



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 12:49 am GMT

PDB ID : 2ZRX
Title : Crystal structure of Sulfolobus shibatae isopentenyl diphosphate isomerase in complex with 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 : 3.00 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	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

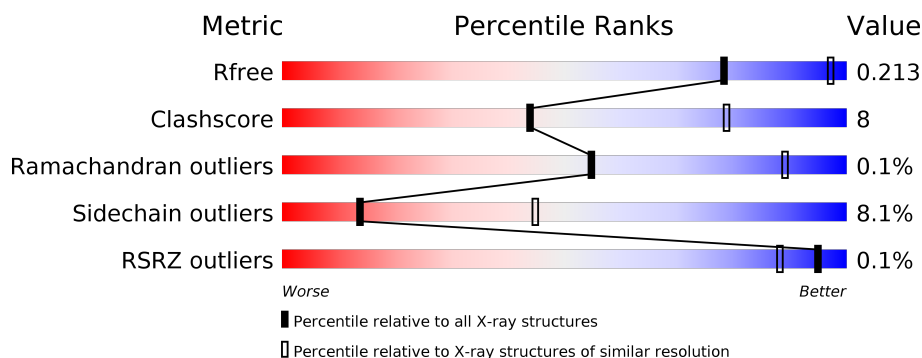
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	100719	1692 (3.00-3.00)
Clashscore	112137	2037 (3.00-3.00)
Ramachandran outliers	110173	1973 (3.00-3.00)
Sidechain outliers	110143	1976 (3.00-3.00)
RSRZ outliers	101464	1716 (3.00-3.00)

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 $\leq 5\%$. 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>79%</div> <div>17%</div> <div>• •</div> </div>
1	B	368	<div> <div>80%</div> <div>16%</div> <div>• •</div> </div>
1	C	368	<div> <div>78%</div> <div>18%</div> <div>• • •</div> </div>
1	D	368	<div> <div>81%</div> <div>15%</div> <div>• •</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	MG	B	702	-	-	-	X

2 Entry composition [i](#)

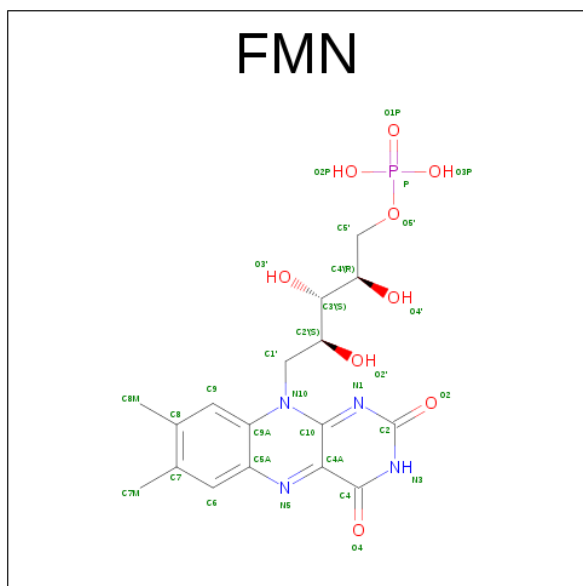
There are 5 unique types of molecules in this entry. The entry contains 11591 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C₁₇H₂₁N₄O₉P).



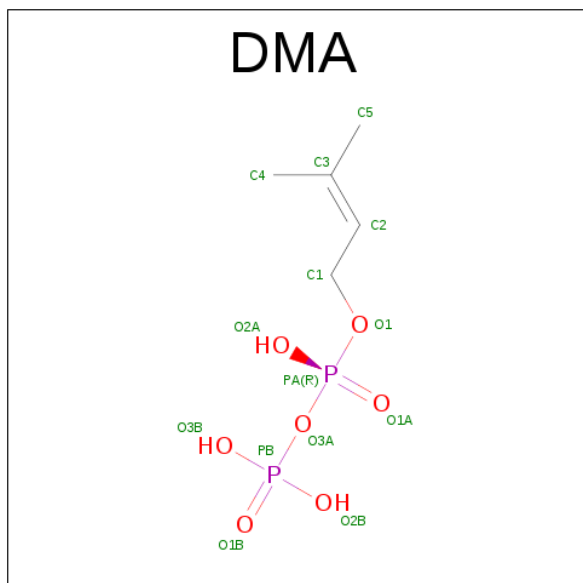
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		
2	B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

