



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:43 PM GMT

PDB ID : 4FWF  
Title : Complex structure of LSD2/AOF1/KDM1b with H3K4 mimic  
Authors : Zhang, Q.; Chen, Z.  
Deposited on : 2012-07-01  
Resolution : 2.70 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](mailto: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.

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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

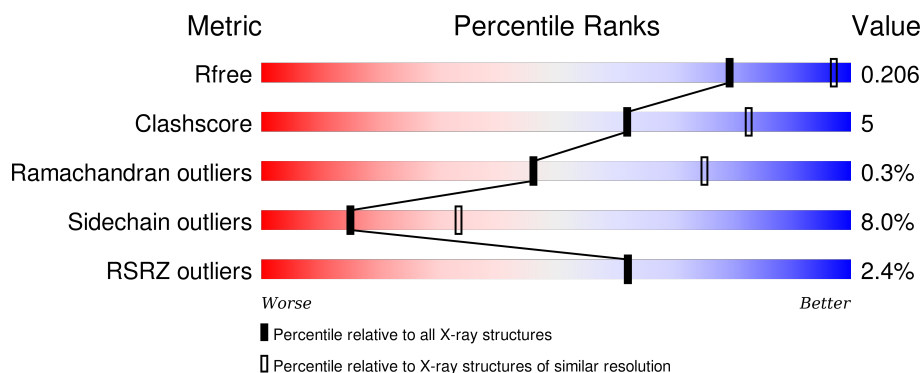
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*


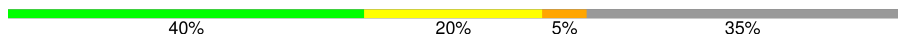
The reported resolution of this entry is 2.70 Å.

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	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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  $\geq 3$ , 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	796	 2% 77% 15% • 7%
2	E	20	 40% 20% 5% 35%

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5826 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 Lysine-specific histone demethylase 1B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	739	Total	C	N	O	S	0	0	0
			5654	3618	959	1037	40			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	27	GLY	-	EXPRESSION TAG	UNP Q8NB78
A	28	HIS	-	EXPRESSION TAG	UNP Q8NB78
A	29	MET	-	EXPRESSION TAG	UNP Q8NB78

- Molecule 2 is a protein called Histone H3.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	13	Total	C	N	O	S	0	0	0
			83	47	17	18	1			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	4	MET	LYS	ENGINEERED MUTATION	UNP P68431

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	Zn	0	0
			3	3		

- Molecule 4 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: C<sub>27</sub>H<sub>33</sub>N<sub>9</sub>O<sub>15</sub>P<sub>2</sub>).



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

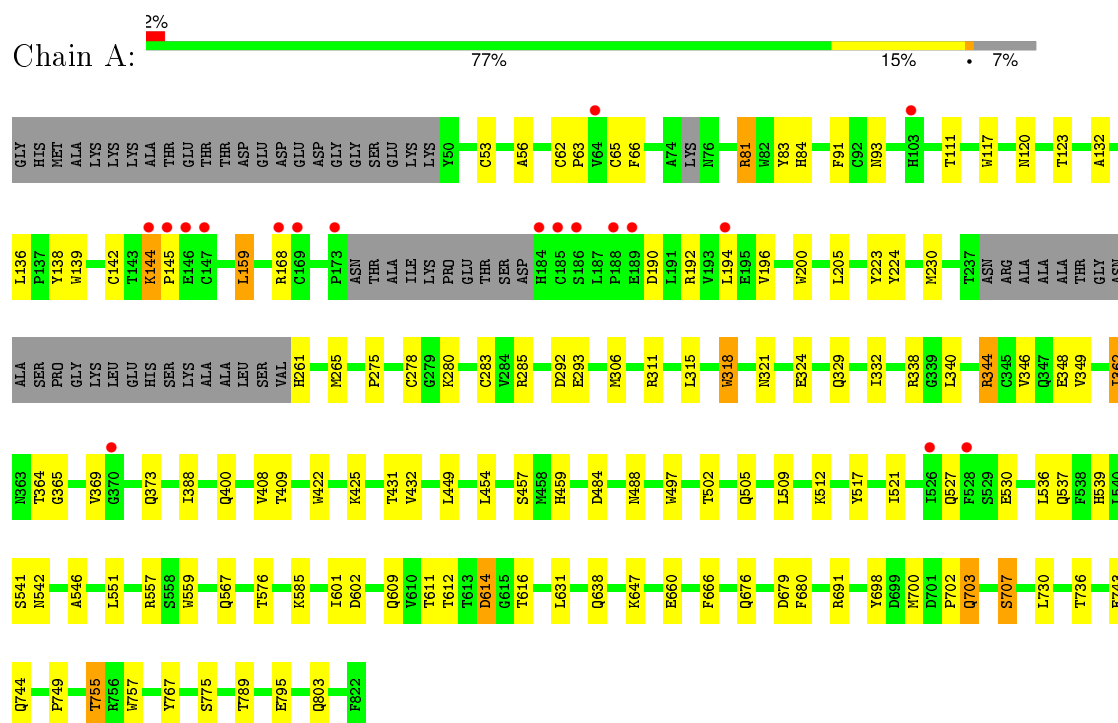
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	33	Total	0	0
			33		

