



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:46 AM UTC

PDB ID : 5H6Q / pdb_00005h6q
Title : Crystal structure of LSD1-CoREST in complex with peptide 11
Authors : Kikuchi, M.; Amano, Y.; Sato, S.; Yokoyama, S.; Umezawa, N.; Higuchi, T.; Umehara, T.
Deposited on : 2016-11-14
Resolution : 2.53 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

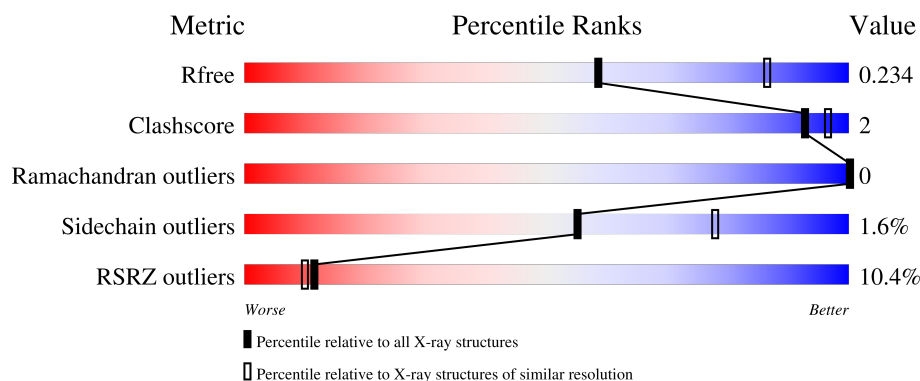
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.53 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	7383 (2.54-2.50)
Clashscore	190562	8079 (2.54-2.50)
Ramachandran outliers	187476	7944 (2.54-2.50)
Sidechain outliers	187428	7946 (2.54-2.50)
RSRZ outliers	180081	7387 (2.54-2.50)

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 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	669	6% 94% 5%
2	B	140	32% 90% 6%
3	C	21	5% 52% 19% 29%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6402 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
1	A	661	Total	C	N	O	S	0	1	0
			5165	3287	900	959	19			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	165	GLY	-	expression tag	UNP O60341
A	166	PRO	-	expression tag	UNP O60341
A	167	LEU	-	expression tag	UNP O60341
A	168	GLY	-	expression tag	UNP O60341
A	169	SER	-	expression tag	UNP O60341
A	170	HIS	-	expression tag	UNP O60341
A	171	MET	-	expression tag	UNP O60341

- Molecule 2 is a protein called REST corepressor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	131	Total	C	N	O	S	0	1	0
			1010	633	175	199	3			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	301	GLY	-	expression tag	UNP Q9UKL0
B	302	SER	-	expression tag	UNP Q9UKL0
B	303	SER	-	expression tag	UNP Q9UKL0
B	304	GLY	-	expression tag	UNP Q9UKL0
B	305	SER	-	expression tag	UNP Q9UKL0
B	306	ALA	-	expression tag	UNP Q9UKL0
B	307	SER	-	expression tag	UNP Q9UKL0

- Molecule 3 is a protein called peptide SRTMQTARKSTGGKAPRKQLK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	15	Total	C	N	O	S	0	0	0
			108	62	24	21	1			

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 5 is FLAVIN-ADENINE DINUCLEOTIDE (CCD ID: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



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

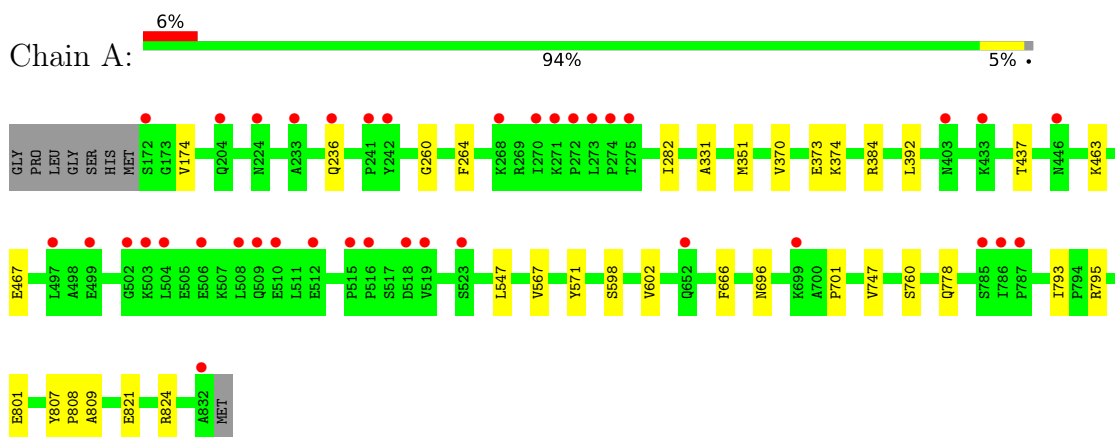
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	40	Total O 40 40	0	0
6	B	2	Total O 2 2	0	0