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

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

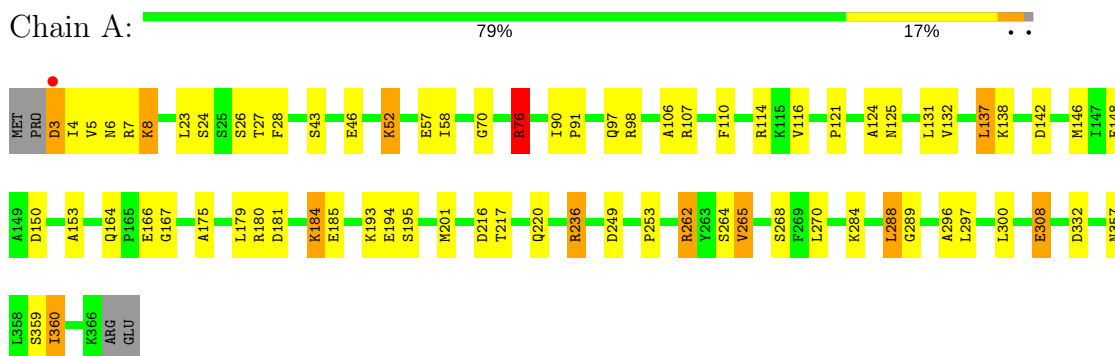
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	48	Total 48	O 48	0	0
5	B	44	Total 44	O 44	0	0
5	C	45	Total 45	O 45	0	0
5	D	38	Total 38	O 38	0	0

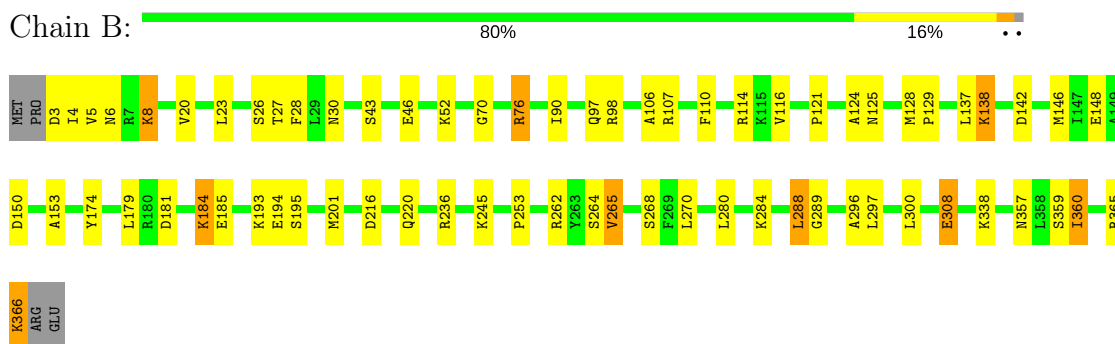
3 Residue-property plots [i](#)

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.

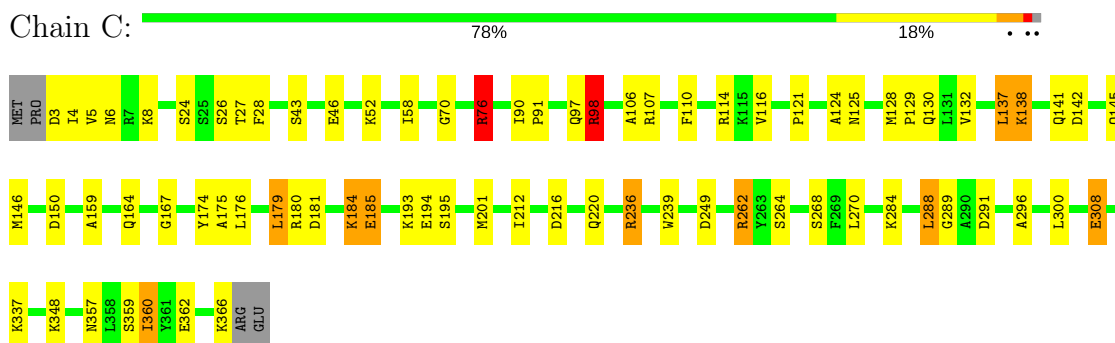
- Molecule 1: Isopentenyl-diphosphate delta-isomerase



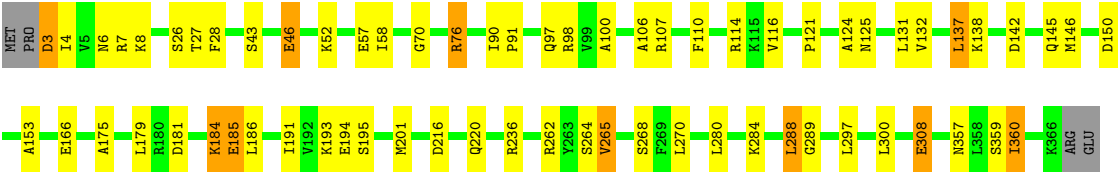
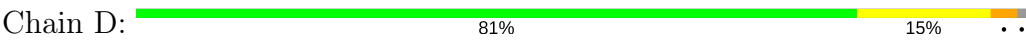
- Molecule 1: Isopentenyl-diphosphate delta-isomerase



- 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	101.07Å 101.07Å 333.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.22 – 3.00 45.20 – 3.00	Depositor EDS
% Data completeness (in resolution range)	96.1 (45.22-3.00) 96.1 (45.20-3.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.184 , 0.215 0.184 , 0.213	Depositor DCC
R_{free} test set	1711 reflections (5.24%)	DCC
Wilson B-factor (Å ²)	55.0	Xtriage
Anisotropy	0.034	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 43.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11591	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.40% 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: FMN, DMA, 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	0.58	0/2855	0.82	7/3846 (0.2%)
1	B	0.62	0/2855	0.76	6/3846 (0.2%)
1	C	0.59	0/2855	0.85	10/3846 (0.3%)
1	D	0.57	0/2855	0.73	5/3846 (0.1%)
All	All	0.59	0/11420	0.79	28/15384 (0.2%)

There are no bond length outliers.

