Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 07:47 am BST

PDB ID	:	4GUR
Title	:	Crystal structure of LSD2-NPAC with H3 in space group P21
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	:	2.51 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 following versions of software and data (see references ⓘ) were used in the production of this report:

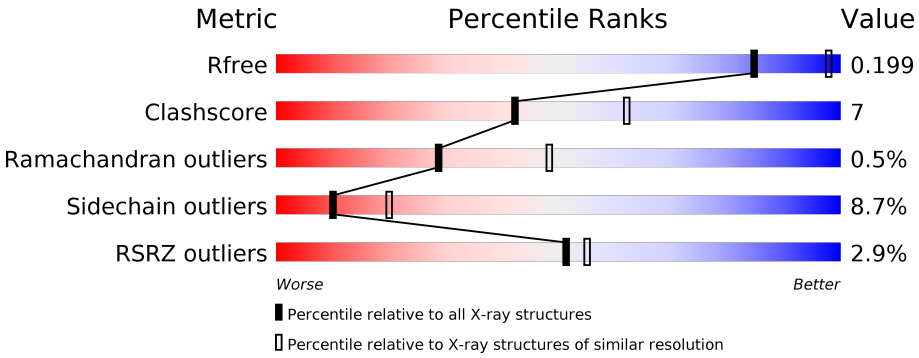
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.51 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 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	2% 75% 17% • 5%
2	B	124	2% 7% • 90%
3	C	21	24% 67% 29% 5%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6234 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	734	Total	C	N	O	S	0	0	0
			5818	3716	990	1071	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

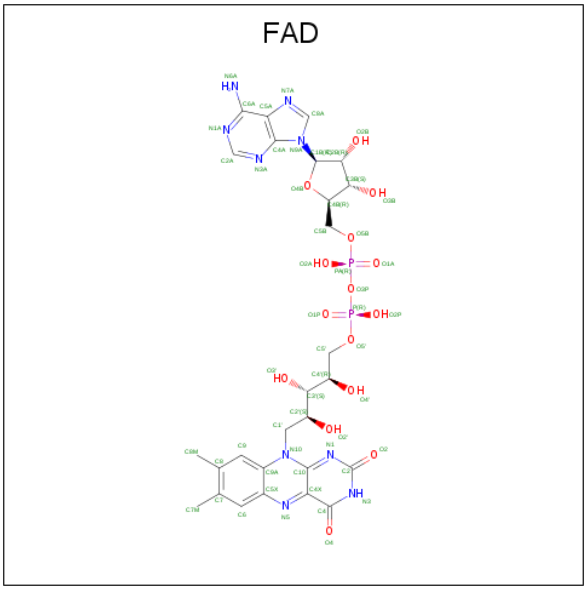
- Molecule 3 is a protein called Histone H3.3.

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:

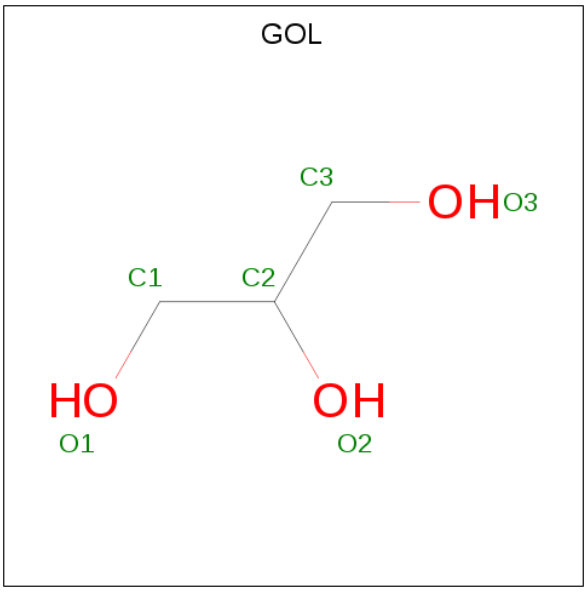
Chain	Residue	Modelled	Actual	Comment	Reference
C	4	MET	LYS	ENGINEERED MUTATION	UNP P84243

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



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

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 7 is water.

