



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 13, 2018 – 03:59 pm GMT

PDB ID : 4Y9U
Title : rat CYPOR mutant - G143del
Authors : Xia, C.; Kim, J.J.P.
Deposited on : 2015-02-17
Resolution : 1.95 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : trunk31020
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk31020

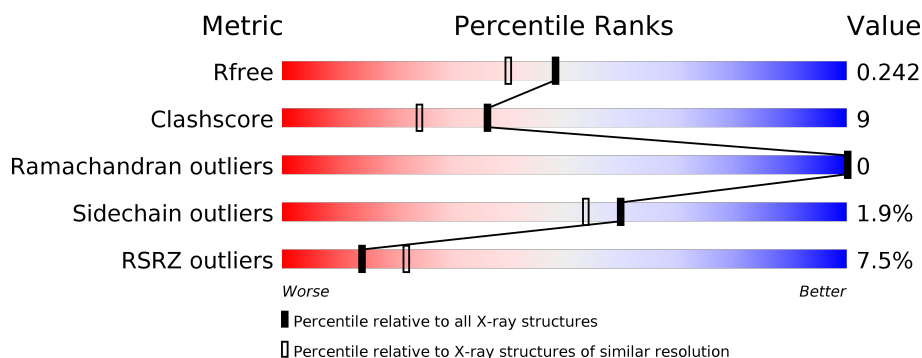
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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}	111664	2220 (1.96-1.96)
Clashscore	122126	2333 (1.96-1.96)
Ramachandran outliers	120053	2314 (1.96-1.96)
Sidechain outliers	120020	2314 (1.96-1.96)
RSRZ outliers	108989	2174 (1.96-1.96)

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	621	<div> <div>2%</div> <div> <div></div> <div>83%</div> <div>14%</div> <div>..</div> </div> </div>
1	B	621	<div> <div>12%</div> <div> <div></div> <div>78%</div> <div>17%</div> <div>..</div> </div> </div>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 10985 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.

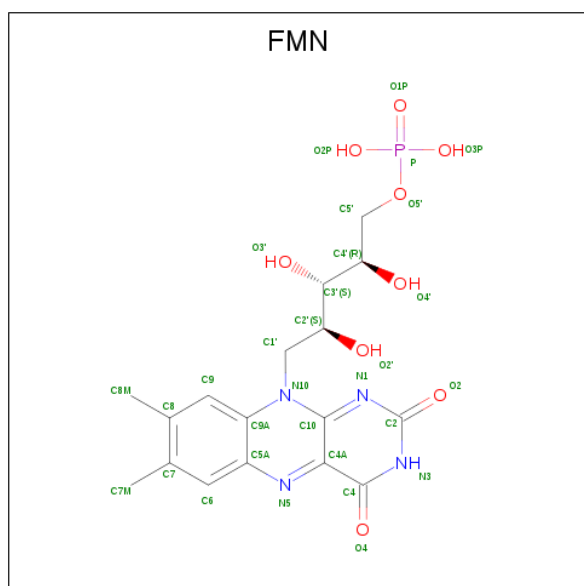
- Molecule 1 is a protein called NADPH–cytochrome P450 reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	608	Total	C	N	O	S	0	0	0
			4872	3090	840	919	23			
1	B	600	Total	C	N	O	S	0	0	0
			4804	3049	832	900	23			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLY	deletion	UNP P00388
B	?	-	GLY	deletion	UNP P00388

- Molecule 2 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C₁₇H₂₁N₄O₉P).