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	76	ARG	NE-CZ-NH2	15.06	127.83	120.30
1	C	180	ARG	NE-CZ-NH1	-14.44	113.08	120.30
1	A	76	ARG	NE-CZ-NH1	-13.64	113.48	120.30
1	C	98	ARG	NE-CZ-NH2	13.12	126.86	120.30
1	C	180	ARG	NE-CZ-NH2	12.21	126.41	120.30
1	C	98	ARG	NE-CZ-NH1	-12.18	114.21	120.30
1	A	236	ARG	NE-CZ-NH2	-11.53	114.54	120.30
1	B	236	ARG	NE-CZ-NH1	-11.36	114.62	120.30
1	C	236	ARG	NE-CZ-NH2	-11.20	114.70	120.30
1	B	236	ARG	NE-CZ-NH2	11.15	125.87	120.30
1	D	236	ARG	NE-CZ-NH1	-10.80	114.90	120.30
1	A	236	ARG	NE-CZ-NH1	10.37	125.48	120.30
1	C	236	ARG	NE-CZ-NH1	10.20	125.40	120.30
1	D	236	ARG	NE-CZ-NH2	10.10	125.35	120.30
1	A	76	ARG	CD-NE-CZ	8.00	134.81	123.60
1	B	76	ARG	NE-CZ-NH1	6.46	123.53	120.30
1	D	76	ARG	NE-CZ-NH1	6.26	123.43	120.30
1	C	76	ARG	NE-CZ-NH1	6.22	123.41	120.30
1	C	236	ARG	CD-NE-CZ	5.74	131.64	123.60
1	A	236	ARG	CD-NE-CZ	5.63	131.48	123.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	98	ARG	CD-NE-CZ	5.58	131.42	123.60
1	C	76	ARG	NE-CZ-NH2	-5.40	117.60	120.30
1	A	98	ARG	NE-CZ-NH1	5.35	122.97	120.30
1	B	76	ARG	NE-CZ-NH2	-5.27	117.66	120.30
1	B	98	ARG	NE-CZ-NH1	5.26	122.93	120.30
1	D	76	ARG	NE-CZ-NH2	-5.13	117.74	120.30
1	D	98	ARG	NE-CZ-NH1	5.12	122.86	120.30
1	B	236	ARG	CD-NE-CZ	5.01	130.62	123.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2808	0	2890	50	0
1	B	2808	0	2890	44	0
1	C	2808	0	2890	44	0
1	D	2808	0	2890	38	0
2	A	31	0	19	1	0
2	B	31	0	19	1	0
2	C	31	0	19	1	0
2	D	31	0	19	0	0
3	A	14	0	9	2	0
3	B	14	0	9	2	0
3	C	14	0	9	1	0
3	D	14	0	9	1	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	48	0	0	8	0
5	B	44	0	0	6	0
5	C	45	0	0	6	0
5	D	38	0	0	2	0
All	All	11591	0	11672	176	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 (176) 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:A:57:GLU:HG3	5:A:741:HOH:O	1.56	1.06
1:B:138:LYS:HD2	5:B:744:HOH:O	1.72	0.88
5:B:733:HOH:O	1:C:348:LYS:HD3	1.74	0.87
1:D:265:VAL:HG22	1:D:268:SER:HB3	1.61	0.81
1:A:265:VAL:HG22	1:A:268:SER:HB3	1.62	0.80
1:A:52:LYS:HE3	5:A:721:HOH:O	1.80	0.79
1:B:265:VAL:HG22	1:B:268:SER:HB3	1.64	0.79
1:C:138:LYS:HG2	5:C:740:HOH:O	1.83	0.77
1:C:239:TRP:NE1	5:C:743:HOH:O	2.17	0.76
1:C:357:ASN:OD1	1:C:360:ILE:HG23	1.87	0.75
1:A:357:ASN:OD1	1:A:360:ILE:HG23	1.87	0.75
1:B:26:SER:H	1:B:220:GLN:HE21	1.35	0.75
1:D:357:ASN:OD1	1:D:360:ILE:HG23	1.88	0.73
1:A:26:SER:H	1:A:220:GLN:HE21	1.35	0.73
1:B:357:ASN:OD1	1:B:360:ILE:HG23	1.89	0.72
1:D:145:GLN:HB3	5:D:749:HOH:O	1.88	0.72
1:A:52:LYS:CD	5:A:721:HOH:O	2.39	0.71
1:A:110:PHE:HB2	1:A:146:MET:HE2	1.74	0.70
1:A:180:ARG:HD2	5:A:728:HOH:O	1.91	0.70
1:C:76:ARG:HG2	5:C:745:HOH:O	1.91	0.69
1:C:195:SER:HB2	3:C:701:DMA:H41	1.73	0.69
1:C:26:SER:H	1:C:220:GLN:HE21	1.40	0.68
1:C:110:PHE:HB2	1:C:146:MET:HE2	1.77	0.67
1:B:195:SER:HB2	3:B:701:DMA:H41	1.76	0.67
1:C:3:ASP:HB2	1:C:6:ASN:HB2	1.77	0.66
1:B:184:LYS:NZ	1:B:184:LYS:HA	2.11	0.66
1:D:26:SER:H	1:D:220:GLN:HE21	1.41	0.66
1:A:70:GLY:HA2	1:A:106:ALA:HB1	1.77	0.65
1:A:195:SER:HB2	3:A:701:DMA:H41	1.79	0.65
1:B:3:ASP:HB2	1:B:6:ASN:HB2	1.79	0.65
1:D:97:GLN:HE21	1:D:125:ASN:H	1.46	0.63
1:A:52:LYS:CE	5:A:721:HOH:O	2.44	0.63
1:B:107:ARG:HA	1:B:146:MET:HE3	1.80	0.62