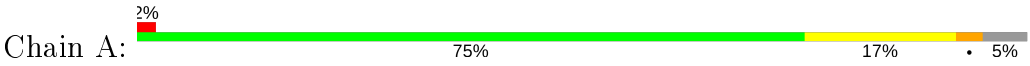
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	90	Total O 90 90	0	0
7	B	3	Total O 3 3	0	0
7	C	5	Total O 5 5	0	0

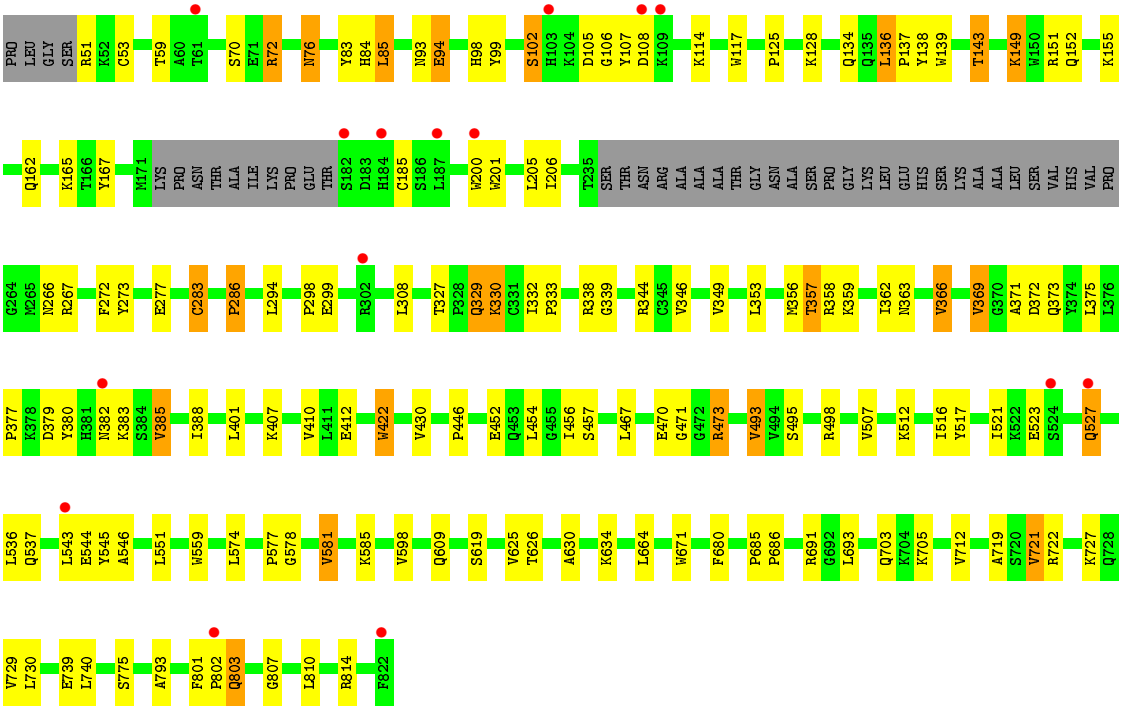
3 Residue-property plots (i)

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: Lysine-specific histone demethylase 1B

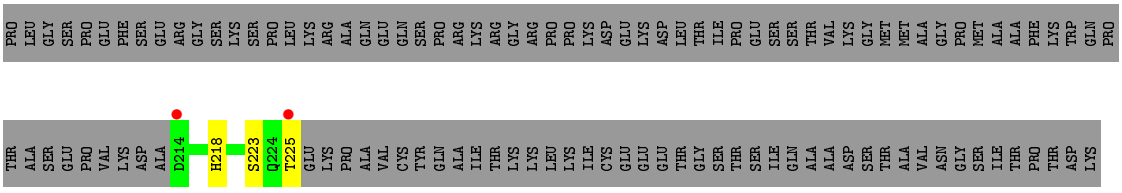
Chain A:





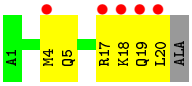
- Molecule 2: Putative oxidoreductase GLYR1

