Full wwPDB X-ray Structure Validation Report ⓘ

Jun 13, 2024 – 11:03 AM EDT

PDB ID	:	4GUS
Title	:	Crystal structure of LSD2-NPAC with H3 in space group P3221
Authors	:	Chen, F.; Dong, Z.; Fang, J.; Yang, Y.; Li, Z.; Xu, Y.; Yang, H.; Wang, P.; Fang, R.; Shi, Y.; Xu, Y.
Deposited on	:	2012-08-29
Resolution	:	2.23 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

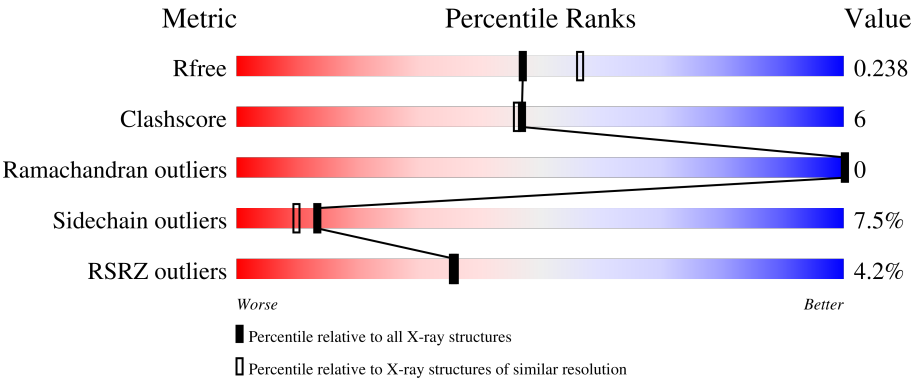
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.23 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}	130704	2391 (2.26-2.22)
Clashscore	141614	2539 (2.26-2.22)
Ramachandran outliers	138981	2489 (2.26-2.22)
Sidechain outliers	138945	2490 (2.26-2.22)
RSRZ outliers	127900	2353 (2.26-2.22)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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 <=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	776	4% 80% 14%
2	B	124	9% 90%
3	C	21	14% 90% 5% 5%

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
5	IOD	A	904	-	-	X	-

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 6515 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	746	Total	C	N	O	S	0	0	0
			5904	3769	1005	1089	41			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	47	PRO	-	expression tag	UNP Q8NB78
A	48	LEU	-	expression tag	UNP Q8NB78
A	49	GLY	-	expression tag	UNP Q8NB78
A	50	SER	-	expression tag	UNP Q8NB78

- Molecule 2 is a protein called Putative oxidoreductase GLYR1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	12	Total	C	N	O	0	0	0
			105	69	19	17			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	145	PRO	-	expression tag	UNP Q49A26
B	146	LEU	-	expression tag	UNP Q49A26
B	147	GLY	-	expression tag	UNP Q49A26
B	148	SER	-	expression tag	UNP Q49A26
B	149	PRO	-	expression tag	UNP Q49A26
B	150	GLU	-	expression tag	UNP Q49A26
B	151	PHE	-	expression tag	UNP Q49A26

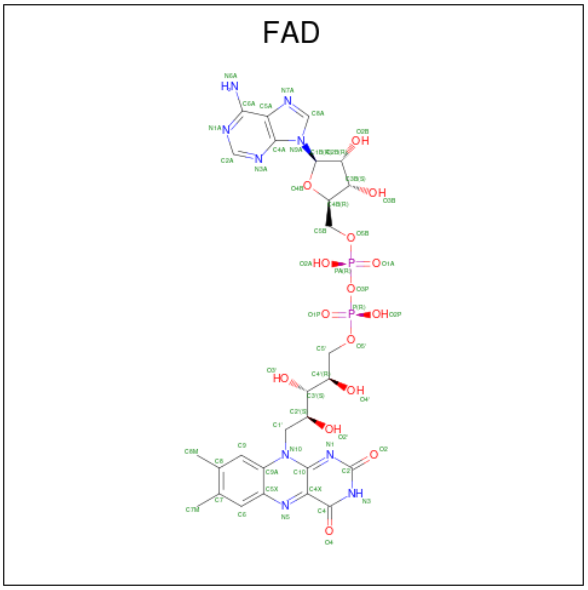
- Molecule 3 is a protein called Histone H3.3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	20	Total	C	N	O	S	0	0	0
			151	90	34	26	1			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	4	MET	LYS	engineered mutation	UNP P84243

- Molecule 4 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).

