



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 19, 2016 – 10:36 AM EST

PDB ID : 5HZJ
Title : Crystal structure of photoinhibitable Intersectin1 containing wildtype LOV2 domain
Authors : Tarnawski, M.; Dagliyan, O.; Chu, P.H.; Shirvanyants, D.; Dokholyan, N.V.; Hahn, K.M.; Schlichting, I.
Deposited on : 2016-02-02
Resolution : 2.60 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-20028442
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-20028442

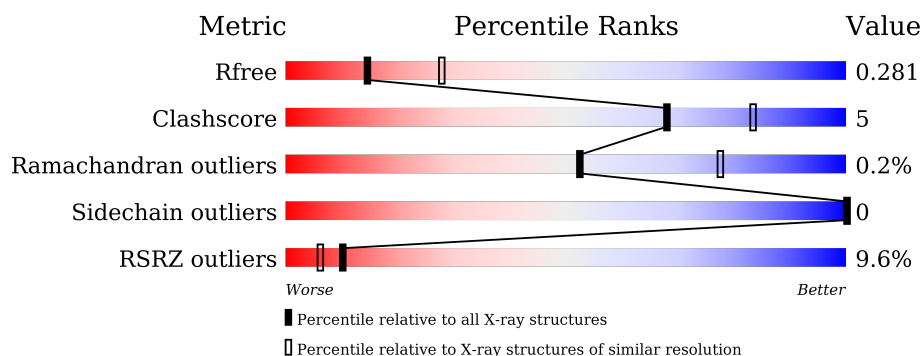
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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	502	<div> <div>9%</div> <div>84%</div> <div>11%</div> <div>5%</div> </div>
1	B	502	<div> <div>9%</div> <div>82%</div> <div>13%</div> <div>5%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7915 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.

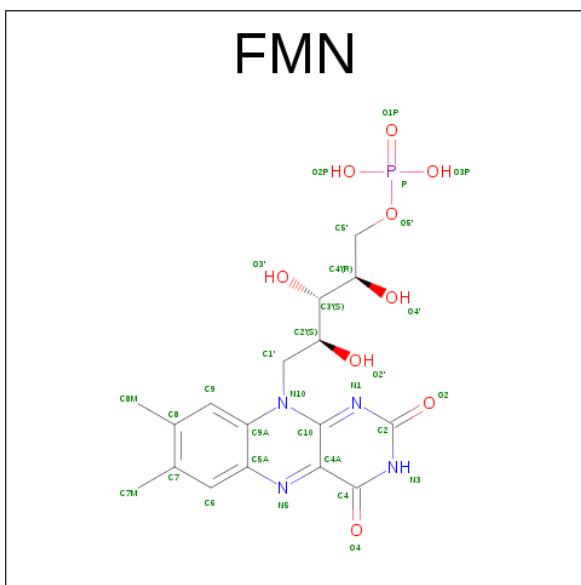
- Molecule 1 is a protein called Intersectin-1,NPH1-1,Intersectin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	476	Total	C	N	O	S	0	0	0
			3889	2481	675	713	20			
1	B	476	Total	C	N	O	S	0	0	0
			3889	2481	675	713	20			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1724	LEU	-	expression tag	UNP Q15811
A	1725	GLU	-	expression tag	UNP Q15811
A	1726	HIS	-	expression tag	UNP Q15811
A	1727	HIS	-	expression tag	UNP Q15811
A	1728	HIS	-	expression tag	UNP Q15811
A	1729	HIS	-	expression tag	UNP Q15811
A	1730	HIS	-	expression tag	UNP Q15811
A	1731	HIS	-	expression tag	UNP Q15811
B	1724	LEU	-	expression tag	UNP Q15811
B	1725	GLU	-	expression tag	UNP Q15811
B	1726	HIS	-	expression tag	UNP Q15811
B	1727	HIS	-	expression tag	UNP Q15811
B	1728	HIS	-	expression tag	UNP Q15811
B	1729	HIS	-	expression tag	UNP Q15811
B	1730	HIS	-	expression tag	UNP Q15811
B	1731	HIS	-	expression tag	UNP Q15811