Chain B:



- Molecule 3: Histone H3.3

Chain C:


A1
M4
Q5
R17
K18
Q19
L20
ALA

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	62.24Å 89.03Å 88.78Å 90.00° 103.30° 90.00°	Depositor
Resolution (Å)	38.87 – 2.51 38.87 – 2.51	Depositor EDS
% Data completeness (in resolution range)	88.6 (38.87-2.51) 94.3 (38.87-2.51)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.60 (at 2.51Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.188 , 0.204 0.183 , 0.199	Depositor DCC
R_{free} test set	1563 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å^2)	42.6	Xtriage
Anisotropy	0.435	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 39.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	6234	wwPDB-VP
Average B, all atoms (Å^2)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.21% 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: GOL, 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	7/5962 (0.1%)	0.65	0/8076
2	B	0.74	0/110	0.59	0/149
3	C	0.38	0/151	0.58	0/198
All	All	0.55	7/6223 (0.1%)	0.64	0/8423

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	559	TRP	CD2-CE2	5.53	1.48	1.41
1	A	139	TRP	CD2-CE2	5.44	1.47	1.41
1	A	671	TRP	CD2-CE2	5.38	1.47	1.41
1	A	117	TRP	CD2-CE2	5.25	1.47	1.41
1	A	200	TRP	CD2-CE2	5.19	1.47	1.41
1	A	422	TRP	CD2-CE2	5.16	1.47	1.41
1	A	201	TRP	CD2-CE2	5.05	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	5818	0	5730	83	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	105	0	91	1	0
3	C	151	0	170	4	0
4	A	53	0	30	3	0
5	A	6	0	8	2	0
6	A	3	0	0	0	0
7	A	90	0	0	2	0
7	B	3	0	0	0	0
7	C	5	0	0	0	0
All	All	6234	0	6029	84	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 7.