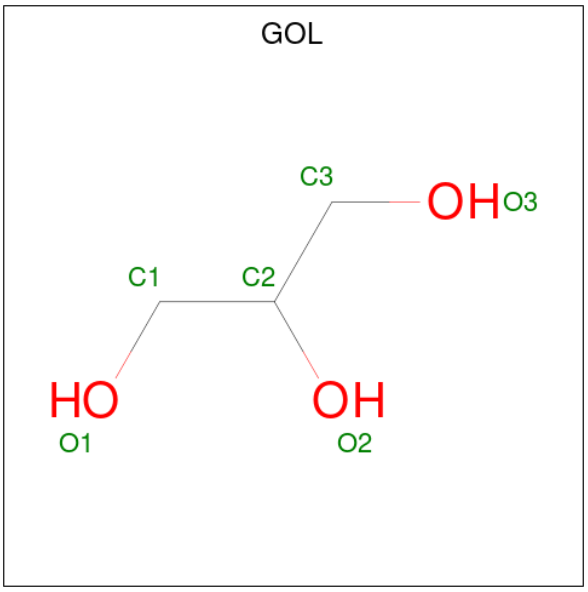


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 5 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	6	Total	I	0	0
			6	6		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 6 3 3	0	0
6	A	1	Total C O 6 3 3	0	0

- Molecule 7 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 8 is water.

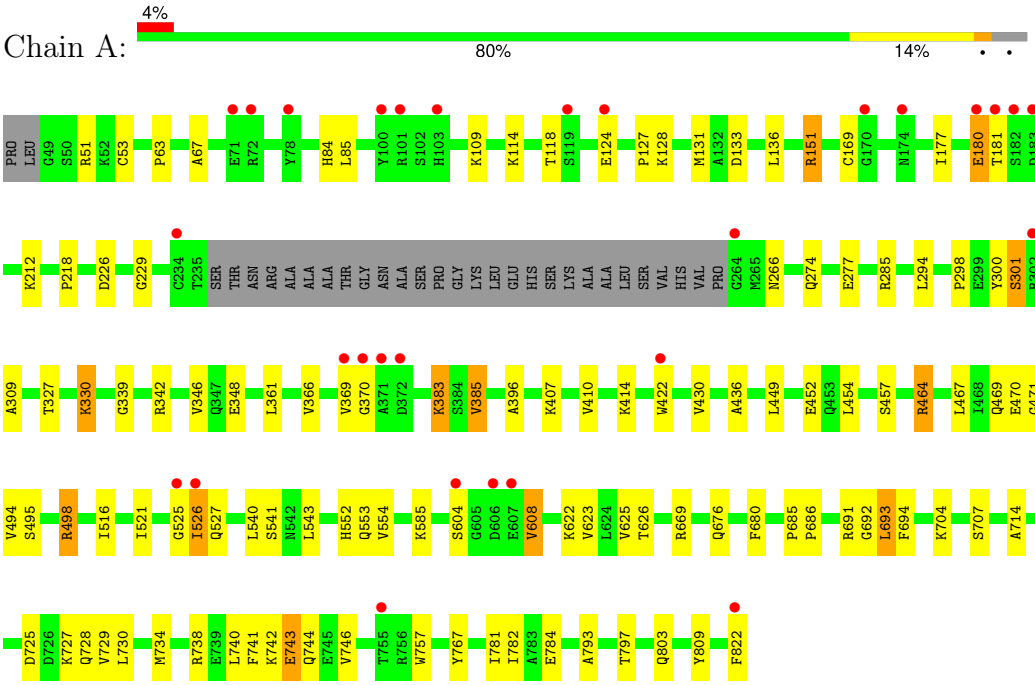
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	264	Total O 264 264	0	0
8	B	6	Total O 6 6	0	0
8	C	11	Total O 11 11	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