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



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

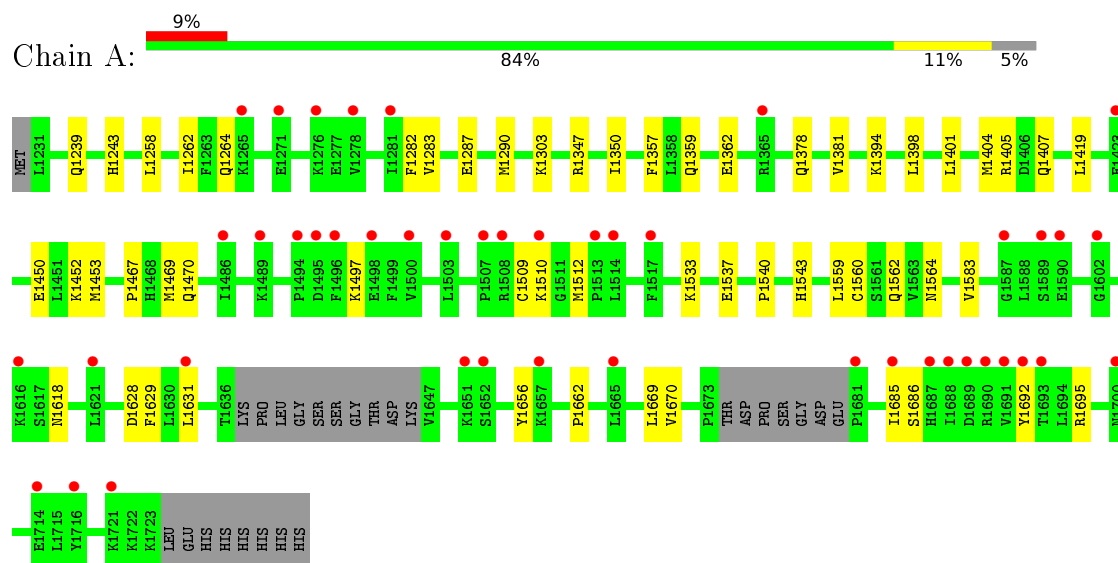
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	33	Total O 33 33	0	0
3	B	42	Total O 42 42	0	0

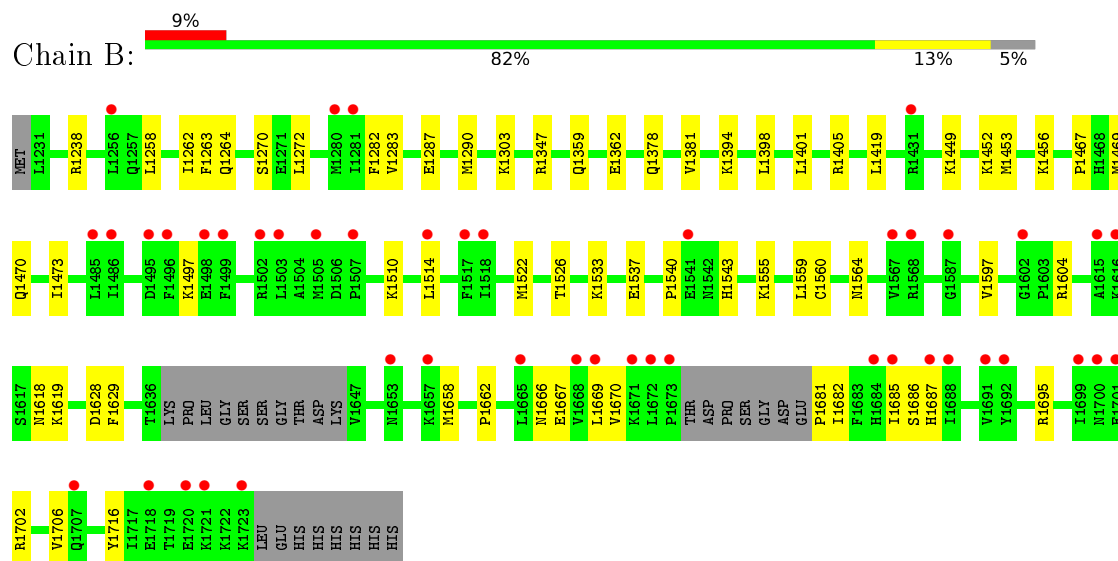
3 Residue-property plots

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: Intersectin-1,NPH1-1,Intersectin-1



• Molecule 1: Intersectin-1,NPH1-1,Intersectin-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	61.65Å 111.17Å 88.19Å 90.00° 90.12° 90.00°	Depositor
Resolution (Å)	47.02 – 2.60 47.02 – 2.60	Depositor EDS
% Data completeness (in resolution range)	96.9 (47.02-2.60) 96.4 (47.02-2.60)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.56 (at 2.61Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.252 , 0.281 0.251 , 0.281	Depositor DCC
R_{free} test set	1775 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	59.3	Xtriage
Anisotropy	0.696	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 31.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.247 for h,-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7915	wwPDB-VP
Average B, all atoms (Å ²)	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.96% 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

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	0.21	0/3962	0.37	0/5338
1	B	0.21	0/3962	0.37	0/5338
All	All	0.21	0/7924	0.37	0/10676

There are no bond length outliers.

