



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:53 AM UTC

PDB ID : 3ZMZ / pdb_00003zmz
Title : LSD1-CoREST in complex with PRSFAV peptide
Authors : Tortorici, M.; Borrello, M.T.; Tardugno, M.; Chiarelli, L.R.; Pilotto, S.; Ciossani, G.; Vellore, N.A.; Cowan, J.; O'Connell, M.; Mai, A.; Baron, R.; Ganesan, A.; Mattevi, A.
Deposited on : 2013-02-13
Resolution : 3.00 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

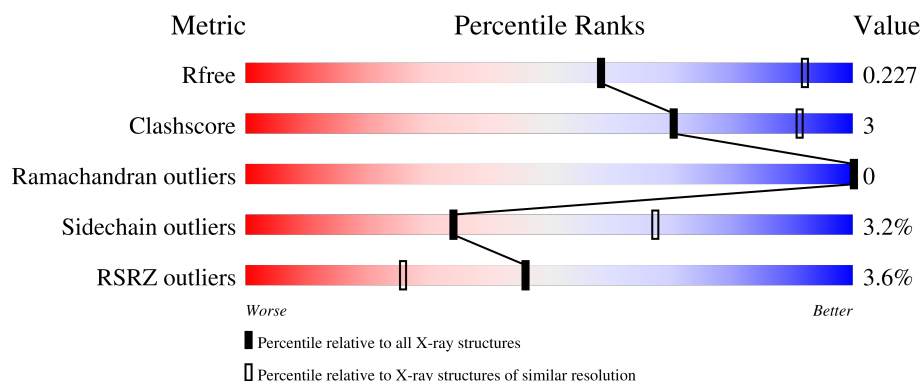
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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 $\leq 5\%$. 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	872	
2	B	482	
3	C	6	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6393 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 1A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	666	5217	3324	906	967	20	0	0	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	171	PRO	ALA	conflict	UNP O60341
A	?	-	ASP	deletion	UNP O60341
A	?	-	THR	deletion	UNP O60341
A	?	-	VAL	deletion	UNP O60341
A	?	-	LYS	deletion	UNP O60341

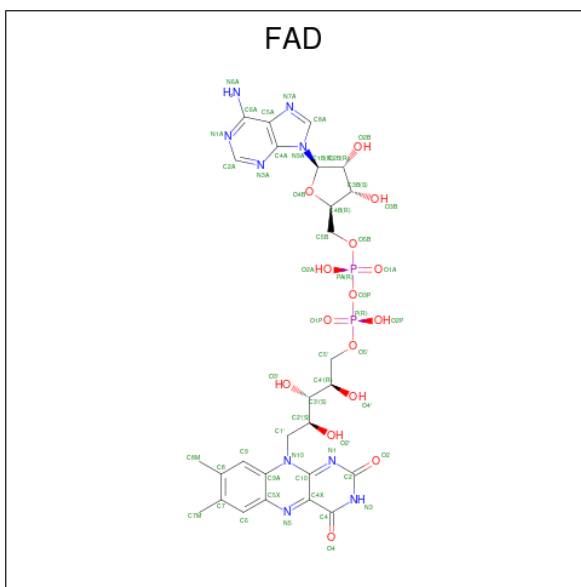
- Molecule 2 is a protein called REST COREPRESSOR 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	133	1076	676	194	203	3	0	0	0

- Molecule 3 is a protein called PEPTIDE.