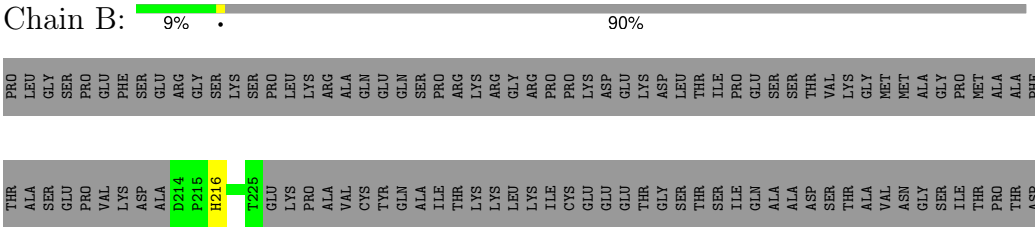
• Molecule 1: Lysine-specific histone demethylase 1B

Chain A:



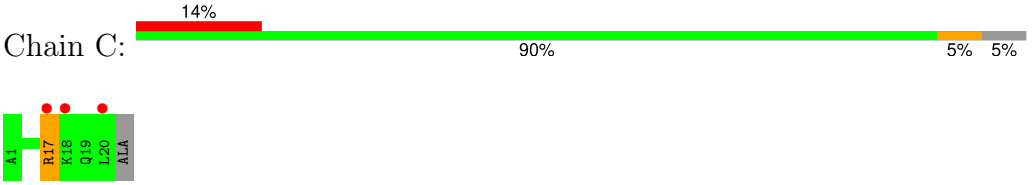
• Molecule 2: Putative oxidoreductase GLYR1

Chain B:



• Molecule 3: Histone H3.3

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	101.08Å 101.08Å 177.37Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.04 – 2.23 49.00 – 2.23	Depositor EDS
% Data completeness (in resolution range)	99.6 (29.04-2.23) 99.6 (49.00-2.23)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.02 (at 2.22Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.207 , 0.237 0.209 , 0.238	Depositor DCC
R_{free} test set	2619 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	42.5	Xtriage
Anisotropy	0.024	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 37.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.019 for -h,-k,l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	6515	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.77% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: FAD, IOD, ZN, GOL

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	0.44	0/6051	0.57	0/8199
2	B	0.44	0/110	0.56	0/149
3	C	0.45	0/151	0.54	0/198
All	All	0.44	0/6312	0.57	0/8546

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	5904	0	5821	73	0
2	B	105	0	91	1	0
3	C	151	0	170	2	0
4	A	53	0	30	2	0
5	A	6	0	0	2	0
6	A	12	0	16	5	0
7	A	3	0	0	0	0
8	A	264	0	0	6	0
8	B	6	0	0	0	0
8	C	11	0	0	0	0
All	All	6515	0	6128	76	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 6.