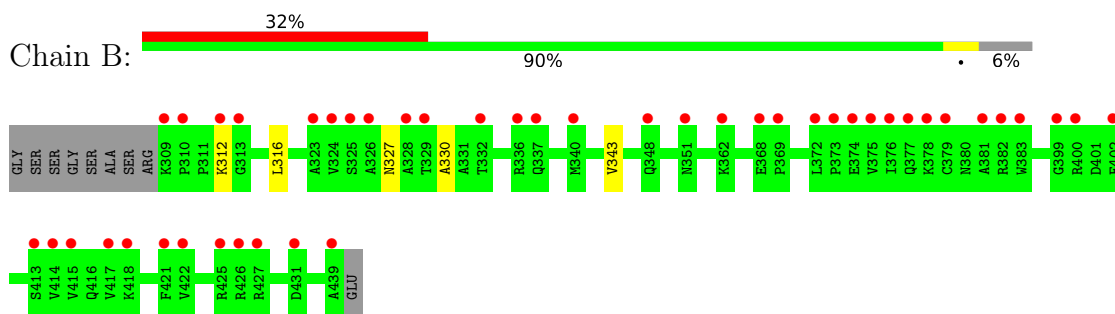
3 Residue-property plots [i](#)

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 1A



- Molecule 2: REST corepressor 1



- Molecule 3: peptide SRTMQTARKSTGGKAPRKQLK



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	120.83Å 180.49Å 233.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.53 40.00 – 2.53	Depositor EDS
% Data completeness (in resolution range)	99.8 (40.00-2.53) 99.7 (40.00-2.53)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.39 (at 2.54Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.224 , 0.247 0.214 , 0.234	Depositor DCC
R_{free} test set	1686 reflections (1.98%)	wwPDB-VP
Wilson B-factor (Å ²)	58.3	Xtriage
Anisotropy	0.712	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 37.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6402	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.82% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, 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	0.76	0/5277	0.90	3/7162 (0.0%)
2	B	0.66	0/1025	0.91	0/1395
3	C	0.77	0/107	1.03	0/139
All	All	0.75	0/6409	0.90	3/8696 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	370	VAL	N-CA-C	-5.73	102.72	108.96
1	A	351	MET	N-CA-C	-5.06	101.00	109.24
1	A	547	LEU	N-CA-C	5.01	117.47	109.96

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	5165	0	5174	16	0
2	B	1010	0	946	2	0
3	C	108	0	118	2	0
4	A	24	0	32	0	0
5	A	53	0	31	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	40	0	0	0	0
6	B	2	0	0	0	0
All	All	6402	0	6301	19	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 2.

All (19) 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:463:LYS:O	1:A:467:GLU:HG2	2.01	0.61
2:B:327:ASN:HB3	2:B:330:ALA:HB2	1.83	0.59
1:A:331:ALA:HA	5:A:905:FAD:N5	2.23	0.53
1:A:801:GLU:HG2	1:A:809:ALA:H	1.73	0.52
1:A:793:ILE:HD11	1:A:795:ARG:CZ	2.41	0.51
3:C:2:ARG:NH2	3:C:12:GLY:O	2.39	0.49
1:A:331:ALA:HA	5:A:905:FAD:C4X	2.44	0.48
1:A:821:GLU:OE2	1:A:824:ARG:NH1	2.47	0.48
1:A:282:ILE:HG21	1:A:602:VAL:HG21	1.95	0.47
1:A:801:GLU:HG2	1:A:809:ALA:N	2.30	0.46
1:A:801:GLU:CG	1:A:809:ALA:HA	2.48	0.44
1:A:384:ARG:NH1	2:B:312:LYS:O	2.48	0.43
1:A:567:VAL:HG11	1:A:571:TYR:HA	2.00	0.43
1:A:760:SER:HB2	5:A:905:FAD:HM83	2.01	0.42
1:A:666:PHE:O	1:A:701:PRO:HG2	2.20	0.42
1:A:807:TYR:N	1:A:808:PRO:CD	2.83	0.41
1:A:236[A]:GLN:OE1	1:A:236[A]:GLN:HA	2.19	0.41
1:A:260:GLY:O	1:A:264:PHE:CD1	2.73	0.41
3:C:8:ARG:O	3:C:9:LYS:C	2.61	0.41