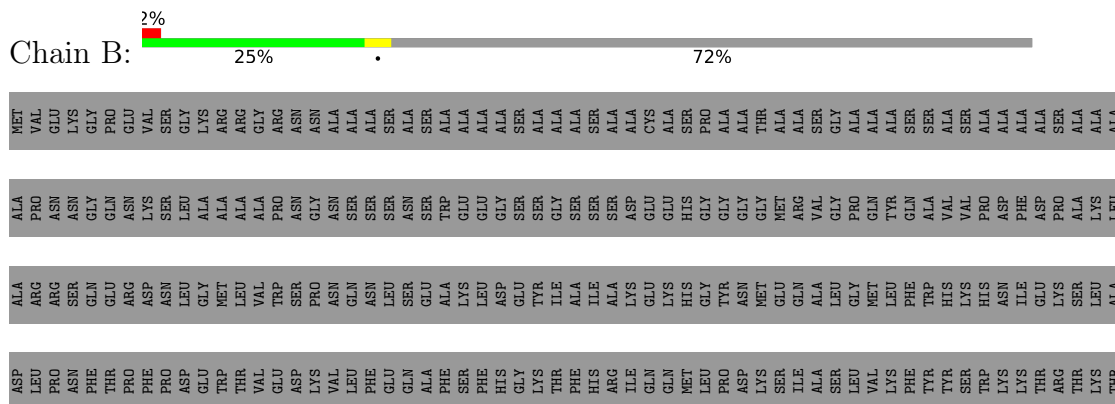
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	6	47	31	9	7	0	0	0

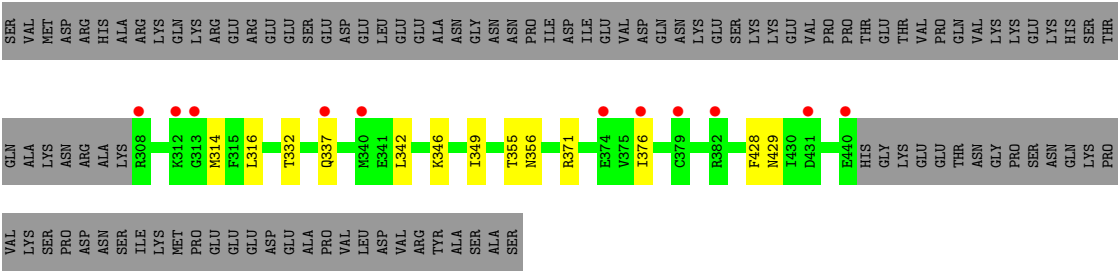
- Molecule 4 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



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

- Molecule 1: LYSINE-SPECIFIC HISTONE DEMETHYLASE 1A





● Molecule 3: PEPTIDE



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	118.95Å 179.27Å 234.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	53.45 – 3.00 53.45 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.6 (53.45-3.00) 99.7 (53.45-3.00)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.84 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.7.0027	Depositor
R, R_{free}	0.208 , 0.227 0.209 , 0.227	Depositor DCC
R_{free} test set	981 reflections (1.94%)	wwPDB-VP
Wilson B-factor (Å ²)	72.4	Xtriage
Anisotropy	0.041	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 41.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6393	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.18% 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: 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	0/5331	0.77	0/7232
2	B	0.42	0/1091	0.80	0/1471
3	C	0.32	0/48	0.71	0/63
All	All	0.53	0/6470	0.78	0/8766

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	5217	0	5252	40	0
2	B	1076	0	1091	9	0
3	C	47	0	50	4	0
4	A	53	0	31	2	0
All	All	6393	0	6424	44	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 3.