All (76) 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:521:ILE:O	1:A:525:GLY:HA2	1.63	0.98
1:A:521:ILE:O	1:A:525:GLY:CA	2.19	0.91
1:A:521:ILE:O	1:A:525:GLY:N	2.25	0.70
1:A:738:ARG:NH2	6:A:909:GOL:O3	2.26	0.69
1:A:304:PRO:HB2	1:A:308:LEU:HD22	1.79	0.65
1:A:741:PHE:C	1:A:743:GLU:OE2	2.37	0.62
1:A:266:ASN:HD22	1:A:452:GLU:HG2	1.65	0.62
1:A:743:GLU:OE1	1:A:744:GLN:NE2	2.33	0.61
1:A:493:VAL:HG11	1:A:516:ILE:HG21	1.84	0.59
1:A:151:ARG:HD2	1:A:169:CYS:SG	2.44	0.58
1:A:114:LYS:O	1:A:118:THR:OG1	2.19	0.57
1:A:498:ARG:HD2	8:A:1170:HOH:O	2.05	0.56
1:A:757:TRP:CD2	6:A:908:GOL:H12	2.41	0.56
1:A:454:LEU:HD21	1:A:585:LYS:HG2	1.87	0.55
1:A:722:ARG:HB3	8:A:1279:HOH:O	2.07	0.55
1:A:194:LEU:HD13	8:A:1183:HOH:O	2.07	0.54
1:A:743:GLU:O	1:A:744:GLN:HB3	2.06	0.54
1:A:127:PRO:O	1:A:131:MET:HG2	2.08	0.53
1:A:51:ARG:NH2	1:A:63:PRO:O	2.42	0.53
1:A:133:ASP:OD1	1:A:212:LYS:NZ	2.41	0.53
1:A:274:GLN:HB2	1:A:277:GLU:HG3	1.90	0.53
1:A:738:ARG:HG2	1:A:746:VAL:HG13	1.91	0.52
1:A:229:GLY:HA3	1:A:309:ALA:HB2	1.90	0.52
1:A:383:LYS:NZ	1:A:822:PHE:O	2.44	0.51
1:A:743:GLU:OE2	1:A:743:GLU:N	2.41	0.51
3:C:17:ARG:NE	3:C:17:ARG:H	2.09	0.51
1:A:526:ILE:HG12	1:A:526:ILE:O	2.11	0.50
1:A:422:TRP:CZ3	6:A:908:GOL:H31	2.48	0.49
1:A:741:PHE:HA	1:A:743:GLU:OE2	2.12	0.49
1:A:494:VAL:O	1:A:498:ARG:HG2	2.13	0.49
3:C:17:ARG:H	3:C:17:ARG:HE	1.59	0.49
1:A:693:LEU:HD22	1:A:694:PHE:CE1	2.47	0.48
1:A:741:PHE:CA	1:A:743:GLU:OE2	2.61	0.48
1:A:218:PRO:O	8:A:1213:HOH:O	2.20	0.48
1:A:53:CYS:SG	1:A:84:HIS:HB2	2.54	0.48
1:A:327:THR:OG1	1:A:330:LYS:HG2	2.14	0.47
1:A:127:PRO:HD2	5:A:904:IOD:I	2.84	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:464:ARG:NH2	1:A:676:GLN:HB2	2.29	0.47
1:A:721:VAL:HG22	1:A:729:VAL:HG22	1.96	0.47
1:A:608:VAL:HG21	1:A:623:VAL:HB	1.97	0.47
1:A:300:TYR:OH	1:A:348:GLU:OE2	2.18	0.46
1:A:469:GLN:OE1	1:A:473:ARG:HG3	2.14	0.46
1:A:526:ILE:O	1:A:526:ILE:HG23	2.16	0.46
8:A:1273:HOH:O	2:B:216:HIS:HB2	2.17	0.45
1:A:469:GLN:HB2	1:A:473:ARG:HG2	1.98	0.45
1:A:725:ASP:OD2	1:A:728:GLN:HG3	2.17	0.45
1:A:342:ARG:O	1:A:346:VAL:HG13	2.17	0.45
1:A:67:ALA:HB2	1:A:131:MET:CE	2.47	0.45
1:A:226:ASP:OD1	1:A:226:ASP:N	2.50	0.45
1:A:669:ARG:CG	1:A:707:SER:HB3	2.46	0.45
1:A:298:PRO:O	1:A:301:SER:OG	2.35	0.44
1:A:626:THR:HA	1:A:793:ALA:O	2.17	0.44
1:A:274:GLN:O	1:A:277:GLU:HB2	2.17	0.44
1:A:128:LYS:HG3	5:A:904:IOD:I	2.88	0.44
1:A:136:LEU:HD13	1:A:339:GLY:HA3	2.00	0.44
1:A:266:ASN:ND2	1:A:452:GLU:HG2	2.30	0.43
1:A:552:HIS:O	1:A:552:HIS:CG	2.70	0.43
1:A:734:MET:HG3	6:A:909:GOL:H2	2.01	0.43
1:A:781:ILE:O	1:A:784:GLU:HB2	2.19	0.43
1:A:180:GLU:H	1:A:180:GLU:HG3	1.39	0.43
1:A:493:VAL:HG13	1:A:516:ILE:HD13	2.00	0.43
1:A:396:ALA:HB2	1:A:809:TYR:CD1	2.54	0.43
1:A:285:ARG:HB2	8:A:1136:HOH:O	2.19	0.42
1:A:369:VAL:HA	1:A:370:GLY:HA3	1.60	0.42
1:A:757:TRP:CE3	6:A:908:GOL:H12	2.54	0.42
1:A:327:THR:H	1:A:330:LYS:HG3	1.83	0.42
1:A:685:PRO:HB3	1:A:691:ARG:HA	2.02	0.42
1:A:685:PRO:HA	1:A:686:PRO:HD3	1.85	0.41
1:A:541:SER:HB2	1:A:691:ARG:HG3	2.03	0.41
1:A:692:GLY:HA3	1:A:714:ALA:O	2.21	0.41
1:A:330:LYS:HB3	1:A:330:LYS:HE3	1.88	0.41
1:A:385:VAL:HB	1:A:622:LYS:HB2	2.02	0.41
1:A:436:ALA:HA	4:A:901:FAD:N5	2.36	0.41
1:A:782:ILE:HG22	1:A:797:THR:HG22	2.02	0.41
1:A:803:GLN:O	4:A:901:FAD:O3'	2.39	0.40
1:A:470:GLU:HA	1:A:471:GLY:HA2	1.60	0.40