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	3889	0	3974	34	0
1	B	3889	0	3974	40	0
2	A	31	0	19	2	0
2	B	31	0	19	1	0
3	A	33	0	0	3	0
3	B	42	0	0	6	0
All	All	7915	0	7986	75	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 (75) 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:1303:LYS:NZ	1:B:1453:MET:O	1.97	0.98
1:A:1303:LYS:NZ	1:A:1453:MET:O	2.12	0.82
1:B:1522:MET:O	3:B:1901:HOH:O	2.06	0.73
1:A:1450:GLU:O	3:A:1901:HOH:O	2.07	0.72
1:B:1449:LYS:HA	1:B:1452:LYS:HE3	1.71	0.72
1:B:1540:PRO:HG2	1:B:1543:HIS:HB2	1.77	0.67
1:A:1378:GLN:O	1:A:1405:ARG:NH2	2.28	0.67
1:A:1560:CYS:O	1:A:1564:ASN:ND2	2.28	0.65
1:B:1706:VAL:O	3:B:1902:HOH:O	2.14	0.65
1:A:1618:ASN:OD1	1:A:1695:ARG:NH2	2.30	0.64
1:A:1540:PRO:HG2	1:A:1543:HIS:HB2	1.80	0.64
1:B:1362:GLU:OE2	1:B:1394:LYS:NZ	2.30	0.64
1:A:1404:MET:HG2	1:A:1452:LYS:HE3	1.81	0.62
1:B:1398:LEU:HB3	1:B:1419:LEU:HB3	1.83	0.60
1:B:1618:ASN:OD1	1:B:1695:ARG:NH2	2.34	0.59
1:A:1359:GLN:NE2	2:A:1801:FMN:O4'	2.35	0.59
1:B:1619:LYS:O	3:B:1903:HOH:O	2.17	0.58
1:B:1560:CYS:O	1:B:1564:ASN:ND2	2.36	0.57
1:B:1398:LEU:HD23	1:B:1419:LEU:HD23	1.85	0.57
1:B:1695:ARG:NH2	3:B:1912:HOH:O	2.38	0.56
1:A:1398:LEU:HB3	1:A:1419:LEU:HB3	1.88	0.56
1:A:1381:VAL:HG12	1:A:1401:LEU:HB3	1.87	0.55
1:A:1497:LYS:NZ	1:A:1497:LYS:HB3	2.22	0.54
1:A:1670:VAL:HG22	1:A:1685:ILE:HG22	1.89	0.54
1:B:1497:LYS:NZ	1:B:1497:LYS:HB3	2.23	0.54
1:B:1669:LEU:O	1:B:1686:SER:N	2.34	0.54
1:A:1628:ASP:OD2	1:A:1629:PHE:HD1	1.91	0.54
1:B:1287:GLU:HA	1:B:1290:MET:HE2	1.91	0.53
1:B:1381:VAL:HG12	1:B:1401:LEU:HB3	1.91	0.53
1:B:1378:GLN:O	1:B:1405:ARG:NH2	2.42	0.53
1:A:1562:GLN:OE1	3:A:1902:HOH:O	2.19	0.52
1:A:1398:LEU:HD23	1:A:1419:LEU:HD23	1.91	0.52
1:B:1628:ASP:OD2	1:B:1629:PHE:HD1	1.92	0.52
1:B:1359:GLN:NE2	2:B:1801:FMN:O4'	2.42	0.52
1:A:1669:LEU:O	1:A:1686:SER:N	2.39	0.50
1:B:1473:ILE:HD12	1:B:1597:VAL:HG22	1.94	0.50
1:B:1670:VAL:HG22	1:B:1685:ILE:HG22	1.94	0.50