All (44) 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:356:ILE:HD11	1:A:566:THR:HG23	1.59	0.83
1:A:384:ARG:HB3	2:B:314:MET:HE3	1.81	0.62
1:A:693:LEU:HD21	3:C:6:VAL:HG21	1.87	0.55
1:A:435:VAL:HG13	2:B:349:ILE:HG13	1.89	0.55
1:A:548:SER:O	1:A:552:TRP:HB3	2.07	0.54
1:A:331:ALA:HA	4:A:900:FAD:C4X	2.39	0.52
1:A:801:GLU:CG	1:A:809:ALA:HA	2.39	0.52
1:A:801:GLU:HG2	1:A:809:ALA:H	1.74	0.51
1:A:331:ALA:HA	4:A:900:FAD:N5	2.26	0.50
1:A:536:LEU:HB3	1:A:544:LEU:HD21	1.93	0.50
1:A:594:ARG:HG2	1:A:640:VAL:HB	1.95	0.48
1:A:501:GLN:O	1:A:505:GLU:HB2	2.14	0.48
1:A:441:LEU:HD23	2:B:356:ASN:HD22	1.77	0.48
3:C:1:PRO:HD2	3:C:4:PHE:CE2	2.48	0.48
1:A:801:GLU:HG2	1:A:809:ALA:N	2.29	0.48
1:A:199:ILE:HD11	1:A:248:LEU:CD1	2.45	0.47
1:A:442:LYS:HE3	2:B:355:THR:HG21	1.97	0.47
1:A:384:ARG:HB3	2:B:314:MET:CE	2.45	0.46
1:A:199:ILE:HD11	1:A:248:LEU:HD11	1.96	0.46
1:A:566:THR:HG21	1:A:697:LEU:HD13	1.98	0.46
1:A:715:MET:HE3	1:A:723:ILE:HG12	1.98	0.45
1:A:809:ALA:HB3	3:C:1:PRO:HD3	1.99	0.45
1:A:537:GLU:HG2	1:A:544:LEU:HG	1.99	0.45
1:A:592:GLN:HB3	1:A:603:ILE:HD12	1.98	0.45
1:A:353:LEU:HB3	1:A:565:LEU:HD22	1.97	0.45
1:A:671:TRP:O	1:A:673:PRO:HD3	2.17	0.44
1:A:205:GLN:O	1:A:209:VAL:HG23	2.17	0.44
1:A:661:LYS:HD3	1:A:704:LEU:HD21	1.99	0.44
1:A:435:VAL:CG1	2:B:349:ILE:HG13	2.48	0.44
1:A:495:ASP:OD1	2:B:371:ARG:NH2	2.51	0.44
1:A:574:VAL:HB	1:A:575:PRO:CD	2.49	0.43
1:A:533:PHE:O	1:A:537:GLU:HG3	2.17	0.43
1:A:428:ILE:O	1:A:432:LYS:HB2	2.18	0.43
3:C:1:PRO:HD2	3:C:4:PHE:CD2	2.53	0.42
1:A:435:VAL:O	1:A:439:GLU:HB2	2.19	0.42
1:A:716:GLU:HG2	1:A:750:ARG:HG2	2.01	0.42
1:A:786:ILE:H	1:A:786:ILE:HD12	1.84	0.42
1:A:791:GLN:HA	1:A:792:PRO:HD3	1.86	0.42
1:A:566:THR:HG21	1:A:697:LEU:HD22	2.01	0.42
1:A:761:TYR:CD1	1:A:809:ALA:HB1	2.55	0.42
1:A:601:GLU:HA	1:A:616:TYR:O	2.20	0.41
1:A:364:GLU:HA	1:A:681:VAL:HB	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:428:PHE:O	2:B:429:ASN:C	2.64	0.40
2:B:342:LEU:O	2:B:346:LYS:HB2	2.22	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	664/872 (76%)	646 (97%)	18 (3%)	0	100	100
2	B	131/482 (27%)	126 (96%)	5 (4%)	0	100	100
3	C	4/6 (67%)	4 (100%)	0	0	100	100
All	All	799/1360 (59%)	776 (97%)	23 (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	566/711 (80%)	548 (97%)	18 (3%)	34	67
2	B	117/395 (30%)	113 (97%)	4 (3%)	32	66
3	C	5/5 (100%)	5 (100%)	0	100	100
All	All	688/1111 (62%)	666 (97%)	22 (3%)	34	67