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	742/776 (96%)	713 (96%)	29 (4%)	0	100	100
2	B	10/124 (8%)	10 (100%)	0	0	100	100
3	C	18/21 (86%)	16 (89%)	2 (11%)	0	100	100
All	All	770/921 (84%)	739 (96%)	31 (4%)	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	640/662 (97%)	591 (92%)	49 (8%)	13	9
2	B	12/106 (11%)	12 (100%)	0	100	100
3	C	15/15 (100%)	14 (93%)	1 (7%)	16	13
All	All	667/783 (85%)	617 (92%)	50 (8%)	13	10

All (50) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	85	LEU
1	A	109	LYS
1	A	124	GLU
1	A	151	ARG
1	A	177	ILE

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Mol	Chain	Res	Type
1	A	180	GLU
1	A	181	THR
1	A	194	LEU
1	A	205	LEU
1	A	294	LEU
1	A	301	SER
1	A	308	LEU
1	A	330	LYS
1	A	361	LEU
1	A	366	VAL
1	A	383	LYS
1	A	385	VAL
1	A	407	LYS
1	A	410	VAL
1	A	414	LYS
1	A	430	VAL
1	A	449	LEU
1	A	457	SER
1	A	464	ARG
1	A	467	LEU
1	A	473	ARG
1	A	493	VAL
1	A	495	SER
1	A	498	ARG
1	A	526	ILE
1	A	527	GLN
1	A	540	LEU
1	A	543	LEU
1	A	553	GLN
1	A	554	VAL
1	A	604	SER
1	A	608	VAL
1	A	625	VAL
1	A	680	PHE
1	A	693	LEU
1	A	704	LYS
1	A	718	VAL
1	A	721	VAL
1	A	727	LYS
1	A	730	LEU
1	A	740	LEU
1	A	742	LYS

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Mol	Chain	Res	Type
1	A	743	GLU
1	A	767	TYR
3	C	17	ARG

Sometimes 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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 9 are monoatomic - leaving 3 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	$\#\|Z\| > 2$
6	GOL	A	908	-	5,5,5	0.53	0	5,5,5	0.33	0
6	GOL	A	909	-	5,5,5	0.41	0	5,5,5	0.87	0
4	FAD	A	901	-	54,58,58	2.38	11 (20%)	71,89,89	2.12	12 (16%)

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
6	GOL	A	908	-	-	3/4/4/4	-
6	GOL	A	909	-	-	2/4/4/4	-
4	FAD	A	901	-	-	2/30/50/50	0/6/6/6