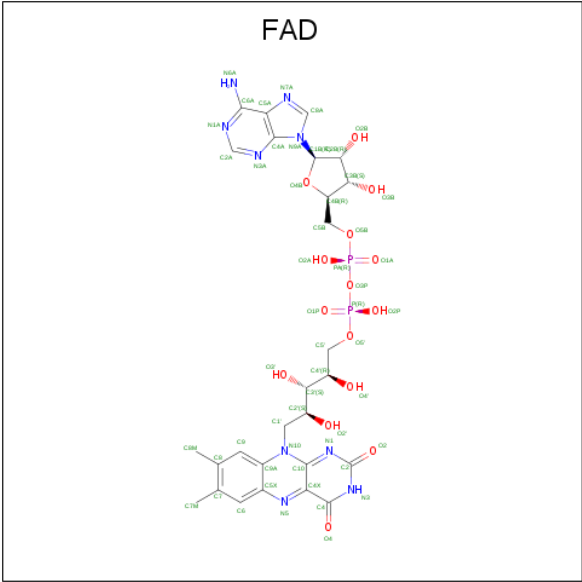
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

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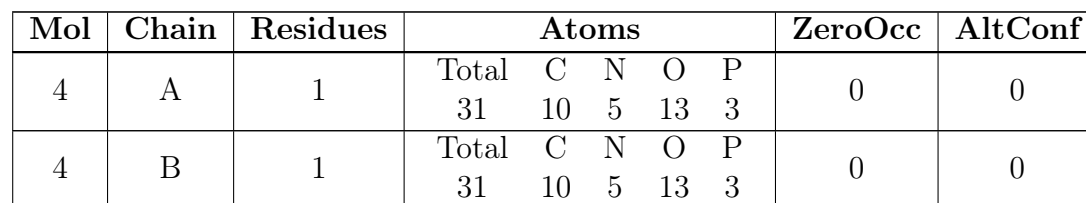
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C₂₇H₃₃N₉O₁₅P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 4 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C₂₁H₂₈N₇O₁₇P₃).



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- Diagram illustrating the Lewis structure of the phosphate ion (PO_4^{3-}). The central phosphorus atom (P) is bonded to four oxygen atoms (O). The bonds are represented by lines: a double bond (orange) to the right (O1) and three single bonds (purple) to the top (O3), left (O2), and bottom (O4). Each oxygen atom has a lone pair (green). The phosphorus atom has a lone pair (green P). The overall charge is indicated by three negative signs (red O⁻) on the single-bonded oxygens.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	O	P	0	0
			5	4	1		

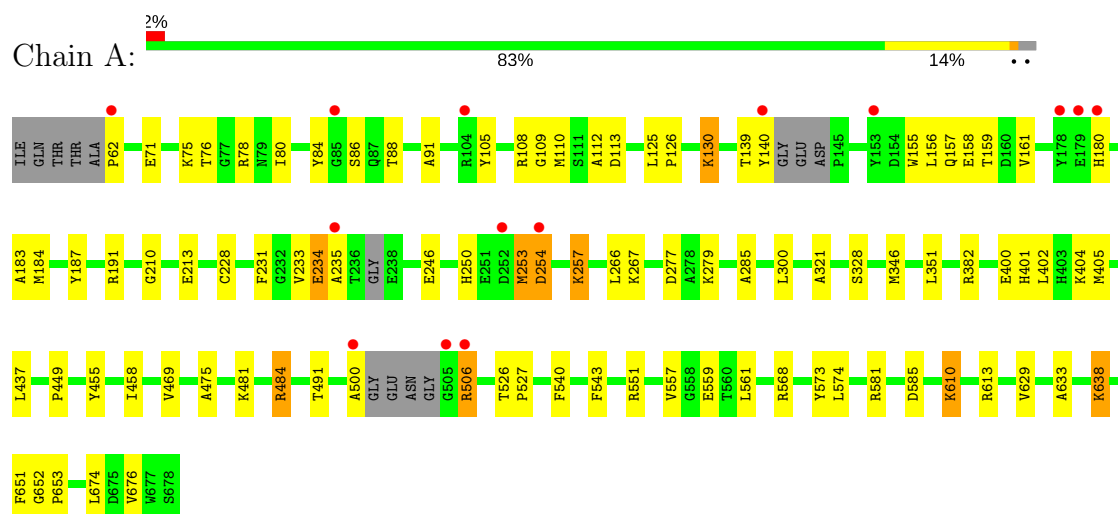
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	609	Total 609	O 609	0	0
6	B	465	Total 465	O 465	0	0