1:A:1362:GLU:OE2	1:A:1394:LYS:NZ	2.42	0.50
1:B:1666:ASN:ND2	3:B:1920:HOH:O	2.44	0.50
1:B:1604:ARG:NH1	1:B:1628:ASP:OD1	2.46	0.47
1:B:1467:PRO:O	1:B:1470:GLN:NE2	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1533:LYS:HE2	1:B:1537:GLU:OE2	2.15	0.47
1:A:1347:ARG:HH22	1:A:1510:LYS:HE2	1.80	0.47
1:A:1287:GLU:HA	1:A:1290:MET:HE2	1.97	0.46
1:A:1533:LYS:HE2	1:A:1537:GLU:OE2	2.15	0.46
1:B:1667:GLU:HG3	1:B:1687:HIS:HE1	1.80	0.46
1:B:1682:ILE:HG13	1:B:1695:ARG:HG3	1.98	0.46
1:B:1238:ARG:NH2	1:B:1456:LYS:O	2.37	0.46
1:B:1526:THR:HG22	1:B:1560:CYS:SG	2.56	0.45
1:A:1629:PHE:HE2	1:A:1631:LEU:HB2	1.82	0.45
1:A:1239:GLN:O	1:A:1243:HIS:ND1	2.25	0.45
1:B:1258:LEU:O	1:B:1262:ILE:HG12	2.17	0.45
1:B:1658:MET:HE1	1:B:1662:PRO:HD3	1.99	0.44
1:B:1264:GLN:HA	1:B:1282:PHE:CE2	2.53	0.44
1:B:1555:LYS:NZ	3:B:1924:HOH:O	2.49	0.44
1:B:1666:ASN:HB3	1:B:1716:TYR:CD1	2.53	0.44
1:B:1681:PRO:HA	1:B:1702:ARG:HD3	1.99	0.44
1:B:1347:ARG:HH12	1:B:1510:LYS:HG3	1.83	0.43
1:A:1469:MET:HB2	1:A:1559:LEU:HG	2.01	0.43
1:B:1469:MET:HB2	1:B:1559:LEU:HG	2.00	0.43
1:A:1629:PHE:CD2	1:A:1662:PRO:HB3	2.54	0.43
1:A:1583:VAL:HG22	1:A:1656:TYR:HB2	2.01	0.43
1:B:1629:PHE:CD2	1:B:1662:PRO:HB3	2.54	0.43
1:B:1263:PHE:CG	1:B:1514:LEU:HD13	2.54	0.42
1:A:1258:LEU:O	1:A:1262:ILE:HG12	2.20	0.42
1:B:1270:SER:HB2	1:B:1272:LEU:HD13	2.01	0.42
1:A:1509:CYS:O	1:A:1512:MET:HG2	2.19	0.42
1:A:1685:ILE:HD11	1:A:1692:TYR:HB2	2.01	0.42
1:A:1347:ARG:HH12	1:A:1510:LYS:HG3	1.84	0.42
1:A:1350:ILE:HD12	1:A:1357:PHE:CZ	2.55	0.42
1:A:1407:GLN:NE2	1:A:1453:MET:SD	2.87	0.41
1:A:1264:GLN:HA	1:A:1282:PHE:CE2	2.55	0.41
1:A:1453:MET:HB2	3:A:1901:HOH:O	2.20	0.41
1:A:1467:PRO:O	1:A:1470:GLN:NE2	2.49	0.40
2:A:1801:FMN:H1'1	2:A:1801:FMN:H9	1.82	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	470/502 (94%)	452 (96%)	17 (4%)	1 (0%)	52	77
1	B	470/502 (94%)	453 (96%)	16 (3%)	1 (0%)	52	77
All	All	940/1004 (94%)	905 (96%)	33 (4%)	2 (0%)	52	77