1:B:110:PHE:HB2	1:B:146:MET:HE2	1.81	0.62
1:C:107:ARG:HA	1:C:146:MET:HE3	1.79	0.62
1:A:3:ASP:HB2	1:A:6:ASN:HB2	1.83	0.61
1:D:107:ARG:HA	1:D:146:MET:HE3	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:ARG:HA	1:A:146:MET:HE3	1.83	0.60
1:B:70:GLY:HA2	1:B:106:ALA:HB1	1.83	0.60
1:C:110:PHE:HB2	1:C:146:MET:CE	2.32	0.60
1:D:3:ASP:HB2	1:D:6:ASN:HB2	1.84	0.60
1:B:97:GLN:HE21	1:B:125:ASN:H	1.49	0.60
1:B:174:TYR:HB3	5:B:742:HOH:O	2.02	0.59
1:B:338:LYS:HE3	1:B:366:LYS:HB3	1.83	0.59
1:C:97:GLN:HE21	1:C:125:ASN:H	1.49	0.59
1:C:174:TYR:CD1	5:C:744:HOH:O	2.52	0.59
1:D:110:PHE:HB2	1:D:146:MET:HE2	1.84	0.59
1:A:121:PRO:HA	1:A:150:ASP:OD2	2.03	0.58
1:C:70:GLY:HA2	1:C:106:ALA:HB1	1.86	0.58
1:C:174:TYR:HD1	5:C:744:HOH:O	1.86	0.58
1:D:308:GLU:CD	1:D:308:GLU:H	2.07	0.57
1:A:137:LEU:HD21	1:A:185:GLU:HB3	1.87	0.57
1:A:52:LYS:HD2	5:A:721:HOH:O	2.04	0.57
1:D:70:GLY:HA2	1:D:106:ALA:HB1	1.86	0.56
1:A:308:GLU:H	1:A:308:GLU:CD	2.07	0.56
1:A:184:LYS:NZ	1:A:184:LYS:HA	2.20	0.56
1:C:184:LYS:HA	1:C:184:LYS:NZ	2.21	0.56
1:C:308:GLU:H	1:C:308:GLU:CD	2.09	0.56
1:D:110:PHE:HB2	1:D:146:MET:CE	2.36	0.56
1:B:308:GLU:CD	1:B:308:GLU:H	2.08	0.55
1:B:201:MET:HB2	1:B:264:SER:HB3	1.88	0.55
1:D:184:LYS:HA	1:D:184:LYS:NZ	2.21	0.55
1:A:110:PHE:HB2	1:A:146:MET:CE	2.36	0.54
1:C:121:PRO:HA	1:C:150:ASP:OD2	2.07	0.54
1:C:137:LEU:HD21	1:C:185:GLU:HB3	1.89	0.54
1:A:262:ARG:NH1	1:A:268:SER:O	2.40	0.54
1:B:110:PHE:HB2	1:B:146:MET:CE	2.37	0.54
1:A:201:MET:HB2	1:A:264:SER:HB3	1.90	0.54
1:C:97:GLN:HE22	1:C:124:ALA:HB1	1.72	0.53
1:A:97:GLN:HE22	1:A:124:ALA:HB1	1.73	0.53
1:B:262:ARG:NH2	1:B:289:GLY:O	2.38	0.53
1:C:201:MET:HB2	1:C:264:SER:HB3	1.90	0.52
1:C:193:LYS:CB	1:C:216:ASP:HB3	2.40	0.52
1:D:137:LEU:HD21	1:D:185:GLU:HB3	1.91	0.52
1:C:43:SER:HB3	1:C:46:GLU:HG2	1.92	0.51
1:B:148:GLU:HB3	5:B:743:HOH:O	2.10	0.51
1:A:43:SER:HB3	1:A:46:GLU:HG2	1.92	0.51
1:C:137:LEU:HD11	1:C:185:GLU:HG2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:43:SER:HB3	1:D:46:GLU:HG2	1.93	0.51
1:C:291:ASP:HA	1:C:337:LYS:HE2	1.93	0.50
1:D:201:MET:HB2	1:D:264:SER:HB3	1.93	0.50
1:D:195:SER:HB2	3:D:701:DMA:H41	1.94	0.50
1:D:97:GLN:HE22	1:D:124:ALA:HB1	1.76	0.50
1:D:97:GLN:NE2	1:D:125:ASN:H	2.07	0.50
1:D:121:PRO:HA	1:D:150:ASP:OD2	2.11	0.50
1:C:98:ARG:HH21	1:C:130:GLN:NE2	2.09	0.50
1:C:262:ARG:NH2	1:C:289:GLY:O	2.35	0.50
1:D:27:THR:O	1:D:28:PHE:HB2	2.12	0.49
1:A:97:GLN:HE21	1:A:125:ASN:H	1.60	0.49
1:A:132:VAL:HG12	1:A:175:ALA:HB2	1.95	0.49
1:B:184:LYS:HZ2	1:B:184:LYS:HA	1.76	0.49
1:C:193:LYS:HB3	1:C:216:ASP:HB3	1.95	0.48
1:D:132:VAL:HG12	1:D:175:ALA:HB2	1.93	0.48
1:D:262:ARG:NH2	1:D:289:GLY:O	2.38	0.48
1:A:193:LYS:CB	1:A:216:ASP:HB3	2.42	0.48
1:D:58:ILE:HG21	1:D:91:PRO:HD3	1.95	0.48
1:B:97:GLN:HE22	1:B:124:ALA:HB1	1.79	0.48
1:B:97:GLN:NE2	1:B:125:ASN:H	2.10	0.48
1:B:245:LYS:HE3	5:B:748:HOH:O	2.13	0.47
1:B:43:SER:HB3	1:B:46:GLU:HG2	1.96	0.47
1:B:121:PRO:HA	1:B:150:ASP:OD2	2.15	0.47
1:B:27:THR:O	1:B:28:PHE:HB2	2.15	0.47
1:C:97:GLN:NE2	1:C:125:ASN:H	2.11	0.47
1:A:193:LYS:HB3	1:A:216:ASP:HB3	1.97	0.47
1:B:193:LYS:HB3	1:B:216:ASP:HB3	1.97	0.47
1:A:262:ARG:NH2	1:A:289:GLY:O	2.37	0.47
1:C:164:GLN:HB3	1:C:167:GLY:HA3	1.96	0.47
1:D:100:ALA:HB1	1:D:146:MET:HE3	1.97	0.47