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	901	FAD	O2'-C2'	-8.66	1.25	1.43
4	A	901	FAD	O2-C2	8.10	1.40	1.24
4	A	901	FAD	O4-C4	7.35	1.37	1.23
4	A	901	FAD	P-O3P	-3.56	1.55	1.59
4	A	901	FAD	C1'-C2'	-3.37	1.47	1.52
4	A	901	FAD	C9A-N10	-2.64	1.36	1.41
4	A	901	FAD	C5B-C4B	-2.57	1.43	1.51
4	A	901	FAD	PA-O3P	-2.35	1.57	1.59
4	A	901	FAD	C4-N3	-2.30	1.34	1.38
4	A	901	FAD	C3B-C4B	-2.18	1.47	1.53
4	A	901	FAD	C4X-N5	2.01	1.35	1.30

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	901	FAD	C1B-N9A-C4A	-12.27	105.08	126.64
4	A	901	FAD	O2'-C2'-C3'	5.18	121.36	109.25
4	A	901	FAD	N3A-C2A-N1A	-4.54	122.52	128.67
4	A	901	FAD	O5'-C5'-C4'	3.02	117.42	109.36
4	A	901	FAD	C4X-C10-N10	2.95	120.70	116.48
4	A	901	FAD	C4-N3-C2	-2.89	120.51	125.64
4	A	901	FAD	C1'-C2'-C3'	2.87	117.44	109.66
4	A	901	FAD	O5B-C5B-C4B	2.78	118.45	108.99
4	A	901	FAD	C5X-C9A-N10	2.72	120.42	117.97
4	A	901	FAD	O4-C4-C4X	-2.32	120.42	126.53
4	A	901	FAD	C4X-C4-N3	2.24	118.96	113.25
4	A	901	FAD	C10-C4X-N5	-2.14	120.44	124.81

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	901	FAD	N10-C1'-C2'-O2'

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Mol	Chain	Res	Type	Atoms
6	A	908	GOL	O1-C1-C2-O2
6	A	908	GOL	O1-C1-C2-C3
6	A	909	GOL	O1-C1-C2-C3
6	A	909	GOL	O1-C1-C2-O2
4	A	901	FAD	PA-O3P-P-O5'
6	A	908	GOL	O2-C2-C3-O3

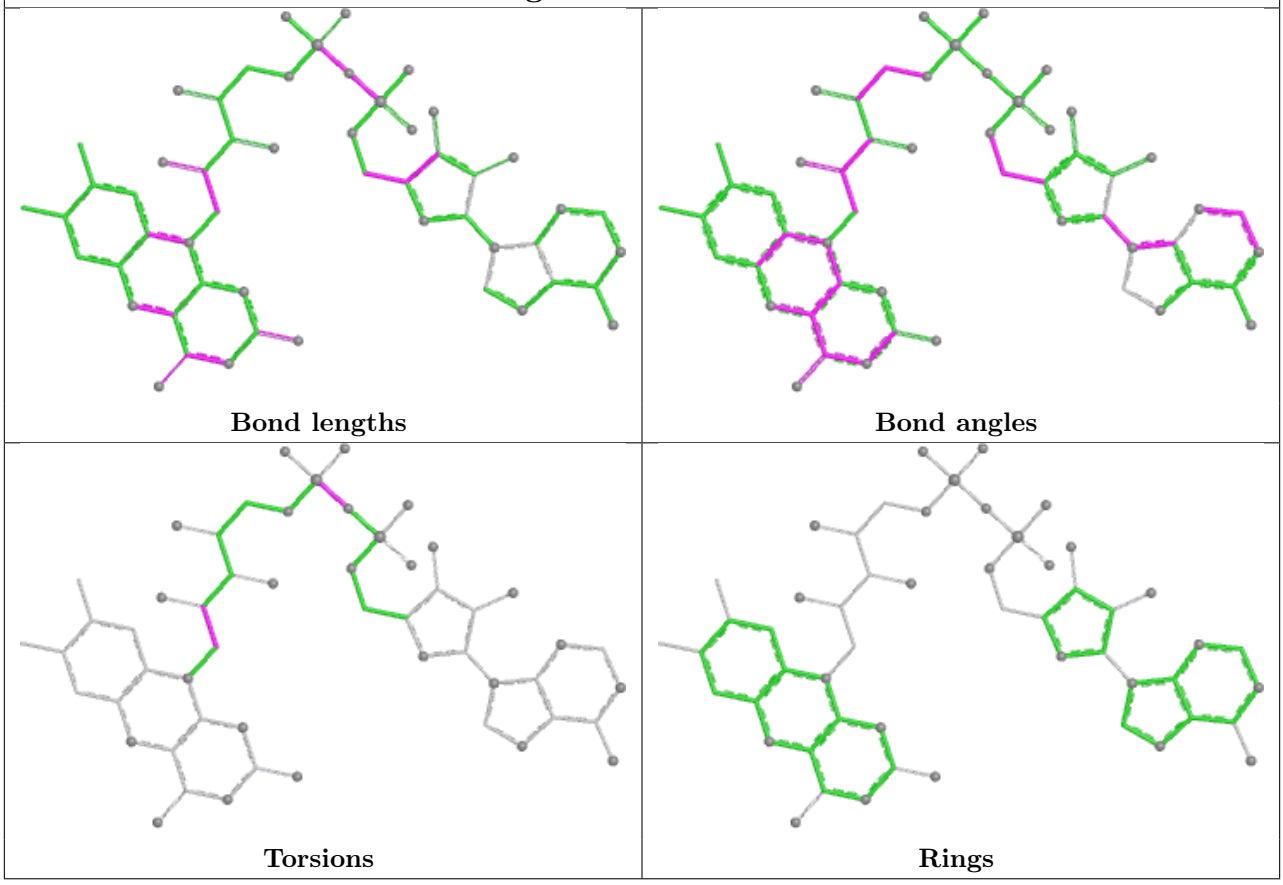
There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	908	GOL	3	0
6	A	909	GOL	2	0
4	A	901	FAD	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand FAD A 901



