.24	0.68
1:D:110:PHE:HB2	1:D:146:MET:HE2	1.76	0.67
1:A:164:GLN:HG2	1:A:166:GLU:HG3	1.76	0.67
1:B:164:GLN:HG2	1:B:166:GLU:HG3	1.76	0.67
1:B:26:SER:H	1:B:220:GLN:HE21	1.42	0.67
1:C:138:LYS:HD3	5:C:723:HOH:O	1.93	0.66
1:D:164:GLN:HG2	1:D:166:GLU:HG3	1.76	0.66
1:D:184:LYS:N	1:D:184:LYS:HE2	2.12	0.65
1:C:110:PHE:HB2	1:C:146:MET:HE2	1.79	0.65
1:A:184:LYS:N	1:A:184:LYS:HE2	2.12	0.65
1:A:338:LYS:HB2	1:A:366:LYS:HD2	1.79	0.65
1:B:184:LYS:HD2	5:B:729:HOH:O	1.97	0.64
1:C:184:LYS:HA	1:C:184:LYS:CE	2.26	0.64
1:D:97:GLN:HE21	1:D:125:ASN:H	1.44	0.64
1:A:166:GLU:HB2	5:A:744:HOH:O	1.98	0.64
1:A:26:SER:H	1:A:220:GLN:HE21	1.45	0.64
1:D:8:LYS:HE2	5:D:760:HOH:O	1.96	0.64
1:B:97:GLN:HE21	1:B:125:ASN:H	1.45	0.63
1:C:97:GLN:HE21	1:C:125:ASN:H	1.45	0.63
1:C:26:SER:H	1:C:220:GLN:HE21	1.46	0.63
1:B:184:LYS:HE2	1:B:184:LYS:N	2.13	0.63
1:D:132:VAL:HG12	1:D:175:ALA:HB2	1.80	0.63
1:C:184:LYS:N	1:C:184:LYS:HE2	2.14	0.63
1:A:184:LYS:CE	1:A:184:LYS:HA	2.28	0.63
1:A:97:GLN:HE22	1:A:124:ALA:HB1	1.63	0.62
1:B:184:LYS:HA	1:B:184:LYS:CE	2.27	0.62
1:C:132:VAL:HG12	1:C:175:ALA:HB2	1.81	0.62
1:A:132:VAL:HG12	1:A:175:ALA:HB2	1.82	0.61
1:C:97:GLN:HE22	1:C:124:ALA:HB1	1.65	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:110:PHE:HB2	1:A:146:MET:HE2	1.80	0.61
1:D:26:SER:H	1:D:220:GLN:HE21	1.46	0.61
1:B:7:ARG:HB2	5:B:745:HOH:O	2.00	0.60
1:D:180:ARG:HD2	5:D:740:HOH:O	2.01	0.60
1:A:97:GLN:HE21	1:A:125:ASN:H	1.47	0.60
1:D:184:LYS:HD2	5:D:752:HOH:O	2.01	0.60
1:C:52:LYS:HE2	5:C:703:HOH:O	2.02	0.59
1:A:110:PHE:HB2	1:A:146:MET:HE3	1.83	0.59
1:B:338:LYS:HB2	1:B:366:LYS:HD2	1.85	0.58
1:D:97:GLN:HE22	1:D:124:ALA:HB1	1.67	0.58
1:B:97:GLN:HE22	1:B:124:ALA:HB1	1.66	0.58
1:C:339:THR:O	1:C:365:ARG:NH2	2.34	0.56
1:C:110:PHE:HB2	1:C:146:MET:HE3	1.88	0.55
1:C:179:LEU:HD13	1:C:212:ILE:HD11	1.88	0.55
1:D:110:PHE:HB2	1:D:146:MET:HE3	1.87	0.55
1:A:339:THR:O	1:A:365:ARG:NH2	2.34	0.55
1:A:50:LYS:HG3	5:A:743:HOH:O	2.07	0.54
1:C:193:LYS:CB	1:C:216:ASP:HB3	2.37	0.54
1:C:338:LYS:HB2	1:C:366:LYS:HD2	1.89	0.54
1:B:195:SER:HB2	3:B:701:DMA:H41	1.91	0.53