All (84) 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:72:ARG:HG2	1:A:72:ARG:HH11	0.94	1.05
1:A:72:ARG:HG2	1:A:72:ARG:NH1	1.70	0.94
1:A:72:ARG:CG	1:A:72:ARG:HH11	1.84	0.89
1:A:473:ARG:HH11	1:A:473:ARG:HG3	1.46	0.80
1:A:266:ASN:HD22	1:A:452:GLU:HG2	1.50	0.77
1:A:51:ARG:N	7:A:1122:HOH:O	2.23	0.70
1:A:143:THR:HB	1:A:167:TYR:O	1.91	0.70
1:A:76:ASN:HD22	1:A:76:ASN:H	1.38	0.70
1:A:369:VAL:HG22	1:A:373:GLN:HB3	1.74	0.69
1:A:609:GLN:HE22	1:A:619:SER:HB3	1.60	0.67
1:A:136:LEU:HD13	1:A:339:GLY:HA3	1.76	0.67
1:A:353:LEU:O	1:A:357:THR:HG23	1.94	0.67
1:A:527:GLN:HA	1:A:527:GLN:HE21	1.59	0.66
1:A:803:GLN:HB3	3:C:4:MET:CE	2.27	0.64
1:A:719:ALA:O	1:A:722:ARG:HG2	1.97	0.64
1:A:53:CYS:SG	1:A:84:HIS:HB2	2.39	0.62
1:A:366:VAL:HG21	1:A:585:LYS:HB3	1.81	0.62
1:A:412:GLU:OE1	4:A:901:FAD:O3B	2.17	0.62
1:A:266:ASN:HD22	1:A:452:GLU:CG	2.14	0.59
1:A:456:ILE:HG23	1:A:577:PRO:HG2	1.85	0.59
2:B:218:HIS:HB3	2:B:223:SER:OG	2.03	0.59
1:A:70:SER:HB2	1:A:98:HIS:HB2	1.85	0.58
1:A:471:GLY:HA2	1:A:739:GLU:O	2.05	0.57
1:A:422:TRP:CZ3	5:A:902:GOL:H31	2.41	0.56
1:A:76:ASN:HD22	1:A:76:ASN:N	2.03	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:266:ASN:ND2	1:A:452:GLU:HG2	2.21	0.54
1:A:99:TYR:HD1	1:A:106:GLY:O	1.91	0.54
1:A:332:ILE:HB	1:A:333:PRO:HD3	1.90	0.53
1:A:454:LEU:HD21	1:A:585:LYS:HG2	1.90	0.53
1:A:366:VAL:HG13	1:A:366:VAL:O	2.09	0.53
1:A:609:GLN:NE2	1:A:619:SER:HB3	2.22	0.52
1:A:537:GLN:HB2	1:A:685:PRO:HG2	1.92	0.52
1:A:517:TYR:O	1:A:521:ILE:HG12	2.10	0.52
1:A:385:VAL:HG11	1:A:401:LEU:HD13	1.91	0.51
1:A:277:GLU:H	3:C:20:LEU:HD12	1.76	0.50
1:A:366:VAL:CG2	1:A:585:LYS:HB3	2.41	0.50
1:A:578:GLY:O	1:A:581:VAL:HG22	2.12	0.50
1:A:546:ALA:HB2	3:C:5:GLN:HG3	1.93	0.50
1:A:273:TYR:CE1	1:A:283:CYS:HB3	2.47	0.49
1:A:507:VAL:HG21	1:A:512:LYS:HE2	1.93	0.49
1:A:544:GLU:HG2	1:A:551:LEU:HG	1.94	0.49
1:A:327:THR:H	1:A:330:LYS:HG3	1.78	0.49
1:A:371:ALA:C	1:A:373:GLN:H	2.16	0.48
1:A:803:GLN:HB3	3:C:4:MET:HE2	1.95	0.48
1:A:137:PRO:HG2	1:A:152:GLN:HE21	1.78	0.48
1:A:98:HIS:HE1	1:A:105:ASP:HB2	1.79	0.48
1:A:272:PHE:HB3	1:A:286:PRO:HG3	1.95	0.48
1:A:470:GLU:HA	1:A:471:GLY:HA2	1.70	0.47
1:A:493:VAL:HG22	1:A:516:ILE:HD13	1.96	0.47
1:A:803:GLN:O	4:A:901:FAD:H1'2	2.14	0.47
1:A:705:LYS:HE2	1:A:705:LYS:HB3	1.46	0.47
1:A:721:VAL:HG22	1:A:729:VAL:HG22	1.96	0.47
1:A:422:TRP:CE3	5:A:902:GOL:H31	2.50	0.47
1:A:298:PRO:HD2	1:A:299:GLU:OE1	2.14	0.46
1:A:149:LYS:NZ	1:A:185:CYS:O	2.49	0.46
1:A:83:TYR:HE2	1:A:93:ASN:HD22	1.63	0.46
1:A:363:ASN:HB3	1:A:375:LEU:HD13	1.97	0.45
1:A:377:PRO:HD2	1:A:380:TYR:CE2	2.52	0.45
1:A:685:PRO:HB3	1:A:691:ARG:HA	1.98	0.45
1:A:802:PRO:O	1:A:803:GLN:HB2	2.16	0.45
1:A:446:PRO:HG3	1:A:810:LEU:HD21	1.99	0.45
1:A:114:LYS:HG3	1:A:125:PRO:HB2	1.99	0.44
1:A:94:GLU:H	1:A:94:GLU:HG2	1.53	0.44
1:A:98:HIS:CE1	1:A:105:ASP:HB2	2.52	0.44
1:A:162:GLN:HA	1:A:162:GLN:NE2	2.33	0.44
1:A:545:TYR:HD1	1:A:712:VAL:HG11	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:685:PRO:HA	1:A:686:PRO:HD3	1.91	0.44
1:A:382:ASN:O	1:A:383:LYS:HB3	2.18	0.44
1:A:102:SER:HA	1:A:107:TYR:CG	2.53	0.44
1:A:801:PHE:O	1:A:807:GLY:HA3	2.18	0.43
1:A:626:THR:HA	1:A:793:ALA:O	2.18	0.43
1:A:609:GLN:NE2	1:A:609:GLN:HA	2.34	0.43
1:A:329:GLN:H	1:A:329:GLN:CD	2.22	0.43
1:A:138:TYR:CZ	1:A:338:ARG:HG2	2.53	0.43
1:A:388:ILE:HG12	1:A:598:VAL:HG21	2.01	0.43
1:A:803:GLN:O	4:A:901:FAD:O3'	2.37	0.43
1:A:85:LEU:HD11	1:A:128:LYS:HB3	1.99	0.43
1:A:473:ARG:HG3	1:A:473:ARG:NH1	2.20	0.42
1:A:473:ARG:CG	1:A:473:ARG:NH1	2.82	0.41
1:A:84:HIS:HD2	1:A:206:ILE:HG12	1.85	0.41
1:A:814:ARG:NH1	7:A:1154:HOH:O	2.49	0.41
1:A:630:ALA:O	1:A:634:LYS:HG2	2.20	0.41
1:A:356:MET:HB3	1:A:362:ILE:HG12	2.04	0.40
1:A:358:ARG:NH2	1:A:359:LYS:HE2	2.37	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	728/776 (94%)	684 (94%)	40 (6%)	4 (0%)	29 48
2	B	10/124 (8%)	9 (90%)	1 (10%)	0	100 100
3	C	18/21 (86%)	16 (89%)	2 (11%)	0	100 100
All	All	756/921 (82%)	709 (94%)	43 (6%)	4 (0%)	29 48

