



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 06:49 PM GMT

PDB ID : 3GFZ
Title : Klebsiella pneumoniae BlrP1 pH 6 manganese/cy-diGMP complex
Authors : Barends, T.; Hartmann, E.; Griesse, J.; Beitlich, T.; Kirienko, N.; Ryjenkov, D.; Reinstein, J.; Shoeman, R.; Gomelsky, M.; Schlichting, I.
Deposited on : 2009-02-27
Resolution : 2.05 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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
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) : rb-20026982

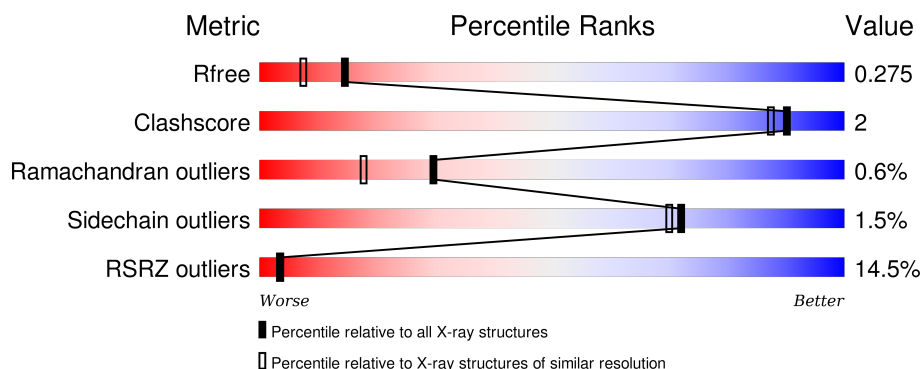
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	1192 (2.04-2.04)
Clashscore	102246	1269 (2.04-2.04)
Ramachandran outliers	100387	1258 (2.04-2.04)
Sidechain outliers	100360	1258 (2.04-2.04)
RSRZ outliers	91569	1194 (2.04-2.04)

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	413	
1	B	413	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	C2E	A	501	X	-	-	-
2	C2E	B	501	X	-	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6678 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.

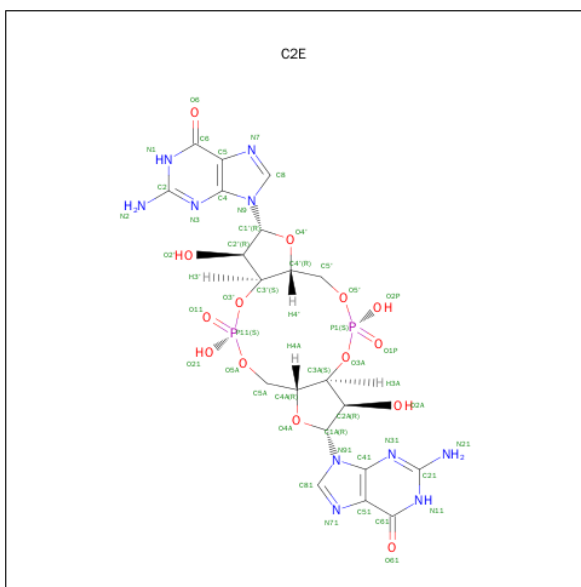
- Molecule 1 is a protein called *Klebsiella pneumoniae* BlrP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	393	Total	C	N	O	S	0	0	0
			3080	1973	533	556	18			
1	B	394	Total	C	N	O	S	0	0	0
			3094	1983	534	559	18			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	ILE	-	EXPRESSION TAG	UNP A6T8V8
A	-6	SER	-	EXPRESSION TAG	UNP A6T8V8
A	-5	GLU	-	EXPRESSION TAG	UNP A6T8V8
A	-4	PHE	-	EXPRESSION TAG	UNP A6T8V8
A	-3	GLY	-	EXPRESSION TAG	UNP A6T8V8
A	-2	SER	-	EXPRESSION TAG	UNP A6T8V8
A	-1	SER	-	EXPRESSION TAG	UNP A6T8V8
A	0	ARG	-	EXPRESSION TAG	UNP A6T8V8
B	-7	ILE	-	EXPRESSION TAG	UNP A6T8V8
B	-6	SER	-	EXPRESSION TAG	UNP A6T8V8
B	-5	GLU	-	EXPRESSION TAG	UNP A6T8V8
B	-4	PHE	-	EXPRESSION TAG	UNP A6T8V8
B	-3	GLY	-	EXPRESSION TAG	UNP A6T8V8
B	-2	SER	-	EXPRESSION TAG	UNP A6T8V8
B	-1	SER	-	EXPRESSION TAG	UNP A6T8V8
B	0	ARG	-	EXPRESSION TAG	UNP A6T8V8