1:D:262:ARG:NH1	1:D:268:SER:O	2.46	0.46
1:D:3:ASP:HA	1:D:6:ASN:H	1.80	0.46
1:A:220:GLN:HG2	1:A:253:PRO:HA	1.97	0.46
1:B:193:LYS:CB	1:B:216:ASP:HB3	2.45	0.46
1:C:141:GLN:O	1:C:145:GLN:HG3	2.16	0.46
1:D:193:LYS:CB	1:D:216:ASP:HB3	2.45	0.46
1:D:193:LYS:HB3	1:D:216:ASP:HB3	1.97	0.46
1:C:296:ALA:HB3	2:C:669:FMN:O3P	2.14	0.46
1:D:57:GLU:HG3	5:D:725:HOH:O	2.16	0.46
1:D:7:ARG:HD3	1:D:166:GLU:OE2	2.15	0.46
1:B:265:VAL:HG22	1:B:265:VAL:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:THR:O	1:A:28:PHE:HB2	2.16	0.45
1:A:114:ARG:HA	1:A:114:ARG:HD3	1.74	0.45
1:B:262:ARG:NH1	1:B:268:SER:O	2.47	0.45
1:B:296:ALA:HB3	2:B:669:FMN:O3P	2.16	0.45
1:D:137:LEU:HD11	1:D:185:GLU:HG2	1.97	0.45
1:B:284:LYS:O	1:B:288:LEU:HB2	2.17	0.45
1:C:58:ILE:HG21	1:C:91:PRO:HD3	1.98	0.45
1:C:132:VAL:HG12	1:C:175:ALA:HB2	1.98	0.44
1:A:137:LEU:HD11	1:A:185:GLU:HG2	1.99	0.44
1:C:114:ARG:HD3	1:C:114:ARG:HA	1.81	0.44
1:A:217:THR:HG23	1:A:270:LEU:HD11	1.99	0.43
1:B:265:VAL:CG2	1:B:268:SER:HB3	2.44	0.43
1:A:3:ASP:HA	1:A:6:ASN:H	1.82	0.43
1:C:362:GLU:O	1:C:366:LYS:HG3	2.17	0.43
1:B:114:ARG:HD3	1:B:114:ARG:HA	1.73	0.43
1:B:137:LEU:CD1	1:B:185:GLU:HB3	2.48	0.43
1:A:164:GLN:HB3	1:A:167:GLY:HA3	2.00	0.43
1:A:265:VAL:O	1:A:265:VAL:HG22	2.17	0.43
1:D:265:VAL:HG22	1:D:265:VAL:O	2.19	0.43
1:A:265:VAL:CG2	1:A:268:SER:HB3	2.41	0.43
1:B:20:VAL:N	5:B:710:HOH:O	2.51	0.43
1:C:284:LYS:O	1:C:288:LEU:HB2	2.19	0.43
1:A:296:ALA:HB3	2:A:669:FMN:O3P	2.19	0.42
1:A:8:LYS:NZ	3:A:701:DMA:O1A	2.47	0.42
1:B:181:ASP:HA	1:B:184:LYS:HG2	2.00	0.42
1:D:181:ASP:HA	1:D:184:LYS:HG2	2.00	0.42
1:D:284:LYS:O	1:D:288:LEU:HB2	2.19	0.42
1:A:332:ASP:HB2	5:A:705:HOH:O	2.19	0.42
1:B:137:LEU:HD13	1:B:185:GLU:HB3	2.01	0.42
1:C:24:SER:O	1:C:249:ASP:HB3	2.19	0.42
1:A:181:ASP:HA	1:A:184:LYS:HG2	2.02	0.42
1:A:76:ARG:NE	5:A:749:HOH:O	2.52	0.42
1:A:7:ARG:HD3	1:A:166:GLU:OE2	2.19	0.42
1:C:181:ASP:HA	1:C:184:LYS:HG2	2.00	0.42
1:D:114:ARG:HA	1:D:114:ARG:HD3	1.75	0.42
1:A:24:SER:O	1:A:249:ASP:HB3	2.20	0.41
1:C:262:ARG:NH1	1:C:268:SER:O	2.52	0.41
1:D:153:ALA:HA	1:D:191:ILE:O	2.20	0.41
1:A:284:LYS:O	1:A:288:LEU:HB2	2.20	0.41
1:D:131:LEU:HD23	1:D:131:LEU:HA	1.86	0.41
1:B:8:LYS:NZ	3:B:701:DMA:O3B	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:159:ALA:HB3	5:C:726:HOH:O	2.20	0.41
1:A:125:ASN:HA	1:A:153:ALA:O	2.21	0.41
1:B:3:ASP:HA	1:B:6:ASN:H	1.84	0.41
1:C:27:THR:O	1:C:28:PHE:HB2	2.21	0.41
1:D:107:ARG:HB3	1:D:107:ARG:HH21	1.86	0.41
1:A:184:LYS:HZ2	1:A:184:LYS:HA	1.85	0.41
1:C:128:MET:N	1:C:129:PRO:CD	2.84	0.41
1:B:3:ASP:HB2	1:B:6:ASN:CB	2.47	0.40
1:A:58:ILE:HG21	1:A:91:PRO:HD3	2.03	0.40
1:B:125:ASN:HA	1:B:153:ALA:O	2.21	0.40
1:B:128:MET:N	1:B:129:PRO:CD	2.84	0.40
1:B:365:ARG:O	1:B:366:LYS:HB2	2.22	0.40
1:A:114:ARG:HG2	1:A:148:GLU:HB2	2.04	0.40
1:A:131:LEU:HD23	1:A:131:LEU:HA	1.81	0.40
1:C:179:LEU:HD13	1:C:212:ILE:HD11	2.04	0.40
1:B:220:GLN:HG2	1:B:253:PRO:HA	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%)	343 (95%)	19 (5%)	0	100	100
1	B	362/368 (98%)	343 (95%)	18 (5%)	1 (0%)	44	81
1	C	362/368 (98%)	341 (94%)	21 (6%)	0	100	100
1	D	362/368 (98%)	344 (95%)	18 (5%)	0	100	100
All	All	1448/1472 (98%)	1371 (95%)	76 (5%)	1 (0%)	55	89