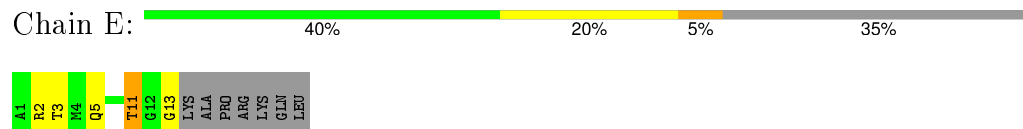
### 3 Residue-property plots [i](#)

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 ( $RSRZ > 2$ ). 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: Lysine-specific histone demethylase 1B



- Molecule 2: Histone H3.1



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	110.44Å 98.54Å 101.36Å 90.00° 96.08° 90.00°	Depositor
Resolution (Å)	50.00 – 2.70 42.98 – 2.65	Depositor EDS
% Data completeness (in resolution range)	93.2 (50.00-2.70) 90.6 (42.98-2.65)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	0.05	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.41 (at 2.65Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, $R_{free}$	0.206 , 0.237 0.205 , 0.206	Depositor DCC
$R_{free}$ test set	1407 reflections (5.33%)	DCC
Wilson B-factor (Å <sup>2</sup> )	34.4	Xtriage
Anisotropy	0.134	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 42.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 28515 reflections	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	5826	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: ZN, 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	0.55	6/5797 (0.1%)	0.60	0/7883
2	E	0.47	0/82	0.65	0/109
All	All	0.55	6/5879 (0.1%)	0.60	0/7992

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	497	TRP	CD2-CE2	5.54	1.48	1.41
1	A	422	TRP	CD2-CE2	5.41	1.47	1.41
1	A	559	TRP	CD2-CE2	5.36	1.47	1.41
1	A	200	TRP	CD2-CE2	5.24	1.47	1.41
1	A	139	TRP	CD2-CE2	5.16	1.47	1.41
1	A	318	TRP	CD2-CE2	5.01	1.47	1.41

There are no bond angle outliers.

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	5654	0	5373	59	0
2	E	83	0	78	6	0
3	A	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	53	0	31	2	0
5	A	33	0	0	0	0
All	All	5826	0	5482	61	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 5.