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	660/669 (99%)	638 (97%)	22 (3%)	0	100	100
2	B	130/140 (93%)	117 (90%)	13 (10%)	0	100	100
3	C	13/21 (62%)	13 (100%)	0	0	100	100
All	All	803/830 (97%)	768 (96%)	35 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	557/567 (98%)	548 (98%)	9 (2%)	55	78
2	B	102/121 (84%)	100 (98%)	2 (2%)	48	73
3	C	11/17 (65%)	11 (100%)	0	100	100
All	All	670/705 (95%)	659 (98%)	11 (2%)	55	78

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	174	VAL
1	A	373	GLU
1	A	374	LYS
1	A	392	LEU
1	A	437	THR
1	A	598	SER
1	A	696	ASN
1	A	747	VAL
1	A	778	GLN
2	B	316	LEU
2	B	343	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	185	HIS
1	A	224	ASN
1	A	514	ASN
2	B	429	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 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	$\# Z > 2$
5	FAD	A	905	-	58,58,58	1.50	10 (17%)	85,89,89	1.75	21 (24%)
4	GOL	A	904	-	5,5,5	0.86	0	5,5,5	0.70	0
4	GOL	A	902	-	5,5,5	0.98	0	5,5,5	0.61	0
4	GOL	A	901	-	5,5,5	0.35	0	5,5,5	0.74	0
4	GOL	A	903	-	5,5,5	1.39	1 (20%)	5,5,5	0.98	0

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	FAD	A	905	-	-	1/34/50/50	0/6/6/6
4	GOL	A	904	-	-	0/4/4/4	-
4	GOL	A	902	-	-	0/4/4/4	-
4	GOL	A	901	-	-	2/4/4/4	-
4	GOL	A	903	-	-	1/4/4/4	-

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	905	FAD	C9A-C5X	4.98	1.49	1.41
5	A	905	FAD	C5A-C4A	4.19	1.46	1.39
5	A	905	FAD	C8-C7	3.27	1.48	1.40
5	A	905	FAD	C5X-N5	-3.21	1.33	1.39
5	A	905	FAD	C1'-C2'	-2.85	1.48	1.52
5	A	905	FAD	C4-N3	-2.52	1.34	1.38
5	A	905	FAD	C5A-C6A	2.35	1.47	1.41
5	A	905	FAD	C4A-N9A	-2.33	1.32	1.37
4	A	903	GOL	O2-C2	2.28	1.50	1.43
5	A	905	FAD	C5A-N7A	-2.17	1.35	1.39
5	A	905	FAD	C8A-N7A	2.17	1.35	1.31