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, 95^{th} 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	746/776 (96%)	0.15	30 (4%) 38 38	26, 43, 63, 83	0
2	B	12/124 (9%)	-0.13	0 100 100	30, 40, 53, 59	0
3	C	20/21 (95%)	0.72	3 (15%) 2 1	30, 37, 66, 67	0
All	All	778/921 (84%)	0.16	33 (4%) 36 35	26, 43, 63, 83	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	17	ARG	5.5
1	A	369	VAL	5.2
1	A	174	ASN	4.4
3	C	20	LEU	4.2
1	A	526	ILE	3.9
1	A	170	GLY	3.6
1	A	370	GLY	3.5
1	A	100	TYR	3.4
1	A	371	ALA	3.3
1	A	822	PHE	3.2
1	A	124	GLU	2.9
1	A	181	THR	2.9
1	A	103	HIS	2.8
1	A	607	GLU	2.8
1	A	264	GLY	2.7
1	A	606	ASP	2.5
1	A	101	ARG	2.4
1	A	604	SER	2.3
1	A	182	SER	2.3
1	A	525	GLY	2.3
1	A	372	ASP	2.2
1	A	755	THR	2.2
1	A	71	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	473	ARG	2.2
1	A	119	SER	2.2
1	A	302	ARG	2.1
1	A	183	ASP	2.1
1	A	234	CYS	2.1
3	C	18	LYS	2.1
1	A	422	TRP	2.1
1	A	72	ARG	2.0
1	A	78	TYR	2.0
1	A	180	GLU	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 monosaccharides in this entry.