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1283	VAL
1	B	1283	VAL

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	435/458 (95%)	435 (100%)	0	100	100
1	B	435/458 (95%)	435 (100%)	0	100	100
All	All	870/916 (95%)	870 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

2 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	1801	-	32,33,33	1.18	3 (9%)	34,50,50	1.66	5 (14%)
2	FMN	B	1801	-	32,33,33	1.17	2 (6%)	34,50,50	1.64	5 (14%)

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	1801	-	-	0/18/18/18	0/3/3/3
2	FMN	B	1801	-	-	0/18/18/18	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1801	FMN	C1'-N10	2.09	1.50	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1801	FMN	C4-N3	2.98	1.38	1.33
2	A	1801	FMN	C4-N3	2.98	1.38	1.33
2	B	1801	FMN	C4A-N5	3.28	1.38	1.33
2	A	1801	FMN	C4A-N5	3.35	1.38	1.33

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1801	FMN	N3-C2-N1	-4.41	120.26	127.69
2	A	1801	FMN	N3-C2-N1	-4.40	120.29	127.69
2	A	1801	FMN	C4A-C4-N3	-2.84	119.81	123.52
2	B	1801	FMN	C4A-C4-N3	-2.82	119.84	123.52
2	A	1801	FMN	C4A-N5-C5A	2.54	119.72	116.72
2	B	1801	FMN	C4A-N5-C5A	2.74	119.95	116.72
2	B	1801	FMN	C5A-C9A-N10	3.48	120.18	117.58
2	A	1801	FMN	C5A-C9A-N10	3.68	120.34	117.58
2	B	1801	FMN	C4-N3-C2	5.91	120.09	115.16
2	A	1801	FMN	C4-N3-C2	6.00	120.16	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1801	FMN	2	0
2	B	1801	FMN	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	476/502 (94%)	0.50	45 (9%)	10 6	38, 75, 149, 276	0
1	B	476/502 (94%)	0.49	46 (9%)	10 6	38, 78, 148, 239	0
All	All	952/1004 (94%)	0.49	91 (9%)	10 6	38, 76, 148, 276	0

All (91) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1502	ARG	8.5
1	A	1498	GLU	8.2
1	B	1721	LYS	8.1
1	B	1496	PHE	6.6
1	A	1507	PRO	6.1
1	A	1271	GLU	6.1
1	A	1688	ILE	5.5
1	B	1720	GLU	5.5
1	B	1684	HIS	4.9
1	B	1615	ALA	4.7
1	B	1486	ILE	4.7
1	A	1716	TYR	4.6
1	A	1495	ASP	4.5
1	A	1278	VAL	4.5
1	A	1494	PRO	4.2
1	A	1517	PHE	4.0
1	A	1616	LYS	4.0
1	B	1671	LYS	4.0
1	B	1507	PRO	4.0
1	B	1505	MET	3.9
1	B	1687	HIS	3.8
1	A	1602	GLY	3.7
1	B	1503	LEU	3.7
1	A	1690	ARG	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	1281	ILE	3.7
1	B	1281	ILE	3.6
1	B	1499	PHE	3.6
1	A	1587	GLY	3.6
1	A	1714	GLU	3.6
1	B	1541	GLU	3.6
1	B	1568	ARG	3.5
1	B	1517	PHE	3.5
1	B	1567	VAL	3.5
1	A	1514	LEU	3.5
1	A	1500	VAL	3.5
1	A	1496	PHE	3.5
1	A	1700	ASN	3.4
1	B	1672	LEU	3.3
1	A	1651	LYS	3.3
1	B	1723	LYS	3.3
1	B	1691	VAL	3.2
1	B	1665	LEU	3.2
1	A	1691	VAL	3.2
1	B	1688	ILE	3.1
1	A	1665	LEU	3.1
1	A	1689	ASP	3.1
1	A	1265	LYS	3.1
1	B	1280	MET	3.0
1	A	1423	GLU	3.0
1	B	1498	GLU	3.0
1	B	1514	LEU	3.0
1	A	1486	ILE	2.9
1	B	1587	GLY	2.8
1	A	1631	LEU	2.8
1	B	1718	GLU	2.8
1	A	1589	SER	2.8
1	B	1495	ASP	2.8
1	B	1669	LEU	2.8
1	B	1668	VAL	2.8
1	B	1685	ILE	2.7
1	A	1685	ILE	2.7
1	A	1687	HIS	2.7
1	A	1276	LYS	2.7
1	A	1508	ARG	2.6
1	A	1489	LYS	2.6
1	B	1616	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	1692	TYR	2.5
1	B	1700	ASN	2.4
1	A	1365	ARG	2.4
1	A	1693	THR	2.4
1	A	1510	LYS	2.3
1	A	1681	PRO	2.3
1	B	1699	ILE	2.3
1	B	1701	GLU	2.3
1	A	1657	LYS	2.3
1	B	1602	GLY	2.2
1	A	1503	LEU	2.2
1	A	1590	GLU	2.2
1	B	1657	LYS	2.2
1	B	1431	ARG	2.2
1	B	1653	ASN	2.2
1	B	1692	TYR	2.2
1	B	1673	PRO	2.1
1	B	1518	ILE	2.1
1	B	1707	GLN	2.1
1	A	1652	SER	2.1
1	A	1721	LYS	2.1
1	B	1485	LEU	2.1
1	A	1513	PRO	2.0
1	A	1621	LEU	2.0
1	B	1256	LEU	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(\AA^2)	Q<0.9
2	FMN	B	1801	31/31	0.93	0.16	-0.21	26,48,62,76	0
2	FMN	A	1801	31/31	0.93	0.15	-0.74	23,47,71,78	0

6.5 Other polymers [i](#)

There are no such residues in this entry.