1:A:179:LEU:HD13	1:A:212:ILE:HD11	1.90	0.53
1:A:174:TYR:HB3	5:A:711:HOH:O	2.08	0.53
1:D:193:LYS:CB	1:D:216:ASP:HB3	2.39	0.53
1:B:193:LYS:CB	1:B:216:ASP:HB3	2.39	0.53
1:B:179:LEU:HD13	1:B:212:ILE:HD11	1.91	0.53
1:D:179:LEU:HD13	1:D:212:ILE:HD11	1.92	0.52
1:C:138:LYS:HG2	5:C:726:HOH:O	2.08	0.52
1:C:181:ASP:HA	1:C:184:LYS:HG2	1.92	0.52
1:A:193:LYS:CB	1:A:216:ASP:HB3	2.40	0.52
1:D:181:ASP:HA	1:D:184:LYS:HG2	1.91	0.52
1:B:110:PHE:CB	1:B:146:MET:HE2	2.37	0.52
1:B:362:GLU:O	1:B:366:LYS:HG3	2.09	0.51
1:B:181:ASP:HA	1:B:184:LYS:HG2	1.92	0.51
1:D:110:PHE:CB	1:D:146:MET:HE2	2.40	0.51
1:B:193:LYS:HB3	1:B:216:ASP:HB3	1.92	0.51
1:D:193:LYS:HB3	1:D:216:ASP:HB3	1.91	0.51
1:C:193:LYS:HB3	1:C:216:ASP:HB3	1.92	0.51
1:B:339:THR:O	1:B:365:ARG:NH2	2.33	0.50
1:A:174:TYR:HE2	5:A:742:HOH:O	1.73	0.50
1:C:138:LYS:CG	5:C:726:HOH:O	2.60	0.50
1:C:11:HIS:HE1	3:C:701:DMA:O1A	1.94	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:97:GLN:NE2	1:D:125:ASN:H	2.07	0.49
1:D:339:THR:O	1:D:365:ARG:NH2	2.36	0.49
1:A:107:ARG:HA	1:A:146:MET:HE1	1.95	0.49
1:C:97:GLN:NE2	1:C:125:ASN:H	2.09	0.48
1:A:181:ASP:HA	1:A:184:LYS:HG2	1.94	0.48
1:B:97:GLN:NE2	1:B:125:ASN:H	2.10	0.48
1:A:193:LYS:HB3	1:A:216:ASP:HB3	1.94	0.48
1:C:95:GLY:N	5:C:737:HOH:O	2.45	0.48
1:B:125:ASN:HB2	5:B:742:HOH:O	2.12	0.48
1:B:6:ASN:HB2	5:B:741:HOH:O	2.14	0.48
1:C:110:PHE:CB	1:C:146:MET:HE2	2.43	0.47
1:B:262:ARG:HD2	1:B:289:GLY:O	2.14	0.47
1:A:35:VAL:HA	5:A:738:HOH:O	2.13	0.47
1:A:71:ARG:HG2	1:A:72:ASN:H	1.79	0.47
1:A:262:ARG:NH1	1:A:268:SER:O	2.43	0.47
1:B:169:PRO:HD2	5:B:743:HOH:O	2.14	0.47
1:D:71:ARG:HG2	1:D:72:ASN:H	1.79	0.47
1:C:141:GLN:O	1:C:145:GLN:HG3	2.15	0.47
1:B:141:GLN:O	1:B:145:GLN:HG3	2.15	0.47
1:A:338:LYS:HB2	1:A:366:LYS:CD	2.44	0.47
1:B:201:MET:HB2	1:B:264:SER:HB3	1.97	0.46
1:B:71:ARG:HG2	1:B:72:ASN:H	1.80	0.46
1:B:8:LYS:NZ	3:B:701:DMA:O3B	2.49	0.46
1:D:262:ARG:HD2	1:D:289:GLY:O	2.16	0.46
1:A:110:PHE:CB	1:A:146:MET:HE2	2.44	0.46
1:C:107:ARG:HA	1:C:146:MET:HE1	1.98	0.46
1:C:338:LYS:HB2	1:C:366:LYS:CD	2.45	0.46
1:D:273:SER:HB2	5:D:763:HOH:O	2.16	0.46