6.4 Ligands (i)

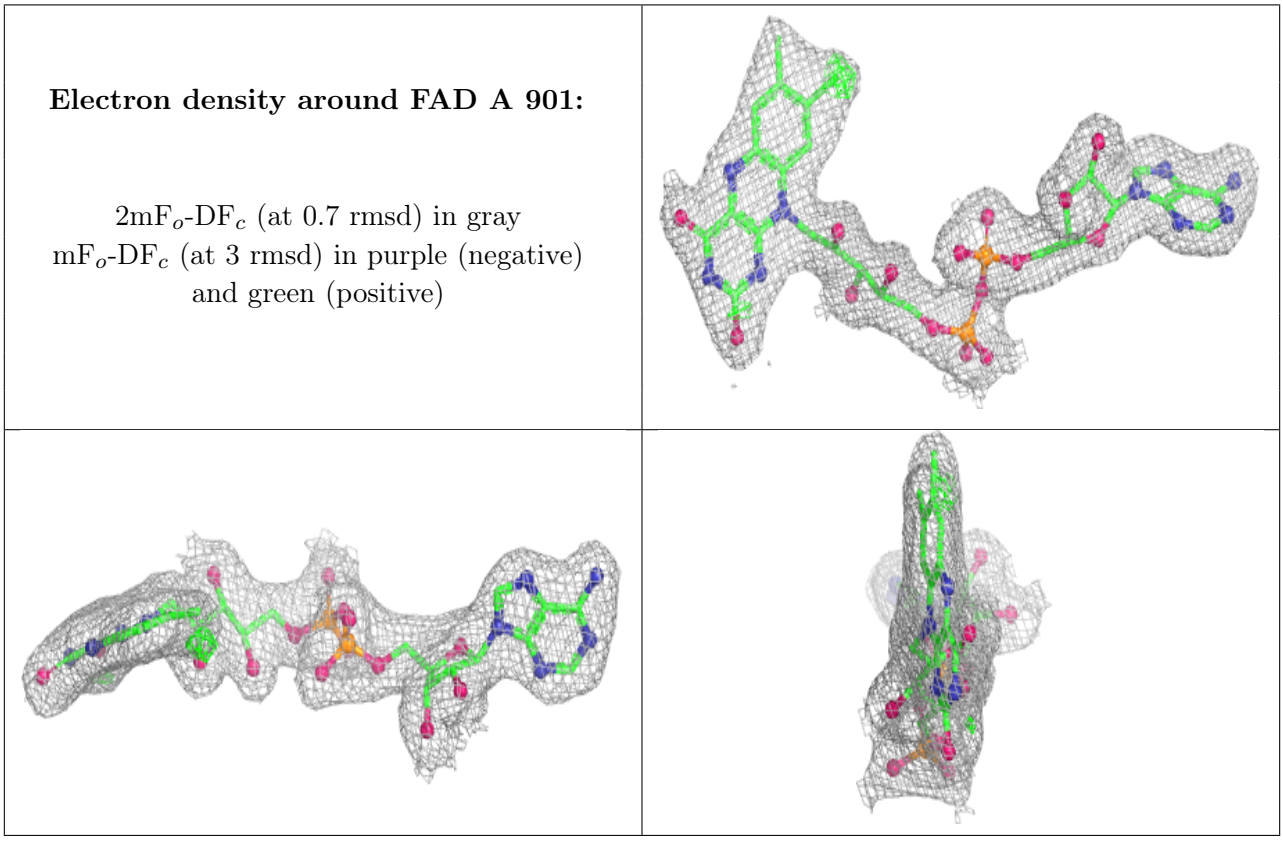
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	IOD	A	907	1/1	0.76	0.11	131,131,131,131	0
5	IOD	A	905	1/1	0.81	0.17	142,142,142,142	0
6	GOL	A	909	6/6	0.88	0.21	48,49,51,53	0
6	GOL	A	908	6/6	0.92	0.23	33,38,40,44	0
4	FAD	A	901	53/53	0.97	0.17	26,30,34,38	0
5	IOD	A	902	1/1	0.97	0.11	60,60,60,60	0
5	IOD	A	904	1/1	0.98	0.06	72,72,72,72	0
5	IOD	A	903	1/1	0.98	0.08	48,48,48,48	0
5	IOD	A	906	1/1	0.98	0.04	78,78,78,78	0
7	ZN	A	910	1/1	0.99	0.13	42,42,42,42	0
7	ZN	A	911	1/1	0.99	0.09	47,47,47,47	0
7	ZN	A	912	1/1	0.99	0.07	57,57,57,57	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around FAD A 901:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



6.5 Other polymers

There are no such residues in this entry.