- Molecule 2 is 9,9'-[(2R,3R,3AS,5S,7AR,9R,10R,10AS,12S,14AR)-3,5,10,12-TETRAHYDROXY-5,12-DIOXIDOOCTAHYDRO-2H,7H-DIFURO[3,2-D:3',2'-J][1,3,7,9,2,8]TETRAOXA DIPHOSPHACYCLODODECINE-2,9-DIYL]BIS(2-AMINO-1,9-DIHYDRO-6H-PURIN-6-ONE) (three-letter code: C2E) (formula: C₂₀H₂₄N₁₀O₁₄P₂).

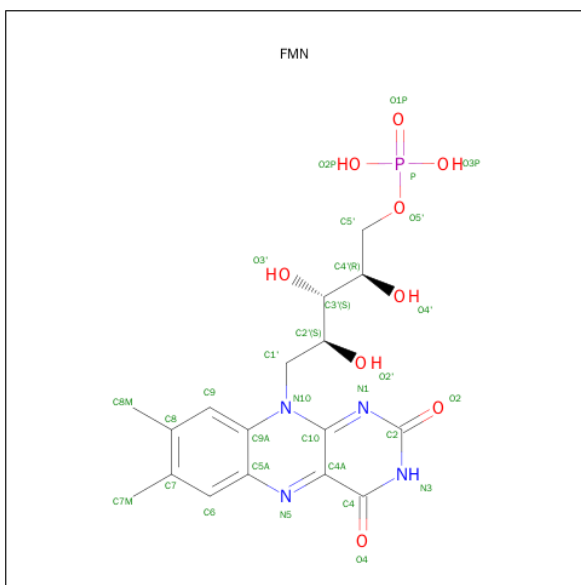


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 46	C 20	N 10	O 14	P 2	0	0
2	B	1	Total 46	C 20	N 10	O 14	P 2	0	0

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	2	Total Mn 2 2	0	0
3	A	2	Total Mn 2 2	0	0

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



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

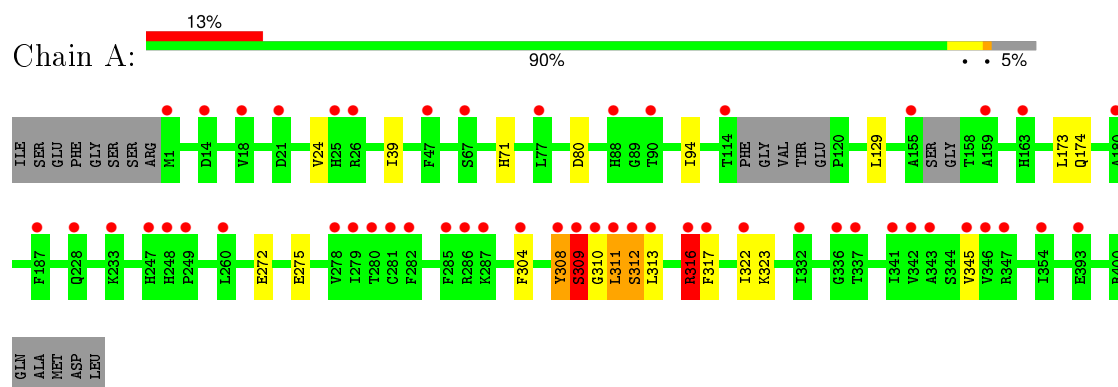
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	208	Total O 208 208	0	0
5	B	138	Total O 138 138	0	0