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	174	VAL
1	A	226	LYS
1	A	429	GLU
1	A	433	LYS
1	A	449	VAL
1	A	458	LEU
1	A	469	LYS
1	A	479	LEU
1	A	492	LYS
1	A	536	LEU
1	A	538	PHE
1	A	556	ASP
1	A	591	ARG
1	A	633	GLN
1	A	652	GLN
1	A	659	LEU
1	A	684	THR
1	A	706	LEU
2	B	316	LEU
2	B	332	THR
2	B	337	GLN
2	B	376	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	191	GLN
1	A	298	GLN
1	A	399	ASN
1	A	403	ASN
1	A	427	GLN
1	A	430	HIS
1	A	459	HIS
1	A	484	HIS
1	A	564	HIS
1	A	606	ASN
1	A	638	GLN
1	A	771	ASN
2	B	348	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

1 ligand is 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	$\# Z > 2$
4	FAD	A	900	-	58,58,58	1.57	11 (18%)	85,89,89	1.55	16 (18%)

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	900	-	-	0/34/50/50	0/6/6/6

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	900	FAD	C9A-C5X	5.53	1.50	1.41
4	A	900	FAD	C5A-C4A	5.01	1.48	1.39
4	A	900	FAD	C8-C7	3.68	1.49	1.40
4	A	900	FAD	C5A-C6A	2.81	1.48	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	900	FAD	P-O3P	2.55	1.62	1.59
4	A	900	FAD	C8A-N7A	2.45	1.36	1.31
4	A	900	FAD	C4-N3	-2.40	1.34	1.38
4	A	900	FAD	PA-O3P	2.36	1.62	1.59
4	A	900	FAD	C4X-N5	2.20	1.35	1.30
4	A	900	FAD	C10-N10	2.15	1.42	1.37
4	A	900	FAD	C5X-N5	-2.08	1.35	1.39

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	900	FAD	C5A-C4A-N3A	-5.06	119.75	126.72
4	A	900	FAD	N3A-C4A-N9A	4.40	134.65	127.17
4	A	900	FAD	N3A-C2A-N1A	-3.63	123.09	128.58
4	A	900	FAD	C2A-N3A-C4A	3.56	120.53	111.83
4	A	900	FAD	C4A-N9A-C8A	3.30	109.20	105.74
4	A	900	FAD	C4A-C5A-N7A	-2.91	107.26	110.58
4	A	900	FAD	C5'-C4'-C3'	-2.81	106.91	112.22
4	A	900	FAD	C4X-C10-N1	-2.65	118.09	124.59
4	A	900	FAD	C4-C4X-N5	2.40	121.53	118.21
4	A	900	FAD	O4-C4-C4X	-2.28	120.52	126.53
4	A	900	FAD	C5A-N7A-C8A	2.24	106.97	103.45
4	A	900	FAD	C6A-C5A-N7A	2.24	136.41	132.09
4	A	900	FAD	C10-N1-C2	2.22	121.65	116.85
4	A	900	FAD	C2A-N1A-C6A	2.17	122.30	118.73
4	A	900	FAD	N9A-C8A-N7A	-2.10	110.96	113.94
4	A	900	FAD	C4X-C4-N3	2.05	118.47	113.25

There are no chirality outliers.

There are no torsion outliers.