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	155	LYS
1	A	372	ASP
1	A	523	GLU
1	A	803	GLN

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	630/662 (95%)	577 (92%)	53 (8%)	11 21
2	B	12/106 (11%)	11 (92%)	1 (8%)	11 22
3	C	15/15 (100%)	12 (80%)	3 (20%)	1 2
All	All	657/783 (84%)	600 (91%)	57 (9%)	10 20

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	59	THR
1	A	72	ARG
1	A	76	ASN
1	A	85	LEU
1	A	94	GLU
1	A	102	SER
1	A	108	ASP
1	A	134	GLN
1	A	136	LEU
1	A	143	THR
1	A	149	LYS
1	A	151	ARG
1	A	165	LYS
1	A	205	LEU
1	A	267	ARG
1	A	283	CYS
1	A	286	PRO
1	A	294	LEU
1	A	308	LEU

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Mol	Chain	Res	Type
1	A	329	GLN
1	A	330	LYS
1	A	344	ARG
1	A	346	VAL
1	A	349	VAL
1	A	357	THR
1	A	366	VAL
1	A	369	VAL
1	A	379	ASP
1	A	385	VAL
1	A	407	LYS
1	A	410	VAL
1	A	430	VAL
1	A	457	SER
1	A	467	LEU
1	A	473	ARG
1	A	493	VAL
1	A	495	SER
1	A	498	ARG
1	A	527	GLN
1	A	536	LEU
1	A	543	LEU
1	A	574	LEU
1	A	581	VAL
1	A	625	VAL
1	A	664	LEU
1	A	680	PHE
1	A	693	LEU
1	A	703	GLN
1	A	721	VAL
1	A	727	LYS
1	A	730	LEU
1	A	740	LEU
1	A	775	SER
2	B	225	THR
3	C	17	ARG
3	C	18	LYS
3	C	19	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	76	ASN
1	A	98	HIS
1	A	134	GLN
1	A	152	GLN
1	A	400	GLN
1	A	440	ASN
1	A	527	GLN
1	A	553	GLN
1	A	609	GLN
1	A	732	GLN
1	A	803	GLN
2	B	218	HIS

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

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 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	$\#\|Z\| > 2$
5	GOL	A	902	-	5,5,5	0.40	0	5,5,5	0.42	0
4	FAD	A	901	-	51,58,58	2.28	24 (47%)	60,89,89	1.84	13 (21%)

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
5	GOL	A	902	-	-	4/4/4/4	-
4	FAD	A	901	-	-	2/30/50/50	0/6/6/6