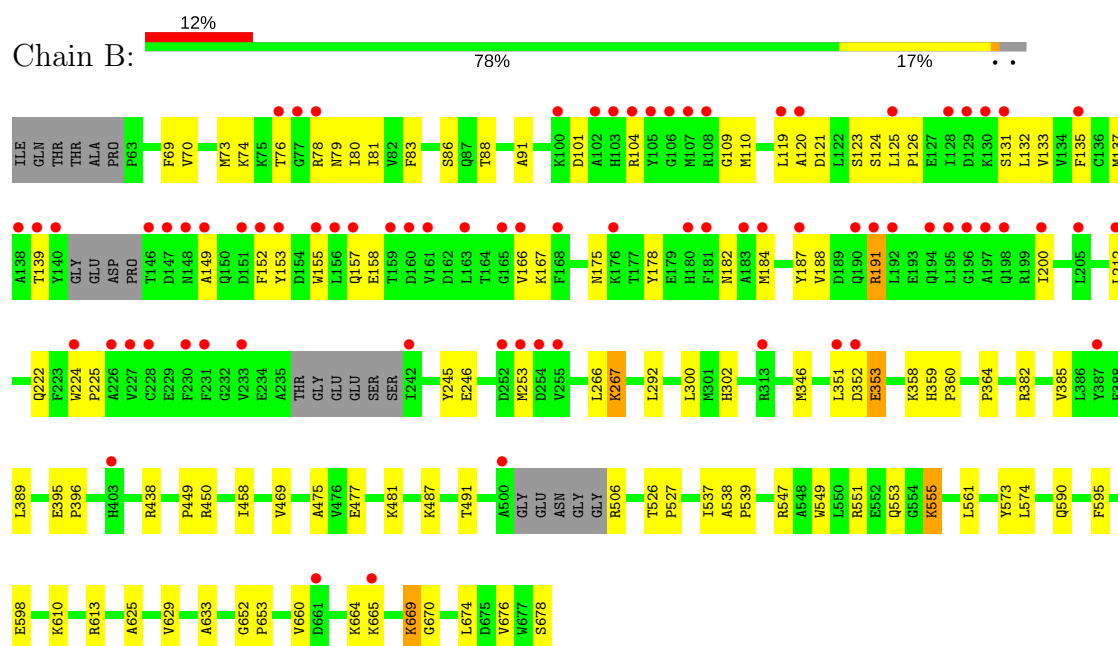
3 Residue-property plots [i](#)

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: NADPH-cytochrome P450 reductase



• Molecule 1: NADPH-cytochrome P450 reductase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	101.79Å 115.05Å 119.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.02 – 1.95 47.02 – 1.94	Depositor EDS
% Data completeness (in resolution range)	95.5 (47.02-1.95) 94.9 (47.02-1.94)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.23 (at 1.94Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.203 , 0.241 0.204 , 0.242	Depositor DCC
R_{free} test set	4923 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	31.6	Xtriage
Anisotropy	0.302	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 48.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.006 for -h,l,k	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10985	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.90% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FMN, PO4, NAP, FAD

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	0.36	0/4988	0.58	2/6747 (0.0%)
1	B	0.33	0/4918	0.57	1/6651 (0.0%)
All	All	0.35	0/9906	0.58	3/13398 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	210	GLY	N-CA-C	-5.38	99.65	113.10
1	B	158	GLU	N-CA-C	5.24	125.15	111.00
1	A	158	GLU	N-CA-C	5.05	124.64	111.00

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	4872	0	4724	77	0
1	B	4804	0	4650	90	0
2	A	31	0	19	0	0
2	B	31	0	19	2	0
3	A	53	0	31	0	0
3	B	53	0	31	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	31	0	11	0	0
4	B	31	0	11	0	0
5	B	5	0	0	0	0
6	A	609	0	0	9	0
6	B	465	0	0	9	0
All	All	10985	0	9496	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 9.