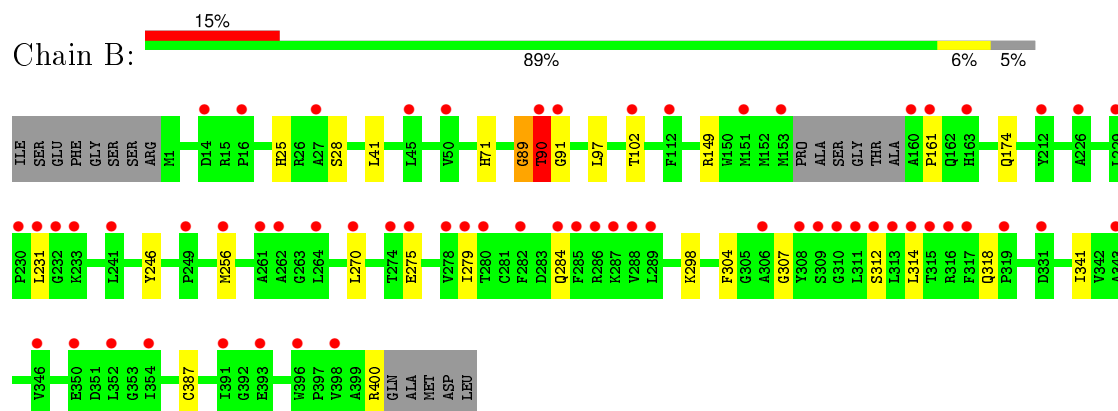
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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 ($\text{RSRZ} > 2$). 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: *Klebsiella pneumoniae* BlrP1



• Molecule 1: *Klebsiella pneumoniae* BlrP1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	68.45Å 97.09Å 127.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.54 – 2.05 48.55 – 2.05	Depositor EDS
% Data completeness (in resolution range)	97.1 (48.54-2.05) 97.1 (48.55-2.05)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.77 (at 2.05Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.229 , 0.272 0.232 , 0.275	Depositor DCC
R_{free} test set	2618 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	28.4	Xtriage
Anisotropy	0.522	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 39.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 52357 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6678	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.75% 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, 0.375 respectively for untwinned datasets, and 0.333, 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, MN, C2E

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	0.41	0/3148	0.65	1/4266 (0.0%)
1	B	0.39	0/3163	0.61	0/4287
All	All	0.40	0/6311	0.63	1/8553 (0.0%)

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	A	0	3
1	B	0	2
All	All	0	5

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	316	ARG	CB-CA-C	-5.16	100.08	110.40

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	308	TYR	Peptide
1	A	309	SER	Peptide
1	A	316	ARG	Peptide
1	B	89	GLY	Peptide
1	B	90	THR	Peptide

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	3080	0	3100	13	0
1	B	3094	0	3110	20	0
2	A	46	0	17	1	0
2	B	46	0	18	1	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	31	0	19	0	0
4	B	31	0	19	0	0
5	A	208	0	0	0	0
5	B	138	0	0	0	0
All	All	6678	0	6283	29	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 2.

All (29) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:90:THR:HG23	1:B:91:GLY:C	1.95	0.87
1:B:90:THR:HG23	1:B:91:GLY:O	1.83	0.77
1:A:310:GLY:O	1:A:313:LEU:N	2.27	0.64
1:B:314:LEU:O	1:B:318:GLN:NE2	2.36	0.59
1:B:89:GLY:O	1:B:90:THR:CB	2.54	0.56
1:A:311:LEU:HD23	1:B:341:ILE:HG23	1.87	0.56
1:B:149:ARG:O	1:B:400:ARG:N	2.39	0.55
1:B:28:SER:HB3	1:B:91:GLY:HA2	1.92	0.52
1:A:24:VAL:HG21	1:A:94:ILE:HB	1.91	0.52
1:B:41:LEU:HB3	1:B:97:LEU:HD21	1.92	0.51
1:A:317:PHE:N	1:A:317:PHE:CD1	2.80	0.50
1:B:89:GLY:O	1:B:90:THR:OG1	2.29	0.50
1:B:246:TYR:CD2	1:B:284:GLN:HB2	2.48	0.49
1:B:275:GLU:O	1:B:279:ILE:HG22	2.13	0.49
1:A:272:GLU:OE1	1:A:323:LYS:NZ	2.41	0.48
1:B:161:PRO:HG3	1:B:387:CYS:SG	2.54	0.47
1:A:39:ILE:HD11	1:A:129:LEU:HD21	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:28:SER:CB	1:B:91:GLY:HA2	2.47	0.44
1:A:304:PHE:CE1	1:A:310:GLY:HA3	2.52	0.44
1:A:174:GLN:OE1	2:A:501:C2E:H8	2.17	0.43
1:A:312:SER:HB3	1:B:307:GLY:O	2.18	0.43
1:B:246:TYR:CE2	1:B:284:GLN:HB2	2.54	0.42
1:A:311:LEU:HD13	1:B:304:PHE:CE2	2.55	0.42
1:A:308:TYR:HA	1:B:312:SER:OG	2.18	0.42
1:B:174:GLN:OE1	2:B:501:C2E:H8	2.19	0.42
1:A:275:GLU:CD	1:A:309:SER:HA	2.40	0.41
1:A:322:ILE:HD11	1:A:345:VAL:CG1	2.50	0.41
1:B:90:THR:CG2	1:B:91:GLY:C	2.78	0.40
1:B:90:THR:HA	1:B:91:GLY:O	2.21	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	387/413 (94%)	378 (98%)	7 (2%)	2 (0%)	34	22
1	B	390/413 (94%)	381 (98%)	6 (2%)	3 (1%)	24	12
All	All	777/826 (94%)	759 (98%)	13 (2%)	5 (1%)	30	18