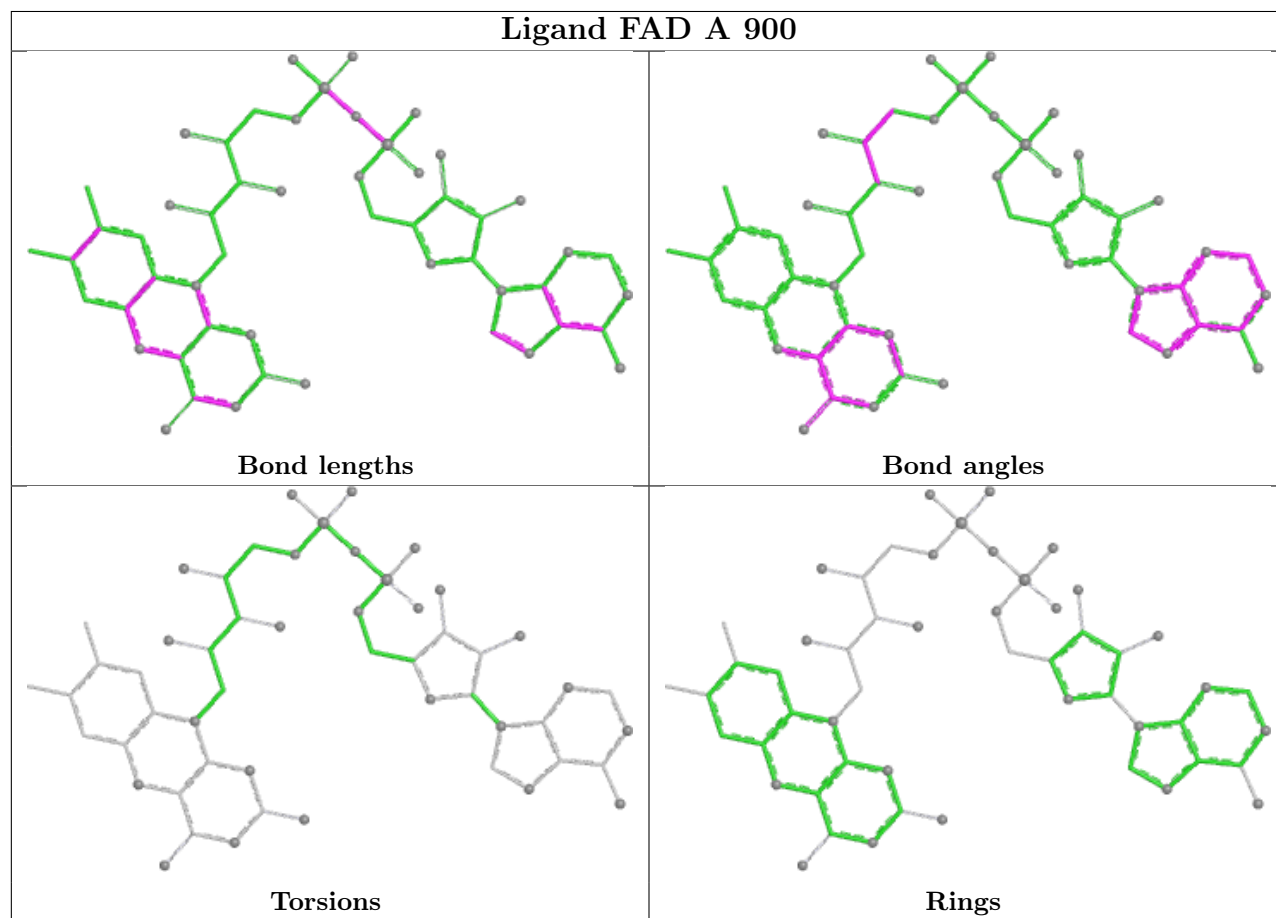
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	900	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 than 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 [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	666/872 (76%)	0.04	18 (2%) 56 33	43, 71, 106, 140	0
2	B	133/482 (27%)	0.60	11 (8%) 17 9	68, 102, 123, 142	0
3	C	6/6 (100%)	0.04	0 100 100	65, 67, 73, 78	0
All	All	805/1360 (59%)	0.13	29 (3%) 46 26	43, 77, 114, 142	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	836	LEU	5.7
1	A	833	MET	4.2
1	A	275	THR	3.9
1	A	377	MET	3.8
1	A	171	PRO	3.7
2	B	340	MET	3.5
2	B	376	ILE	3.4
1	A	273	LEU	3.0
1	A	373	GLU	3.0
1	A	403	ASN	3.0
2	B	312	LYS	2.8
1	A	467	GLU	2.8
1	A	271	LYS	2.8
2	B	337	GLN	2.7
2	B	440	GLU	2.6
1	A	645	GLU	2.5
2	B	374	GLU	2.4
2	B	379	CYS	2.4
2	B	313	GLY	2.3
1	A	453	GLU	2.3
1	A	272	PRO	2.3
1	A	770	GLY	2.3
1	A	652	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	510	GLU	2.2
2	B	382	ARG	2.2
2	B	308	ARG	2.1
2	B	431	ASP	2.1
1	A	771	ASN	2.1
1	A	358	GLN	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](#)