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	905	FAD	C5A-C4A-N3A	-4.84	120.05	126.72
5	A	905	FAD	N3A-C2A-N1A	-4.34	122.01	128.58
5	A	905	FAD	N3A-C4A-N9A	4.14	134.20	127.17
5	A	905	FAD	C2A-N3A-C4A	3.63	120.70	111.83
5	A	905	FAD	C4A-N9A-C8A	3.02	108.91	105.74
5	A	905	FAD	O4-C4-C4X	-2.92	118.82	126.53
5	A	905	FAD	C5'-C4'-C3'	-2.71	107.10	112.22
5	A	905	FAD	C5X-C9A-N10	2.68	120.39	117.97
5	A	905	FAD	C2A-N1A-C6A	2.67	123.12	118.73
5	A	905	FAD	C9A-C5X-N5	-2.64	119.66	122.45
5	A	905	FAD	O2-C2-N1	-2.61	117.47	121.80
5	A	905	FAD	O2A-PA-O1A	2.59	124.47	112.44
5	A	905	FAD	C4'-C3'-C2'	-2.58	109.27	113.57
5	A	905	FAD	C4A-C5A-N7A	-2.49	107.74	110.58
5	A	905	FAD	C4X-C10-N1	-2.38	118.75	124.59
5	A	905	FAD	C8M-C8-C9	-2.33	115.46	119.57
5	A	905	FAD	O3'-C3'-C2'	2.31	114.19	108.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	905	FAD	C6-C5X-C9A	2.22	122.10	119.05
5	A	905	FAD	C6A-C5A-N7A	2.22	136.37	132.09
5	A	905	FAD	C4A-N9A-C1B	-2.17	121.56	126.63
5	A	905	FAD	C10-N1-C2	2.17	121.55	116.85

There are no chirality outliers.

All (4) torsion outliers are listed below:

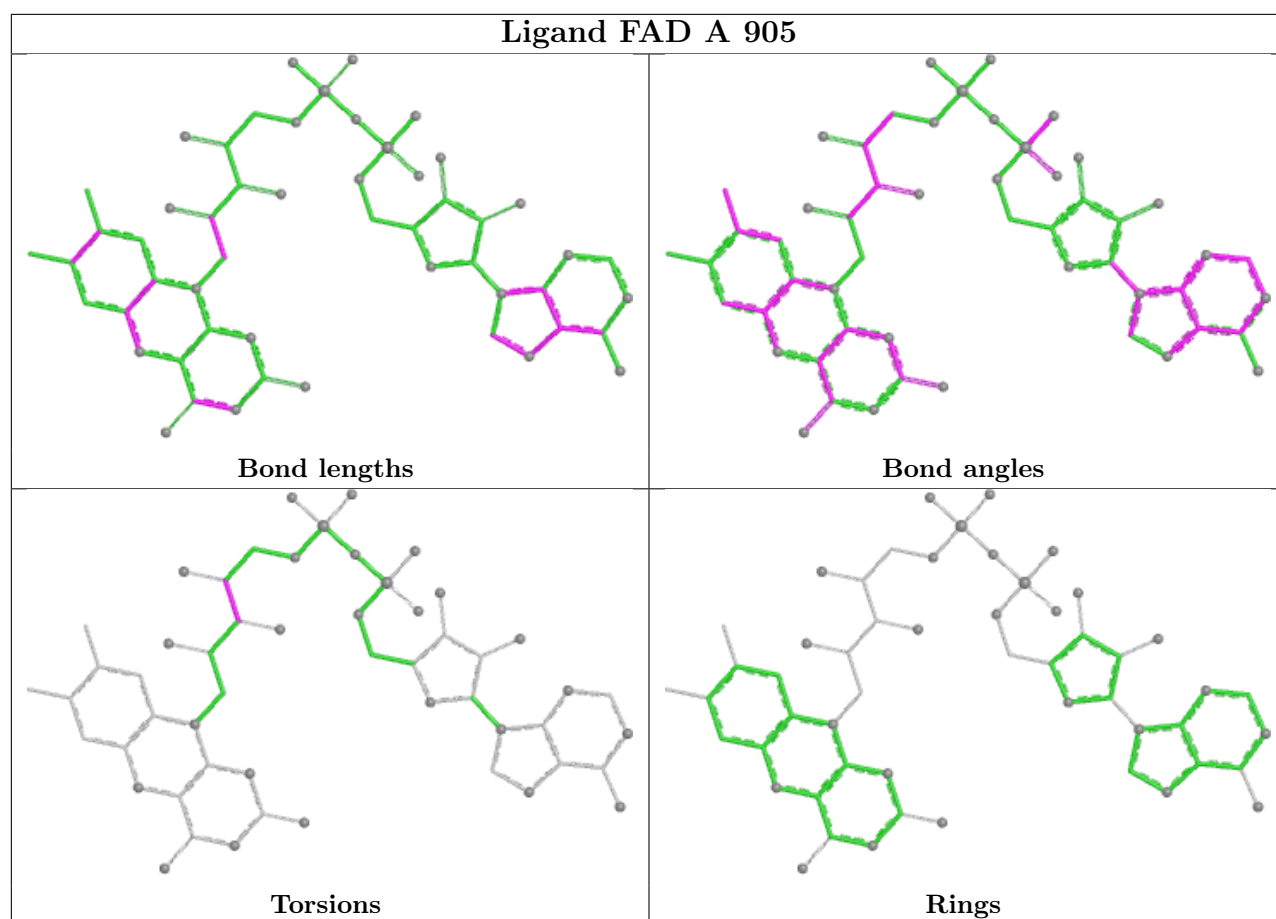
Mol	Chain	Res	Type	Atoms
4	A	901	GOL	C1-C2-C3-O3
4	A	901	GOL	O2-C2-C3-O3
4	A	903	GOL	O1-C1-C2-O2
5	A	905	FAD	C2'-C3'-C4'-O4'