All (61) 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:81:ARG:HG2	1:A:81:ARG:HH11	1.12	1.08
2:E:2:ARG:HH22	2:E:13:GLY:H	1.17	0.89
1:A:81:ARG:NH1	1:A:81:ARG:HG2	1.90	0.77
1:A:83:TYR:HE2	1:A:93:ASN:HD22	1.38	0.70
1:A:703:GLN:HA	1:A:703:GLN:HE21	1.57	0.69
1:A:132:ALA:HA	1:A:136:LEU:HD12	1.75	0.68
1:A:755:THR:HG23	1:A:757:TRP:CD1	2.30	0.67
1:A:459:HIS:HE1	1:A:679:ASP:OD1	1.80	0.64
1:A:660:GLU:OE1	1:A:755:THR:HG22	1.99	0.63
1:A:81:ARG:CG	1:A:81:ARG:HH11	2.01	0.62
1:A:612:THR:HG22	1:A:614:ASP:H	1.64	0.61
1:A:369:VAL:HG22	1:A:373:GLN:HB2	1.82	0.60
1:A:541:SER:HB3	1:A:691:ARG:HG2	1.82	0.60
1:A:223:TYR:CE2	1:A:275:PRO:HD3	2.37	0.60
1:A:755:THR:CG2	1:A:757:TRP:CD1	2.86	0.59
1:A:567:GLN:OE1	2:E:3:THR:HG21	2.04	0.57
1:A:795:GLU:HB2	4:A:904:FAD:H5'2	1.87	0.57
1:A:117:TRP:HE1	1:A:123:THR:HG23	1.72	0.55
1:A:285:ARG:O	1:A:311:ARG:NH2	2.41	0.54
1:A:614:ASP:C	1:A:614:ASP:OD2	2.48	0.52
1:A:280:LYS:HG2	1:A:283:CYS:SG	2.50	0.51
1:A:196:VAL:HG12	1:A:344:ARG:HG2	1.92	0.51
1:A:509:LEU:HD23	1:A:551:LEU:HD22	1.92	0.51
1:A:332:ILE:HG12	1:A:346:VAL:HG13	1.93	0.50
1:A:546:ALA:HB2	2:E:5:GLN:HG3	1.93	0.49
1:A:537:GLN:OE1	1:A:691:ARG:HD3	2.13	0.49
1:A:660:GLU:OE1	1:A:755:THR:CG2	2.61	0.48
1:A:459:HIS:CE1	1:A:679:ASP:OD1	2.65	0.48
1:A:190:ASP:OD1	1:A:192:ARG:HD3	2.14	0.48
1:A:454:LEU:HD21	1:A:585:LYS:HG2	1.95	0.47
1:A:364:THR:HG22	1:A:400:GLN:OE1	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:315:LEU:HA	1:A:362:ILE:HD11	1.96	0.47
1:A:306:MET:HE2	1:A:348:GLU:HG3	1.97	0.47
2:E:2:ARG:NH2	2:E:13:GLY:H	1.99	0.47
1:A:318:TRP:HB2	1:A:362:ILE:HG13	1.98	0.46
1:A:364:THR:HB	1:A:365:GLY:H	1.53	0.45
1:A:698:TYR:HB3	1:A:700:MET:CE	2.47	0.45
1:A:120:ASN:O	1:A:224:TYR:HD1	2.00	0.45
1:A:81:ARG:NH1	1:A:81:ARG:CG	2.67	0.44
1:A:66:PHE:CE1	1:A:91:PHE:HB3	2.53	0.44
1:A:62:CYS:HA	1:A:63:PRO:HD3	1.74	0.44
1:A:803:GLN:O	4:A:904:FAD:H1'2	2.18	0.43
1:A:459:HIS:CD2	1:A:702:PRO:HB3	2.54	0.43
1:A:142:CYS:SG	1:A:168:ARG:HA	2.59	0.43
1:A:144:LYS:HA	1:A:145:PRO:HD3	1.79	0.43
1:A:138:TYR:CG	1:A:159:LEU:HB2	2.54	0.43
1:A:293:GLU:OE2	1:A:311:ARG:HD3	2.19	0.42
1:A:602:ASP:HB3	1:A:609:GLN:HB3	2.02	0.42
1:A:315:LEU:HD23	1:A:362:ILE:CD1	2.50	0.42
1:A:755:THR:CG2	1:A:757:TRP:HD1	2.31	0.42
1:A:542:ASN:HB3	2:E:5:GLN:HE21	1.85	0.42
1:A:517:TYR:O	1:A:521:ILE:HG12	2.20	0.41
1:A:502:THR:OG1	1:A:505:GLN:HG3	2.20	0.41
1:A:321:ASN:HD21	1:A:324:GLU:CD	2.23	0.41
1:A:730:LEU:HD11	1:A:749:PRO:HG3	2.02	0.41
1:A:484:ASP:OD1	1:A:539:HIS:CE1	2.73	0.41
1:A:53:CYS:SG	1:A:84:HIS:HB2	2.61	0.41
1:A:388:ILE:CD1	1:A:601:ILE:HD11	2.51	0.41
1:A:666:PHE:HB2	1:A:707:SER:HB2	2.03	0.41
1:A:136:LEU:O	1:A:338:ARG:HD3	2.21	0.40
1:A:488:ASN:ND2	2:E:11:THR:H	2.19	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	731/796 (92%)	695 (95%)	34 (5%)	2 (0%)	46	75
2	E	11/20 (55%)	10 (91%)	1 (9%)	0	100	100
All	All	742/816 (91%)	705 (95%)	35 (5%)	2 (0%)	46	75

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	743	GLU
1	A	56	ALA

### 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	580/678 (86%)	534 (92%)	46 (8%)	15	34
2	E	7/15 (47%)	6 (86%)	1 (14%)	4	10
All	All	587/693 (85%)	540 (92%)	47 (8%)	15	33