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	901	FAD	PA-O5B	-5.00	1.39	1.59
4	A	901	FAD	PA-O1A	-3.94	1.36	1.50
4	A	901	FAD	P-O2P	-3.81	1.37	1.55
4	A	901	FAD	O4B-C1B	-3.73	1.35	1.41
4	A	901	FAD	PA-O2A	-3.58	1.38	1.55
4	A	901	FAD	C6-C5X	-3.54	1.36	1.41
4	A	901	FAD	P-O1P	-3.52	1.38	1.50
4	A	901	FAD	P-O5'	-3.06	1.46	1.59
4	A	901	FAD	C4-C4X	-3.04	1.36	1.41
4	A	901	FAD	C4A-N3A	-3.00	1.31	1.35
4	A	901	FAD	C5A-N7A	-2.87	1.29	1.39
4	A	901	FAD	O3'-C3'	-2.81	1.36	1.43
4	A	901	FAD	C9A-C5X	-2.72	1.37	1.42
4	A	901	FAD	C2-N3	-2.72	1.32	1.38
4	A	901	FAD	C5A-C4A	-2.64	1.33	1.40
4	A	901	FAD	O5B-C5B	-2.56	1.34	1.44
4	A	901	FAD	C2-N1	-2.53	1.33	1.38
4	A	901	FAD	C2B-C1B	-2.53	1.49	1.53
4	A	901	FAD	C2A-N1A	-2.51	1.29	1.33
4	A	901	FAD	C8A-N7A	-2.51	1.30	1.34
4	A	901	FAD	O4'-C4'	-2.44	1.38	1.43
4	A	901	FAD	C9-C9A	-2.41	1.35	1.40
4	A	901	FAD	C4X-C10	-2.28	1.36	1.38
4	A	901	FAD	C1'-N10	-2.25	1.45	1.48

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	901	FAD	C4-N3-C2	6.05	120.25	115.14
4	A	901	FAD	C1'-N10-C9A	6.05	123.05	118.29
4	A	901	FAD	C9A-N10-C10	-4.29	116.29	121.91
4	A	901	FAD	C5X-C9A-N10	3.97	120.59	117.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	901	FAD	N3A-C2A-N1A	-3.81	122.72	128.68
4	A	901	FAD	C4A-C5A-N7A	-2.55	106.74	109.40
4	A	901	FAD	O4B-C1B-C2B	-2.53	103.23	106.93
4	A	901	FAD	C4X-C4-N3	-2.46	120.07	123.43
4	A	901	FAD	C1'-N10-C10	2.29	120.46	118.41
4	A	901	FAD	O4'-C4'-C5'	-2.28	104.79	109.92
4	A	901	FAD	C4'-C3'-C2'	2.27	118.09	113.36
4	A	901	FAD	C4-C4X-N5	2.21	121.13	118.60
4	A	901	FAD	C4-C4X-C10	-2.18	118.51	119.95

There are no chirality outliers.

All (6) torsion outliers are listed below:

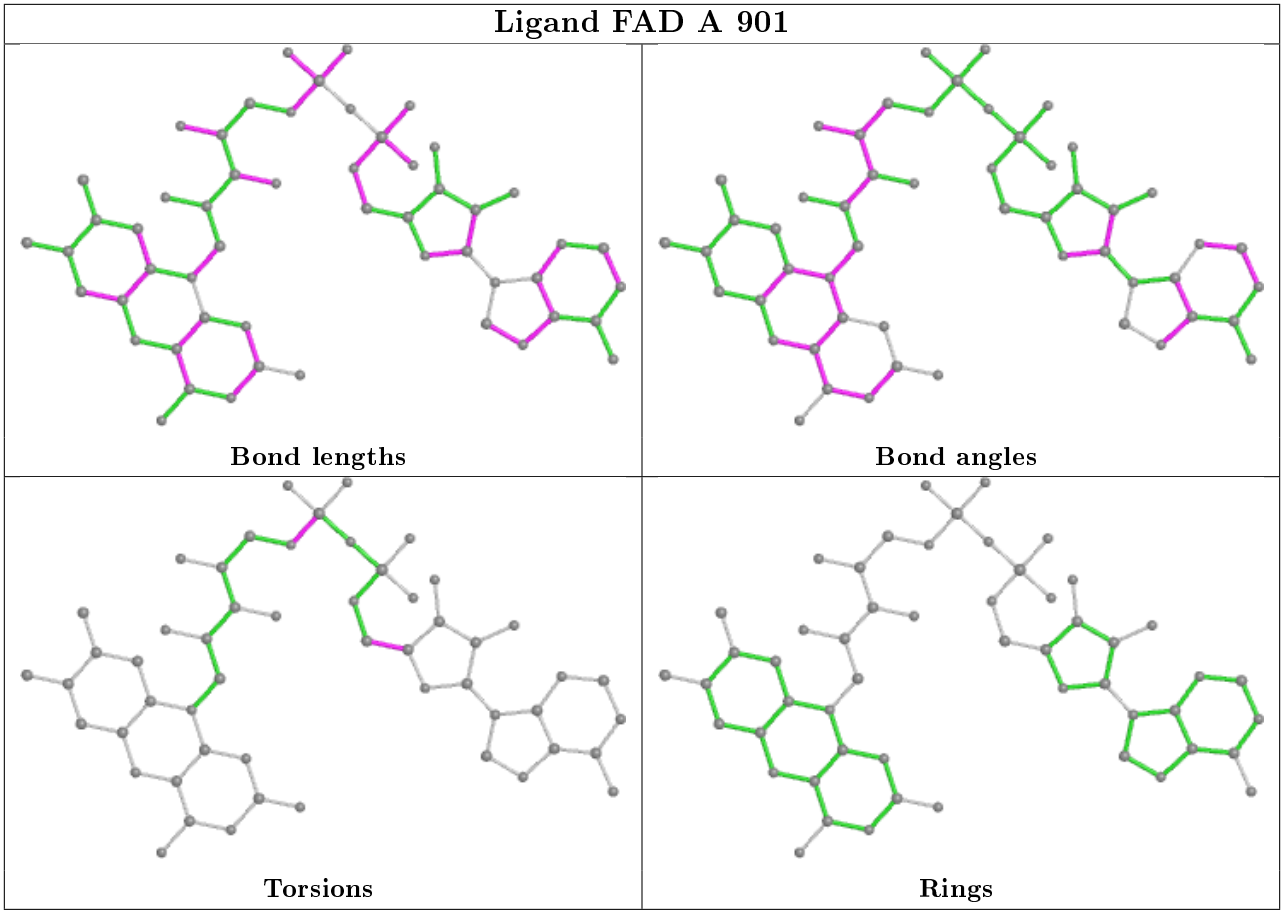
Mol	Chain	Res	Type	Atoms
5	A	902	GOL	O1-C1-C2-C3
5	A	902	GOL	C1-C2-C3-O3
4	A	901	FAD	C5'-O5'-P-O3P
5	A	902	GOL	O1-C1-C2-O2
5	A	902	GOL	O2-C2-C3-O3
4	A	901	FAD	O4B-C4B-C5B-O5B

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	902	GOL	2	0
4	A	901	FAD	3	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.



5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	734/776 (94%)	-0.00	15 (2%) 65 68	26, 47, 83, 102	0
2	B	12/124 (9%)	0.68	2 (16%) 1 1	46, 66, 82, 90	0
3	C	20/21 (95%)	0.77	5 (25%) 0 0	47, 55, 90, 95	0
All	All	766/921 (83%)	0.03	22 (2%) 51 55	26, 47, 84, 102	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	822	PHE	6.3
1	A	527	GLN	4.7
1	A	200	TRP	3.6
3	C	18	LYS	3.4
2	B	225	THR	3.2
1	A	382	ASN	3.2
3	C	20	LEU	3.2
2	B	214	ASP	2.7
1	A	103	HIS	2.7
1	A	61	THR	2.5
1	A	187	LEU	2.5
3	C	17	ARG	2.5
1	A	182	SER	2.4
1	A	302	ARG	2.4
1	A	108	ASP	2.4
1	A	109	LYS	2.3
1	A	802	PRO	2.2
1	A	543	LEU	2.2
3	C	4	MET	2.2
1	A	184	HIS	2.1
3	C	19	GLN	2.1
1	A	524	SER	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)