1:A:141:GLN:O	1:A:145:GLN:HG3	2.16	0.46
1:A:97:GLN:NE2	1:A:125:ASN:H	2.11	0.45
1:C:128:MET:N	1:C:129:PRO:HD2	2.30	0.45
1:C:262:ARG:HD2	1:C:289:GLY:O	2.16	0.45
1:A:174:TYR:HE2	5:A:735:HOH:O	1.96	0.45
1:B:110:PHE:HB2	1:B:146:MET:HE3	1.95	0.45
1:A:262:ARG:HD2	1:A:289:GLY:O	2.17	0.45
1:B:132:VAL:HG22	1:B:175:ALA:HB2	1.98	0.45
1:B:195:SER:CB	3:B:701:DMA:H41	2.47	0.44
1:C:71:ARG:HG2	1:C:72:ASN:H	1.81	0.44
1:D:128:MET:N	1:D:129:PRO:HD2	2.32	0.44
1:A:201:MET:HB2	1:A:264:SER:HB3	2.00	0.44
1:C:201:MET:HB2	1:C:264:SER:HB3	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:174:TYR:CE2	5:A:735:HOH:O	2.55	0.44
1:B:114:ARG:HD3	1:B:114:ARG:HA	1.75	0.44
1:C:262:ARG:NH1	1:C:268:SER:O	2.47	0.44
1:D:296:ALA:HB3	2:D:669:FNR:O3P	2.18	0.43
1:D:201:MET:HB2	1:D:264:SER:HB3	2.00	0.43
1:B:128:MET:N	1:B:129:PRO:HD2	2.33	0.43
1:D:141:GLN:O	1:D:145:GLN:HG3	2.19	0.43
1:D:107:ARG:HA	1:D:146:MET:HE1	2.01	0.43
1:D:183:SER:HB3	1:D:190:ILE:HD12	2.01	0.43
1:B:183:SER:HB3	1:B:190:ILE:HD12	2.01	0.43
1:D:338:LYS:HE3	1:D:338:LYS:HB3	1.87	0.42
1:A:183:SER:HB3	1:A:190:ILE:HD12	2.01	0.42
1:A:128:MET:N	1:A:129:PRO:HD2	2.34	0.42
1:B:4:ILE:HG13	1:B:4:ILE:O	2.19	0.42
1:A:114:ARG:HA	1:A:114:ARG:HD3	1.74	0.41
1:C:121:PRO:HA	1:C:150:ASP:OD2	2.21	0.41
1:A:217:THR:HG23	1:A:270:LEU:HD11	2.01	0.41
1:C:114:ARG:HA	1:C:114:ARG:HD3	1.77	0.41
1:A:121:PRO:HA	1:A:150:ASP:OD2	2.20	0.41
1:D:332:ASP:HB2	5:D:729:HOH:O	2.19	0.41
1:A:338:LYS:HB3	1:A:338:LYS:HE3	1.88	0.41
1:C:13:GLU:CD	1:C:235:ARG:HH22	2.24	0.41
1:B:262:ARG:NH1	1:B:268:SER:O	2.46	0.41
1:A:4:ILE:HG13	1:A:4:ILE:O	2.17	0.41
1:C:56:LYS:NZ	5:C:716:HOH:O	2.49	0.41
1:C:183:SER:HB3	1:C:190:ILE:HD12	2.02	0.41
1:C:338:LYS:HB3	1:C:338:LYS:HE3	1.86	0.40
1:A:284:LYS:O	1:A:288:LEU:HB2	2.21	0.40
1:D:43:SER:HB3	1:D:46:GLU:HG2	2.03	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%)	348 (96%)	13 (4%)	1 (0%)	46	79
1	B	362/368 (98%)	348 (96%)	13 (4%)	1 (0%)	46	79
1	C	362/368 (98%)	347 (96%)	14 (4%)	1 (0%)	46	79
1	D	362/368 (98%)	349 (96%)	12 (3%)	1 (0%)	46	79
All	All	1448/1472 (98%)	1392 (96%)	52 (4%)	4 (0%)	46	79