The worst 5 of 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:A:159:THR:OG1	1:A:161:VAL:HG13	1.56	1.05
1:B:70:VAL:HA	1:B:73:MET:HE2	1.50	0.93
1:A:257:LYS:HA	1:A:266:LEU:HD21	1.53	0.90
1:B:86:SER:HB3	1:B:91:ALA:HB3	1.61	0.83
1:A:159:THR:HG1	1:A:161:VAL:HG13	1.44	0.79

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	600/621 (97%)	586 (98%)	14 (2%)	0	100	100
1	B	592/621 (95%)	570 (96%)	22 (4%)	0	100	100
All	All	1192/1242 (96%)	1156 (97%)	36 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	519/531 (98%)	508 (98%)	11 (2%)	56	49
1	B	507/531 (96%)	499 (98%)	8 (2%)	65	61
All	All	1026/1062 (97%)	1007 (98%)	19 (2%)	60	54

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	573	TYR
1	A	638	LYS
1	B	353	GLU
1	A	506	ARG
1	B	555	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

7 ligands are modelled in this entry.

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	701	-	31,33,33	2.92	11 (35%)	39,50,50	3.33	16 (41%)
3	FAD	A	702	-	51,58,58	2.59	11 (21%)	57,89,89	2.35	10 (17%)
4	NAP	A	703	-	29,33,52	1.69	4 (13%)	34,52,80	2.56	4 (11%)
2	FMN	B	701	-	31,33,33	2.93	13 (41%)	39,50,50	3.35	15 (38%)
3	FAD	B	702	-	51,58,58	2.58	11 (21%)	57,89,89	2.33	10 (17%)
4	NAP	B	703	-	29,33,52	1.70	5 (17%)	34,52,80	2.55	4 (11%)
5	PO4	B	704	-	4,4,4	1.35	0	6,6,6	0.39	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	701	-	-	0/16/18/18	0/3/3/3
3	FAD	A	702	-	-	0/28/50/50	0/6/6/6
4	NAP	A	703	-	-	0/17/37/67	0/3/3/5
2	FMN	B	701	-	-	0/16/18/18	0/3/3/3
3	FAD	B	702	-	-	0/28/50/50	0/6/6/6
4	NAP	B	703	-	-	0/17/37/67	0/3/3/5
5	PO4	B	704	-	-	0/0/0/0	0/0/0/0

The worst 5 of 55 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	701	FMN	C8M-C8	-6.55	1.38	1.51
2	A	701	FMN	C8M-C8	-6.22	1.38	1.51
3	A	702	FAD	C8M-C8	-5.88	1.39	1.51
3	B	702	FAD	C7M-C7	-5.85	1.39	1.51
3	A	702	FAD	C7M-C7	-5.84	1.39	1.51

The worst 5 of 59 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	702	FAD	N3A-C2A-N1A	-13.46	117.34	128.86
3	B	702	FAD	N3A-C2A-N1A	-13.22	117.55	128.86
4	A	703	NAP	N3A-C2A-N1A	-13.05	117.69	128.86
4	B	703	NAP	N3A-C2A-N1A	-13.05	117.70	128.86
2	B	701	FMN	C4-C4A-C10	-6.79	114.88	119.95

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	701	FMN	2	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	608/621 (97%)	0.23	14 (2%) 60 70	22, 32, 52, 81	0
1	B	600/621 (96%)	0.72	76 (12%) 3 6	22, 36, 71, 101	0
All	All	1208/1242 (97%)	0.47	90 (7%) 14 22	22, 33, 67, 101	0

The worst 5 of 90 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	200	ILE	7.6
1	B	195	LEU	6.7
1	B	104	ARG	6.3
1	B	192	LEU	6.1
1	A	235	ALA	6.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	PO4	B	704	5/5	0.76	0.23	106,106,107,107	0
2	FMN	B	701	31/31	0.87	0.24	60,70,74,74	0
2	FMN	A	701	31/31	0.94	0.14	32,38,41,43	0
4	NAP	B	703	31/48	0.97	0.10	21,25,42,50	0
3	FAD	A	702	53/53	0.98	0.11	21,25,32,37	0
4	NAP	A	703	31/48	0.98	0.10	22,24,36,46	0
3	FAD	B	702	53/53	0.98	0.12	20,24,32,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.