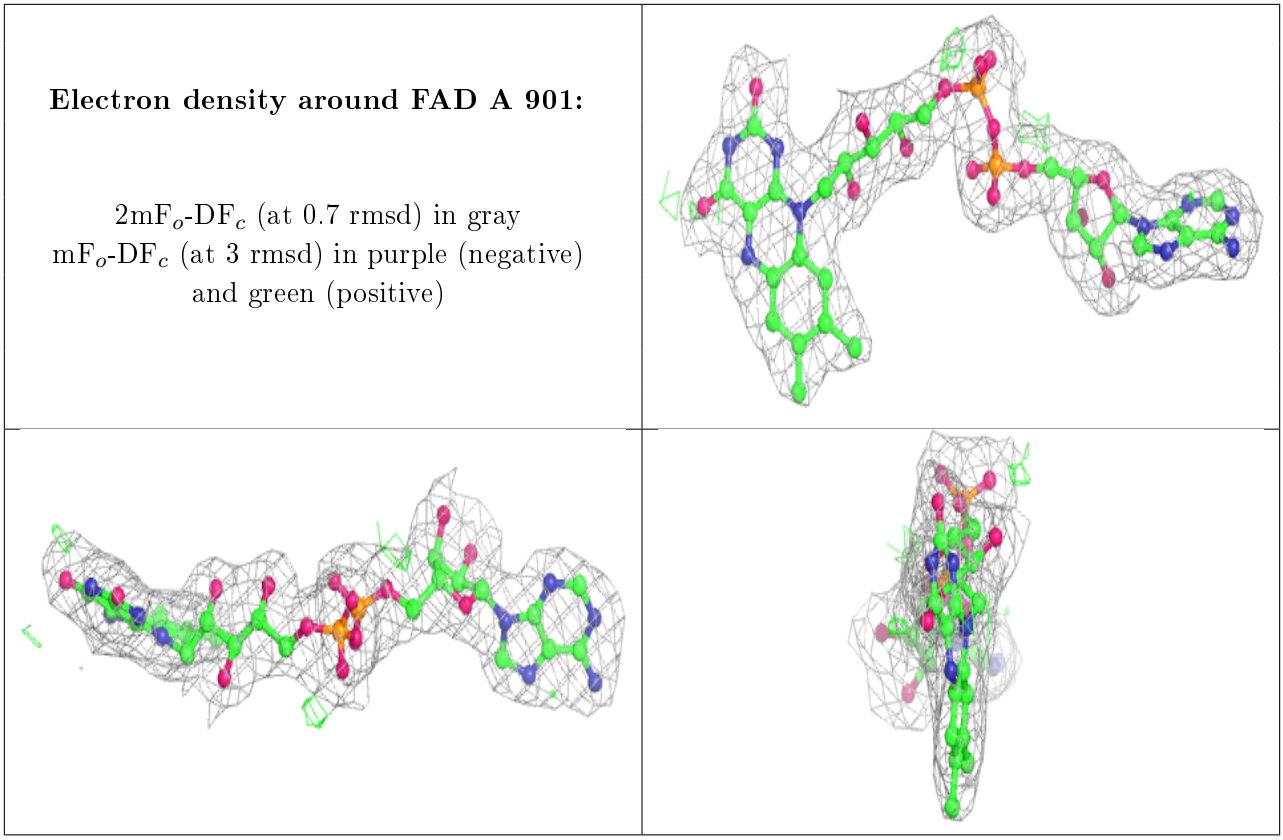
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	GOL	A	902	6/6	0.85	0.28	48,51,54,60	0
4	FAD	A	901	53/53	0.96	0.17	26,32,38,43	0
6	ZN	A	903	1/1	0.97	0.07	63,63,63,63	0
6	ZN	A	904	1/1	0.99	0.10	54,54,54,54	0
6	ZN	A	905	1/1	0.99	0.07	55,55,55,55	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 (i)

There are no such residues in this entry.