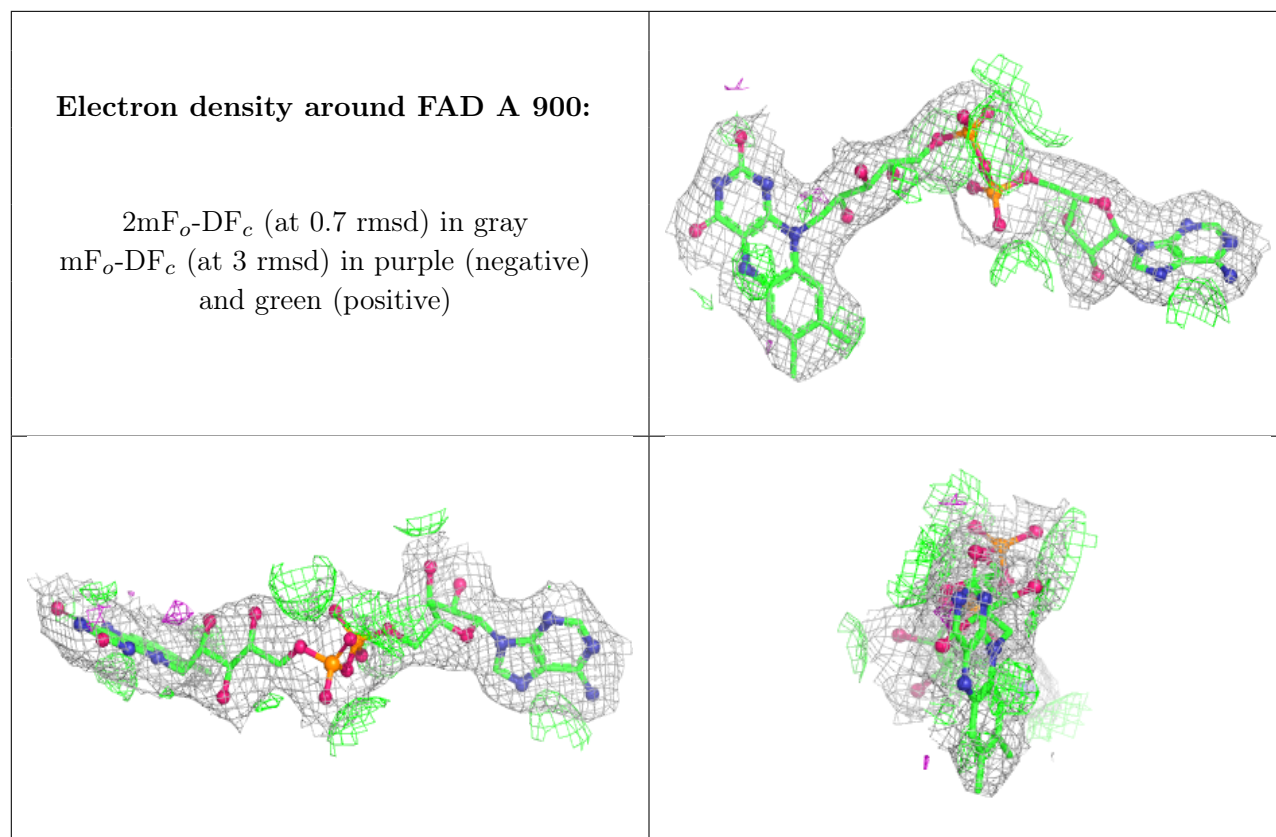
There are no oligosaccharides in this entry.

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($\text{\AA}^2$)	Q<0.9
4	FAD	A	900	53/53	0.97	0.07	43,54,64,66	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.