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	90	THR
1	A	311	LEU
1	A	309	SER
1	B	102	THR
1	B	231	LEU

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	330/346 (95%)	325 (98%)	5 (2%)	72	70
1	B	332/346 (96%)	327 (98%)	5 (2%)	72	70
All	All	662/692 (96%)	652 (98%)	10 (2%)	72	70

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	71	HIS
1	A	80	ASP
1	A	173	LEU
1	A	312	SER
1	A	316	ARG
1	B	25	HIS
1	B	71	HIS
1	B	256	MET
1	B	270	LEU
1	B	298	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	66	GLN
1	B	268	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	C2E	A	501	3	44,52,52	2.98	9 (20%)	50,82,82	2.63	18 (36%)
4	FMN	A	504	-	32,33,33	1.23	4 (12%)	34,50,50	1.69	7 (20%)
2	C2E	B	501	3	44,52,52	2.92	9 (20%)	50,82,82	2.83	22 (44%)
4	FMN	B	504	-	32,33,33	1.19	3 (9%)	34,50,50	1.74	7 (20%)

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	C2E	A	501	3	1/1/10/10	0/22/62/62	0/6/7/7
4	FMN	A	504	-	-	0/18/18/18	0/3/3/3
2	C2E	B	501	3	1/1/10/10	0/22/62/62	0/6/7/7
4	FMN	B	504	-	-	0/18/18/18	0/3/3/3

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	C2E	C2'-C1'	-12.33	1.34	1.53
2	B	501	C2E	C2'-C1'	-12.31	1.34	1.53
2	A	501	C2E	C2A-C1A	-12.10	1.34	1.53
2	B	501	C2E	C2A-C1A	-11.59	1.35	1.53
2	A	501	C2E	O2'-C2'	-3.94	1.33	1.43
2	B	501	C2E	O2'-C2'	-3.83	1.33	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	C2E	O2A-C2A	-3.78	1.34	1.43
2	A	501	C2E	O2A-C2A	-3.60	1.34	1.43
2	B	501	C2E	C8-N7	-2.71	1.29	1.34
2	A	501	C2E	C2'-C3'	-2.56	1.47	1.53
2	A	501	C2E	C8-N7	-2.26	1.30	1.34
2	B	501	C2E	C2'-C3'	-2.20	1.48	1.53
2	B	501	C2E	P11-O11	2.16	1.59	1.51
2	A	501	C2E	O4A-C1A	2.17	1.44	1.41
2	A	501	C2E	P11-O11	2.22	1.59	1.51
4	A	504	FMN	C5A-N5	2.39	1.39	1.35
2	B	501	C2E	O4A-C1A	2.46	1.44	1.41
4	B	504	FMN	C1'-N10	2.69	1.51	1.48
4	A	504	FMN	C4-N3	2.82	1.38	1.33
4	A	504	FMN	C1'-N10	2.82	1.51	1.48
4	B	504	FMN	C4A-N5	3.02	1.38	1.33
4	B	504	FMN	C4-N3	3.19	1.38	1.33
4	A	504	FMN	C4A-N5	3.54	1.38	1.33
2	B	501	C2E	O4'-C1'	4.43	1.47	1.41
2	A	501	C2E	O4'-C1'	4.81	1.48	1.41