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	30	ASN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	298/302 (99%)	274 (92%)	24 (8%)	14	45
1	B	298/302 (99%)	275 (92%)	23 (8%)	15	48
1	C	298/302 (99%)	274 (92%)	24 (8%)	14	45
1	D	298/302 (99%)	273 (92%)	25 (8%)	13	43
All	All	1192/1208 (99%)	1096 (92%)	96 (8%)	14	45

All (96) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ASP
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
1	A	116	VAL
1	A	137	LEU
1	A	138	LYS
1	A	142	ASP
1	A	179	LEU
1	A	184	LYS
1	A	194	GLU
1	A	236	ARG
1	A	262	ARG
1	A	265	VAL
1	A	288	LEU
1	A	297	LEU
1	A	300	LEU

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Mol	Chain	Res	Type
1	A	308	GLU
1	A	359	SER
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	116	VAL
1	B	138	LYS
1	B	142	ASP
1	B	179	LEU
1	B	184	LYS
1	B	194	GLU
1	B	265	VAL
1	B	270	LEU
1	B	280	LEU
1	B	288	LEU
1	B	297	LEU
1	B	300	LEU
1	B	308	GLU
1	B	359	SER
1	B	360	ILE
1	B	366	LYS
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	98	ARG
1	C	116	VAL
1	C	137	LEU
1	C	138	LYS
1	C	142	ASP
1	C	176	LEU
1	C	179	LEU
1	C	184	LYS
1	C	185	GLU
1	C	194	GLU