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	237	GLY
1	C	237	GLY
1	D	237	GLY
1	B	237	GLY

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	298/302 (99%)	274 (92%)	24 (8%)	15	39
1	B	298/302 (99%)	271 (91%)	27 (9%)	12	34
1	C	298/302 (99%)	273 (92%)	25 (8%)	14	37
1	D	298/302 (99%)	270 (91%)	28 (9%)	11	32
All	All	1192/1208 (99%)	1088 (91%)	104 (9%)	13	36

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

Mol	Chain	Res	Type
1	A	4	ILE
1	A	5	VAL
1	A	8	LYS
1	A	23	LEU
1	A	52	LYS
1	A	76	ARG
1	A	90	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	98	ARG
1	A	116	VAL
1	A	132	VAL
1	A	137	LEU
1	A	142	ASP
1	A	174	TYR
1	A	179	LEU
1	A	185	GLU
1	A	194	GLU
1	A	236	ARG
1	A	265	VAL
1	A	288	LEU
1	A	297	LEU
1	A	300	LEU
1	A	338	LYS
1	A	339	THR
1	A	360	ILE
1	B	4	ILE
1	B	5	VAL
1	B	8	LYS
1	B	23	LEU
1	B	52	LYS
1	B	76	ARG
1	B	90	ILE
1	B	98	ARG
1	B	116	VAL
1	B	142	ASP
1	B	166	GLU
1	B	174	TYR
1	B	179	LEU
1	B	184	LYS
1	B	185	GLU
1	B	194	GLU
1	B	236	ARG
1	B	265	VAL
1	B	270	LEU
1	B	280	LEU
1	B	288	LEU
1	B	292	ILE
1	B	297	LEU
1	B	300	LEU
1	B	338	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	339	THR
1	B	360	ILE
1	C	4	ILE
1	C	5	VAL
1	C	8	LYS
1	C	52	LYS
1	C	76	ARG
1	C	90	ILE
1	C	116	VAL
1	C	132	VAL
1	C	137	LEU
1	C	142	ASP
1	C	166	GLU
1	C	174	TYR
1	C	176	LEU
1	C	179	LEU
1	C	184	LYS
1	C	185	GLU
1	C	194	GLU
1	C	236	ARG
1	C	270	LEU
1	C	288	LEU
1	C	292	ILE
1	C	300	LEU
1	C	338	LYS
1	C	339	THR
1	C	360	ILE
1	D	4	ILE
1	D	5	VAL
1	D	8	LYS
1	D	52	LYS
1	D	76	ARG
1	D	90	ILE
1	D	98	ARG
1	D	116	VAL
1	D	132	VAL
1	D	137	LEU
1	D	142	ASP
1	D	166	GLU
1	D	174	TYR
1	D	179	LEU
1	D	184	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	185	GLU
1	D	194	GLU
1	D	236	ARG
1	D	265	VAL
1	D	270	LEU
1	D	280	LEU
1	D	288	LEU
1	D	292	ILE
1	D	297	LEU
1	D	300	LEU
1	D	338	LYS
1	D	339	THR
1	D	360	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	HIS
1	A	97	GLN
1	A	220	GLN
1	B	11	HIS
1	B	97	GLN
1	B	220	GLN
1	C	11	HIS
1	C	97	GLN
1	C	130	GLN
1	C	220	GLN
1	D	11	HIS
1	D	97	GLN
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	#$|Z| > 2$
2	FNR	A	669	-	30,33,33	1.50	4 (13%)	33,50,50	2.59	8 (24%)
3	DMA	A	701	4	11,13,13	0.55	0	16,19,19	1.21	2 (12%)
2	FNR	B	669	-	30,33,33	1.38	3 (10%)	33,50,50	2.58	8 (24%)
3	DMA	B	701	4	11,13,13	0.60	0	16,19,19	1.21	1 (6%)
2	FNR	C	669	-	30,33,33	1.32	3 (10%)	33,50,50	2.40	8 (24%)
3	DMA	C	701	4	11,13,13	0.63	0	16,19,19	1.39	2 (12%)
2	FNR	D	669	-	30,33,33	1.39	4 (13%)	33,50,50	2.46	8 (24%)
3	DMA	D	701	4	11,13,13	0.60	0	16,19,19	1.35	2 (12%)

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

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	669	FNR	CAA-N10	2.16	1.41	1.39
2	A	669	FNR	CAA-N10	2.39	1.41	1.39
2	D	669	FNR	C9A-N10	3.07	1.43	1.38
2	C	669	FNR	C9A-N10	3.37	1.43	1.38
2	B	669	FNR	C9A-N10	3.39	1.43	1.38
2	C	669	FNR	C4-C4A	3.41	1.48	1.41
2	C	669	FNR	C4A-CAA	3.69	1.47	1.41
2	B	669	FNR	C4A-CAA	3.77	1.48	1.41
2	A	669	FNR	C4-C4A	3.83	1.48	1.41
2	A	669	FNR	C9A-N10	3.87	1.44	1.38
2	B	669	FNR	C4-C4A	3.89	1.49	1.41
2	D	669	FNR	C4-C4A	3.89	1.49	1.41
2	D	669	FNR	C4A-CAA	4.28	1.49	1.41
2	A	669	FNR	C4A-CAA	4.53	1.49	1.41