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	C2E	C4A-O4A-C1A	-7.68	101.50	109.64
2	A	501	C2E	C4A-O4A-C1A	-6.74	102.50	109.64
2	B	501	C2E	N31-C21-N11	-4.84	120.97	127.56
2	A	501	C2E	N31-C21-N11	-4.48	121.47	127.56
2	B	501	C2E	N3-C2-N1	-4.36	121.62	127.56
4	A	504	FMN	N3-C2-N1	-4.28	120.48	127.69
4	B	504	FMN	N3-C2-N1	-4.26	120.51	127.69
2	A	501	C2E	N3-C2-N1	-4.19	121.86	127.56
2	A	501	C2E	C5-C6-N1	-4.13	118.13	123.52
2	B	501	C2E	C5-C6-N1	-3.90	118.42	123.52
2	A	501	C2E	C51-C61-N11	-3.50	118.95	123.52
2	B	501	C2E	C51-C61-N11	-3.15	119.41	123.52
2	B	501	C2E	O5A-C5A-C4A	-3.08	97.99	109.09
4	B	504	FMN	C4A-C4-N3	-2.88	119.75	123.52
2	B	501	C2E	C1'-N9-C4	-2.81	123.67	126.81
2	B	501	C2E	C5'-C4'-C3'	-2.36	105.61	114.30
2	A	501	C2E	O5'-P1-O1P	-2.30	99.80	109.21
2	A	501	C2E	C5'-C4'-C3'	-2.27	105.95	114.30
4	A	504	FMN	C4A-C4-N3	-2.20	120.64	123.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	C2E	O3A-P1-O1P	-2.14	100.59	109.34
2	B	501	C2E	O5A-P11-O11	-2.02	100.95	109.21
4	B	504	FMN	C4-C4A-N5	2.05	121.19	118.70
2	B	501	C2E	O3A-C3A-C2A	2.07	119.42	111.73
2	B	501	C2E	C2A-C1A-N91	2.08	119.04	113.47
2	B	501	C2E	O4'-C4'-C5'	2.10	116.81	109.29
2	A	501	C2E	O4'-C4'-C5'	2.11	116.82	109.29
2	A	501	C2E	N21-C21-N11	2.12	120.70	117.20
2	B	501	C2E	O21-P11-O5A	2.29	119.16	108.24
4	A	504	FMN	C4-C4A-N5	2.33	121.53	118.70
2	A	501	C2E	C2A-C1A-N91	2.63	120.50	113.47
2	B	501	C2E	C2'-C1'-N9	2.65	120.56	113.47
4	B	504	FMN	C5A-C9A-N10	2.74	119.63	117.58
4	A	504	FMN	C5A-C9A-N10	2.74	119.63	117.58
2	A	501	C2E	C2'-C1'-N9	2.89	121.19	113.47
2	A	501	C2E	O21-P11-O5A	2.92	122.16	108.24
2	B	501	C2E	N21-C21-N11	2.94	122.05	117.20
4	B	504	FMN	C1'-N10-C9A	2.96	122.26	118.83
2	A	501	C2E	O4'-C1'-N9	2.99	113.76	108.11
4	A	504	FMN	C4A-N5-C5A	3.12	120.40	116.72
2	B	501	C2E	C3'-C2'-C1'	3.30	107.24	100.06
4	B	504	FMN	C4A-N5-C5A	3.33	120.65	116.72
2	A	501	C2E	C3'-C2'-C1'	3.40	107.45	100.06
4	A	504	FMN	C1'-N10-C9A	3.62	123.03	118.83
2	A	501	C2E	C61-N11-C21	3.76	120.29	115.88
2	B	501	C2E	C61-N11-C21	3.94	120.50	115.88
2	B	501	C2E	O2'-C2'-C1'	4.12	124.51	111.61
2	A	501	C2E	O2'-C2'-C1'	4.36	125.26	111.61
2	B	501	C2E	C6-N1-C2	4.42	121.06	115.88
4	A	504	FMN	C4-N3-C2	4.54	118.94	115.16
2	B	501	C2E	O4'-C1'-N9	4.82	117.20	108.11
2	A	501	C2E	C6-N1-C2	4.95	121.69	115.88
4	B	504	FMN	C4-N3-C2	5.63	119.86	115.16
2	A	501	C2E	O4A-C1A-N91	8.95	125.02	108.11
2	B	501	C2E	O4A-C1A-N91	9.34	125.76	108.11

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	501	C2E	C1A
2	B	501	C2E	C1A

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	C2E	1	0
2	B	501	C2E	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 ⓘ

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	393/413 (95%)	1.13	52 (13%) 4 4	35, 41, 50, 55	0
1	B	394/413 (95%)	1.16	62 (15%) 3 2	34, 41, 49, 53	0
All	All	787/826 (95%)	1.14	114 (14%) 3 3	34, 41, 50, 55	0