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	CYS
1	A	81	ARG
1	A	111	THR
1	A	144	LYS
1	A	159	LEU
1	A	194	LEU
1	A	205	LEU
1	A	230	MET
1	A	261	HIS
1	A	265	MET
1	A	278	CYS

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Mol	Chain	Res	Type
1	A	292	ASP
1	A	329	GLN
1	A	340	LEU
1	A	344	ARG
1	A	349	VAL
1	A	362	ILE
1	A	408	VAL
1	A	409	THR
1	A	425	LYS
1	A	431	THR
1	A	432	VAL
1	A	449	LEU
1	A	457	SER
1	A	512	LYS
1	A	527	GLN
1	A	530	GLU
1	A	536	LEU
1	A	557	ARG
1	A	576	THR
1	A	611	THR
1	A	614	ASP
1	A	616	THR
1	A	631	LEU
1	A	638	GLN
1	A	647	LYS
1	A	676	GLN
1	A	680	PHE
1	A	703	GLN
1	A	707	SER
1	A	736	THR
1	A	744	GLN
1	A	755	THR
1	A	767	TYR
1	A	775	SER
1	A	789	THR
2	E	11	THR

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	93	ASN
1	A	141	GLN

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Mol	Chain	Res	Type
1	A	321	ASN
1	A	329	GLN
1	A	382	ASN
1	A	459	HIS
1	A	488	ASN
1	A	505	GLN
1	A	539	HIS
1	A	552	HIS
1	A	561	HIS
1	A	665	GLN
1	A	703	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 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 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
4	FAD	A	904	-	48,58,58	1.51	5 (10%)	54,89,89	2.09	11 (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
4	FAD	A	904	-	-	0/30/50/50	0/6/6/6

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	904	FAD	C10-N1	2.51	1.39	1.35
4	A	904	FAD	C9A-N10	3.16	1.43	1.38
4	A	904	FAD	C5X-N5	3.48	1.40	1.35
4	A	904	FAD	C4-N3	4.44	1.41	1.33
4	A	904	FAD	C4X-N5	5.91	1.42	1.33

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	904	FAD	N3A-C2A-N1A	-10.21	121.08	128.89
4	A	904	FAD	P-O3P-PA	-3.92	121.73	132.73
4	A	904	FAD	C1B-N9A-C4A	-3.51	121.65	126.94
4	A	904	FAD	C2B-C1B-N9A	-2.97	109.75	114.29
4	A	904	FAD	C4A-C5A-N7A	-2.68	107.01	109.48
4	A	904	FAD	C4X-C4-N3	-2.46	120.23	123.59
4	A	904	FAD	C5B-C4B-C3B	-2.25	106.28	115.21
4	A	904	FAD	C9A-C5X-N5	-2.00	119.39	122.36
4	A	904	FAD	C4X-N5-C5X	2.15	119.23	116.76
4	A	904	FAD	C5X-C9A-N10	2.23	119.31	117.62
4	A	904	FAD	C4-N3-C2	5.46	119.97	115.25

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
4	A	904	FAD	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	739/796 (92%)	-0.14	18 (2%) 62 62	10, 40, 82, 110	2 (0%)
2	E	13/20 (65%)	0.39	0 100 100	49, 56, 69, 70	5 (38%)
All	All	752/816 (92%)	-0.13	18 (2%) 62 62	10, 41, 81, 110	7 (0%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	185	CYS	4.7
1	A	186	SER	4.2
1	A	147	CYS	3.9
1	A	184	HIS	3.4
1	A	188	PRO	3.1
1	A	370	GLY	3.0
1	A	528	PHE	2.9
1	A	145	PRO	2.7
1	A	103	HIS	2.6
1	A	194	LEU	2.6
1	A	189	GLU	2.3
1	A	144	LYS	2.2
1	A	146	GLU	2.2
1	A	526	ILE	2.1
1	A	168	ARG	2.1
1	A	173	PRO	2.1
1	A	64	VAL	2.0
1	A	169	CYS	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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
4	FAD	A	904	53/53	0.98	0.17	0.51	12,14,15,16	0
3	ZN	A	902	1/1	0.98	0.06	-2.17	61,61,61,61	0
3	ZN	A	901	1/1	0.98	0.07	-2.25	67,67,67,67	0
3	ZN	A	903	1/1	0.94	0.06	-2.44	109,109,109,109	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.