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Mol	Chain	Res	Type
1	C	236	ARG
1	C	262	ARG
1	C	270	LEU
1	C	288	LEU
1	C	300	LEU
1	C	308	GLU
1	C	359	SER
1	C	360	ILE
1	D	3	ASP
1	D	4	ILE
1	D	8	LYS
1	D	46	GLU
1	D	52	LYS
1	D	76	ARG
1	D	90	ILE
1	D	116	VAL
1	D	137	LEU
1	D	138	LYS
1	D	142	ASP
1	D	179	LEU
1	D	184	LYS
1	D	185	GLU
1	D	186	LEU
1	D	194	GLU
1	D	265	VAL
1	D	270	LEU
1	D	280	LEU
1	D	288	LEU
1	D	297	LEU
1	D	300	LEU
1	D	308	GLU
1	D	359	SER
1	D	360	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	ASN
1	A	97	GLN
1	A	130	GLN
1	A	197	ASN
1	A	220	GLN

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Mol	Chain	Res	Type
1	A	312	GLN
1	B	97	GLN
1	B	130	GLN
1	B	164	GLN
1	B	220	GLN
1	B	312	GLN
1	C	97	GLN
1	C	130	GLN
1	C	164	GLN
1	C	220	GLN
1	C	312	GLN
1	D	97	GLN
1	D	130	GLN
1	D	220	GLN
1	D	312	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	FMN	A	669	-	31,33,33	1.55	4 (12%)	38,50,50	2.47	8 (21%)
3	DMA	A	701	4	12,13,13	0.60	0	12,19,19	1.22	1 (8%)
2	FMN	B	669	-	31,33,33	1.55	4 (12%)	38,50,50	2.29	9 (23%)
3	DMA	B	701	4	12,13,13	0.80	1 (8%)	12,19,19	1.30	1 (8%)
2	FMN	C	669	-	31,33,33	1.52	4 (12%)	38,50,50	2.37	11 (28%)
3	DMA	C	701	4	12,13,13	0.67	0	12,19,19	1.21	0
2	FMN	D	669	-	31,33,33	1.54	4 (12%)	38,50,50	2.24	9 (23%)
3	DMA	D	701	4	12,13,13	0.61	0	12,19,19	1.15	0

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	FMN	A	669	-	-	0/16/18/18	0/3/3/3
3	DMA	A	701	4	-	0/13/13/13	0/0/0/0
2	FMN	B	669	-	-	0/16/18/18	0/3/3/3
3	DMA	B	701	4	-	0/13/13/13	0/0/0/0
2	FMN	C	669	-	-	0/16/18/18	0/3/3/3
3	DMA	C	701	4	-	0/13/13/13	0/0/0/0
2	FMN	D	669	-	-	0/16/18/18	0/3/3/3
3	DMA	D	701	4	-	0/13/13/13	0/0/0/0

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	669	FMN	C10-N1	2.01	1.36	1.33
3	B	701	DMA	PB-O3A	2.14	1.63	1.60
2	B	669	FMN	C10-N1	2.22	1.36	1.33
2	D	669	FMN	C10-N1	2.78	1.37	1.33
2	A	669	FMN	C10-N1	2.81	1.37	1.33
2	D	669	FMN	C9A-N10	2.97	1.42	1.38
2	B	669	FMN	C9A-N10	3.53	1.43	1.38
2	A	669	FMN	C9A-N10	3.75	1.43	1.38
2	B	669	FMN	C4A-C10	3.96	1.48	1.41
2	C	669	FMN	C4-C4A	4.05	1.49	1.41
2	C	669	FMN	C9A-N10	4.11	1.44	1.38
2	C	669	FMN	C4A-C10	4.13	1.48	1.41
2	A	669	FMN	C4-C4A	4.37	1.49	1.41
2	A	669	FMN	C4A-C10	4.40	1.48	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	669	FMN	C4A-C10	4.43	1.48	1.41
2	D	669	FMN	C4-C4A	4.73	1.50	1.41
2	B	669	FMN	C4-C4A	4.74	1.50	1.41