All (114) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	308	TYR	10.0
1	B	279	ILE	9.2
1	B	308	TYR	8.6
1	A	281	CYS	8.6
1	A	282	PHE	8.3
1	A	279	ILE	7.9
1	B	284	GLN	7.0
1	A	247	HIS	7.0
1	B	311	LEU	6.9
1	B	282	PHE	6.4
1	A	312	SER	6.1
1	B	102	THR	5.9
1	B	14	ASP	5.6
1	A	311	LEU	5.3
1	B	316	ARG	5.0
1	B	231	LEU	4.7
1	B	161	PRO	4.4
1	B	232	GLY	4.4
1	A	248	HIS	4.4
1	B	264	LEU	4.4
1	B	285	PHE	4.3
1	B	249	PRO	4.2
1	B	313	LEU	4.2
1	B	233	LYS	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	18	VAL	3.9
1	A	159	ALA	3.8
1	B	286	ARG	3.8
1	B	153	MET	3.7
1	A	280	THR	3.7
1	B	90	THR	3.7
1	A	180	ALA	3.6
1	A	26	ARG	3.5
1	B	229	LEU	3.5
1	B	314	LEU	3.5
1	A	278	VAL	3.5
1	A	233	LYS	3.5
1	A	1	MET	3.4
1	B	315	THR	3.4
1	B	230	PRO	3.2
1	A	114	THR	3.2
1	A	322	ILE	3.1
1	B	27	ALA	3.1
1	B	112	PHE	3.1
1	B	312	SER	3.1
1	B	280	THR	3.0
1	A	342	VAL	3.0
1	B	398	VAL	3.0
1	A	310	GLY	3.0
1	B	354	ILE	2.9
1	B	261	ALA	2.9
1	A	67	SER	2.9
1	A	341	ILE	2.9
1	A	14	ASP	2.8
1	A	317	PHE	2.8
1	B	319	PRO	2.8
1	B	256	MET	2.8
1	A	309	SER	2.8
1	A	316	ARG	2.7
1	B	287	LYS	2.7
1	A	285	PHE	2.7
1	B	163	HIS	2.7
1	B	262	ALA	2.7
1	B	306	ALA	2.7
1	A	393	GLU	2.7
1	A	346	VAL	2.6
1	B	309	SER	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	88	HIS	2.6
1	B	160	ALA	2.6
1	B	45	LEU	2.6
1	B	278	VAL	2.5
1	A	90	THR	2.5
1	A	163	HIS	2.5
1	B	352	LEU	2.5
1	A	343	ALA	2.5
1	A	332	ILE	2.5
1	B	289	LEU	2.4
1	A	249	PRO	2.4
1	A	77	LEU	2.4
1	B	393	GLU	2.4
1	A	336	GLY	2.4
1	B	343	ALA	2.3
1	A	337	THR	2.3
1	B	350	GLU	2.3
1	A	228	GLN	2.3
1	A	25	HIS	2.2
1	B	241	LEU	2.2
1	A	313	LEU	2.2
1	A	187	PHE	2.2
1	B	275	GLU	2.2
1	A	286	ARG	2.2
1	A	345	VAL	2.2
1	A	347	ARG	2.1
1	B	310	GLY	2.1
1	B	16	PRO	2.1
1	B	391	ILE	2.1
1	A	21	ASP	2.1
1	B	396	TRP	2.1
1	B	226	ALA	2.1
1	B	274	THR	2.1
1	A	287	LYS	2.1
1	A	155	ALA	2.1
1	A	260	LEU	2.1
1	B	270	LEU	2.1
1	B	50	VAL	2.1
1	B	288	VAL	2.1
1	A	304	PHE	2.1
1	B	317	PHE	2.1
1	A	354	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	331	ASP	2.0
1	B	346	VAL	2.0
1	A	47	PHE	2.0
1	B	151	MET	2.0
1	B	91	GLY	2.0
1	B	212	TYR	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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
4	FMN	A	504	31/31	0.87	0.17	-0.12	34,37,52,52	0
4	FMN	B	504	31/31	0.88	0.14	-0.83	36,38,52,53	0
2	C2E	B	501	46/46	0.92	0.11	-1.58	36,40,43,46	0
2	C2E	A	501	46/46	0.92	0.11	-2.22	36,39,44,47	0
3	MN	B	502	1/1	0.99	0.03	-7.08	41,41,41,41	0
3	MN	A	502	1/1	0.96	0.05	-8.03	43,43,43,43	0
3	MN	A	503	1/1	0.92	0.07	-	49,49,49,49	0
3	MN	B	503	1/1	0.93	0.14	-	53,53,53,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.