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	669	FNR	C4-C4A-CAA	-6.65	115.69	119.94
2	B	669	FNR	C4-C4A-CAA	-6.39	115.86	119.94
2	C	669	FNR	C4-C4A-CAA	-6.27	115.93	119.94
2	D	669	FNR	C4-C4A-CAA	-6.15	116.00	119.94
2	C	669	FNR	C4A-CAA-N10	-4.79	117.70	120.52
2	B	669	FNR	C4A-CAA-N10	-4.62	117.79	120.52
2	A	669	FNR	C4A-CAA-N10	-4.62	117.80	120.52
2	A	669	FNR	C4A-C4-N3	-4.22	117.81	123.59
2	B	669	FNR	C4A-C4-N3	-4.11	117.96	123.59
2	D	669	FNR	C4A-C4-N3	-3.90	118.25	123.59
2	C	669	FNR	C4A-C4-N3	-3.81	118.38	123.59
2	D	669	FNR	C4A-CAA-N10	-3.68	118.35	120.52
3	D	701	DMA	PA-O3A-PB	-3.16	122.08	132.67
3	A	701	DMA	PA-O3A-PB	-2.40	124.64	132.67
3	C	701	DMA	PA-O3A-PB	-2.35	124.80	132.67
2	D	669	FNR	C4A-N5-C5A	2.06	119.13	116.76
3	B	701	DMA	C5-C3-C4	2.08	119.76	114.64
3	A	701	DMA	O3B-PB-O2B	2.19	115.72	107.38
2	A	669	FNR	C4A-N5-C5A	2.28	119.39	116.76
3	D	701	DMA	O3B-PB-O1B	2.47	118.52	110.58
2	C	669	FNR	C4A-N5-C5A	2.52	119.66	116.76
3	C	701	DMA	O2B-PB-O1B	2.67	119.19	110.58
2	C	669	FNR	C5A-C9A-N10	2.82	119.76	117.62
2	B	669	FNR	C4A-N5-C5A	3.15	120.38	116.76
2	D	669	FNR	C1'-N10-C9A	3.23	122.49	118.86

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	669	FNR	C1'-N10-C9A	3.34	122.61	118.86
2	C	669	FNR	C4-C4A-N5	3.35	122.78	118.72
2	A	669	FNR	C1'-N10-C9A	3.46	122.74	118.86
2	D	669	FNR	C5A-C9A-N10	3.49	120.27	117.62
2	B	669	FNR	C1'-N10-C9A	3.52	122.81	118.86
2	A	669	FNR	C4-C4A-N5	3.53	123.01	118.72
2	A	669	FNR	C5A-C9A-N10	3.61	120.36	117.62
2	B	669	FNR	C4-C4A-N5	3.77	123.29	118.72
2	D	669	FNR	C4-C4A-N5	3.83	123.36	118.72
2	B	669	FNR	C5A-C9A-N10	3.90	120.58	117.62
2	C	669	FNR	C4-N3-C2	7.67	121.88	115.25
2	B	669	FNR	C4-N3-C2	8.22	122.36	115.25
2	D	669	FNR	C4-N3-C2	8.43	122.54	115.25
2	A	669	FNR	C4-N3-C2	8.96	123.00	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 5 short contacts:

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

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 (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	364/368 (98%)	-0.37	4 (1%)	82	80	29, 43, 65, 80	0
1	B	364/368 (98%)	-0.34	3 (0%)	87	86	29, 43, 65, 80	0
1	C	364/368 (98%)	-0.38	2 (0%)	91	90	29, 43, 65, 80	0
1	D	364/368 (98%)	-0.40	1 (0%)	94	94	29, 43, 65, 80	0
All	All	1456/1472 (98%)	-0.37	10 (0%)	89	88	29, 43, 65, 80	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	174	TYR	3.2
1	D	167	GLY	3.2
1	B	3	ASP	3.0
1	C	174	TYR	2.9
1	A	3	ASP	2.9
1	B	5	VAL	2.8
1	A	167	GLY	2.7
1	C	5	VAL	2.3
1	A	115	LYS	2.2
1	A	166	GLU	2.1

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
2	FNR	B	669	31/31	0.97	0.14	0.24	41,42,43,43	0
2	FNR	A	669	31/31	0.97	0.15	0.17	41,42,43,43	0
4	MG	C	702	1/1	0.82	0.15	0.14	62,62,62,62	0
2	FNR	C	669	31/31	0.97	0.14	-0.17	41,42,43,43	0
4	MG	D	702	1/1	0.89	0.15	-0.18	57,57,57,57	0
3	DMA	B	701	14/14	0.96	0.15	-0.28	64,67,69,69	0
2	FNR	D	669	31/31	0.97	0.13	-0.65	41,42,43,43	0
3	DMA	C	701	14/14	0.96	0.13	-0.77	62,65,65,66	0
4	MG	A	702	1/1	0.89	0.14	-0.84	47,47,47,47	0
4	MG	B	702	1/1	0.85	0.12	-1.33	65,65,65,65	0
3	DMA	D	701	14/14	0.98	0.11	-1.45	55,58,60,60	0
3	DMA	A	701	14/14	0.98	0.11	-1.78	59,61,62,62	0

6.5 Other polymers (i)

There are no such residues in this entry.