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	669	FMN	C4-C4A-C10	-4.55	116.28	119.96
2	B	669	FMN	C4-C4A-C10	-4.42	116.39	119.96
2	A	669	FMN	C4A-C4-N3	-4.16	117.56	123.48
2	A	669	FMN	C4-C4A-C10	-4.16	116.60	119.96
2	D	669	FMN	C4-C4A-C10	-4.13	116.62	119.96
2	C	669	FMN	C4A-C10-N10	-4.05	117.71	120.52
2	A	669	FMN	C4A-C10-N10	-3.80	117.88	120.52
2	C	669	FMN	C4A-C4-N3	-3.75	118.15	123.48
2	B	669	FMN	C4A-C10-N10	-3.67	117.97	120.52
2	B	669	FMN	C4A-C4-N3	-3.60	118.36	123.48
2	D	669	FMN	C4A-C4-N3	-3.31	118.76	123.48
2	D	669	FMN	C4A-C10-N10	-3.04	118.41	120.52
2	C	669	FMN	O5'-P-O1P	-2.28	100.09	106.47
2	D	669	FMN	O3P-P-O5'	-2.14	101.05	106.73
3	A	701	DMA	C1-C2-C3	-2.11	123.35	126.68
2	C	669	FMN	C1'-N10-C10	-2.08	116.37	118.50
3	B	701	DMA	C5-C3-C4	2.03	119.34	114.60
2	B	669	FMN	P-O5'-C5'	2.27	124.54	118.30
2	C	669	FMN	P-O5'-C5'	2.34	124.75	118.30
2	B	669	FMN	C1'-N10-C9A	2.89	120.99	118.35
2	C	669	FMN	C5A-C9A-N10	2.99	119.88	117.66
2	D	669	FMN	C5A-C9A-N10	3.17	120.01	117.66
2	A	669	FMN	C5A-C9A-N10	3.19	120.03	117.66
2	B	669	FMN	C5A-C9A-N10	3.47	120.24	117.66
2	C	669	FMN	C4A-N5-C5A	3.64	120.60	116.76
2	D	669	FMN	C4A-N5-C5A	3.78	120.75	116.76
2	D	669	FMN	C1'-N10-C9A	3.81	121.84	118.35
2	C	669	FMN	C4-C4A-N5	4.10	123.18	118.68
2	A	669	FMN	C1'-N10-C9A	4.24	122.23	118.35
2	C	669	FMN	C1'-N10-C9A	4.25	122.24	118.35
2	B	669	FMN	C4A-N5-C5A	4.55	121.57	116.76
2	A	669	FMN	C4A-N5-C5A	4.59	121.61	116.76
2	B	669	FMN	C4-C4A-N5	4.81	123.95	118.68
2	A	669	FMN	C4-C4A-N5	4.87	124.02	118.68
2	D	669	FMN	C4-C4A-N5	5.28	124.47	118.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	669	FMN	C4-N3-C2	7.71	121.90	115.16
2	B	669	FMN	C4-N3-C2	7.84	122.01	115.16
2	C	669	FMN	C4-N3-C2	8.52	122.61	115.16
2	A	669	FMN	C4-N3-C2	9.44	123.42	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	669	FMN	1	0
3	A	701	DMA	2	0
2	B	669	FMN	1	0
3	B	701	DMA	2	0
2	C	669	FMN	1	0
3	C	701	DMA	1	0
3	D	701	DMA	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%)	-0.60	1 (0%) 93 82	31, 45, 66, 77	0
1	B	364/368 (98%)	-0.59	0 100 100	31, 45, 66, 77	0
1	C	364/368 (98%)	-0.61	0 100 100	31, 45, 66, 77	0
1	D	364/368 (98%)	-0.59	0 100 100	31, 45, 66, 77	0
All	All	1456/1472 (98%)	-0.60	1 (0%) 95 88	31, 45, 67, 77	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	ASP	2.4

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(\AA^2)	Q<0.9
4	MG	B	702	1/1	0.73	0.23	6.18	60,60,60,60	0
4	MG	D	702	1/1	0.79	0.21	1.18	60,60,60,60	0
2	FMN	D	669	31/31	0.97	0.18	0.86	43,45,46,46	0
2	FMN	B	669	31/31	0.98	0.16	0.83	43,45,46,46	0
2	FMN	C	669	31/31	0.97	0.15	0.29	43,45,46,46	0
2	FMN	A	669	31/31	0.97	0.15	0.18	43,45,46,46	0
4	MG	C	702	1/1	0.94	0.14	0.05	62,62,62,62	0
3	DMA	D	701	14/14	0.98	0.16	-0.40	59,63,64,64	0
3	DMA	C	701	14/14	0.98	0.14	-0.47	59,63,64,64	0
3	DMA	B	701	14/14	0.97	0.12	-0.82	59,63,64,65	0
3	DMA	A	701	14/14	0.98	0.12	-1.43	59,63,64,64	0
4	MG	A	702	1/1	0.80	0.10	-1.70	63,63,63,63	0

6.5 Other polymers [i](#)

There are no such residues in this entry.