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	905	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 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	661/669 (98%)	0.38	38 (5%) 29 26	36, 64, 104, 137	1 (0%)
2	B	131/140 (93%)	1.74	45 (34%) 1 1	41, 99, 131, 153	1 (0%)
3	C	15/21 (71%)	0.56	1 (6%) 24 21	49, 59, 82, 95	0
All	All	807/830 (97%)	0.61	84 (10%) 11 10	36, 68, 117, 153	2 (0%)

All (84) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	309	LYS	8.9
3	C	15	ALA	6.3
1	A	832	ALA	6.2
1	A	236[A]	GLN	6.0
2	B	377	GLN	5.3
2	B	439	ALA	4.9
1	A	786	ILE	4.7
2	B	376	ILE	4.5
1	A	272	PRO	4.2
2	B	382	ARG	4.2
2	B	379	CYS	4.1
2	B	351[A]	ASN	4.0
2	B	313	GLY	4.0
2	B	414	VAL	3.9
2	B	332	THR	3.8
2	B	399	GLY	3.8
1	A	271	LYS	3.7
2	B	378	LYS	3.7
1	A	172	SER	3.6
1	A	506	GLU	3.6
2	B	383	TRP	3.5
2	B	375	VAL	3.5
2	B	326	ALA	3.5

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Mol	Chain	Res	Type	RSRZ
2	B	336	ARG	3.5
2	B	325	SER	3.4
2	B	340	MET	3.4
1	A	508	LEU	3.4
2	B	373	PRO	3.4
2	B	312	LYS	3.3
1	A	509	GLN	3.3
2	B	310	PRO	3.3
1	A	699	LYS	3.3
1	A	787	PRO	3.2
2	B	362	LYS	3.2
1	A	503	LYS	3.0
2	B	374	GLU	2.9
2	B	425	ARG	2.9
1	A	433	LYS	2.9
2	B	431	ASP	2.9
2	B	324	VAL	2.9
2	B	328	ALA	2.9
2	B	381	ALA	2.9
1	A	241	PRO	2.8
2	B	329	THR	2.8
2	B	426	ARG	2.8
1	A	519	VAL	2.8
1	A	497	LEU	2.8
1	A	518	ASP	2.8
1	A	270	ILE	2.8
2	B	421	PHE	2.8
1	A	403	ASN	2.7
2	B	368	GLU	2.7
1	A	504	LEU	2.7
2	B	415	VAL	2.7
1	A	512	GLU	2.7
2	B	400	ARG	2.6
2	B	422	VAL	2.6
1	A	515	PRO	2.6
2	B	402	PHE	2.5
2	B	348	GLN	2.5
1	A	274	PRO	2.4
1	A	273	LEU	2.4
2	B	413	SER	2.4
2	B	372	LEU	2.4
1	A	242	TYR	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	224	ASN	2.4
1	A	502	GLY	2.3
1	A	785	SER	2.3
2	B	323	ALA	2.3
2	B	418	LYS	2.3
2	B	427	ARG	2.3
2	B	369	PRO	2.2
1	A	204	GLN	2.2
1	A	275	THR	2.2
1	A	652	GLN	2.2
1	A	499	GLU	2.2
1	A	510	GLU	2.2
1	A	233	ALA	2.1
2	B	337	GLN	2.1
1	A	268	LYS	2.1
1	A	523	SER	2.1
1	A	516	PRO	2.0
2	B	417	VAL	2.0
1	A	446	ASN	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.

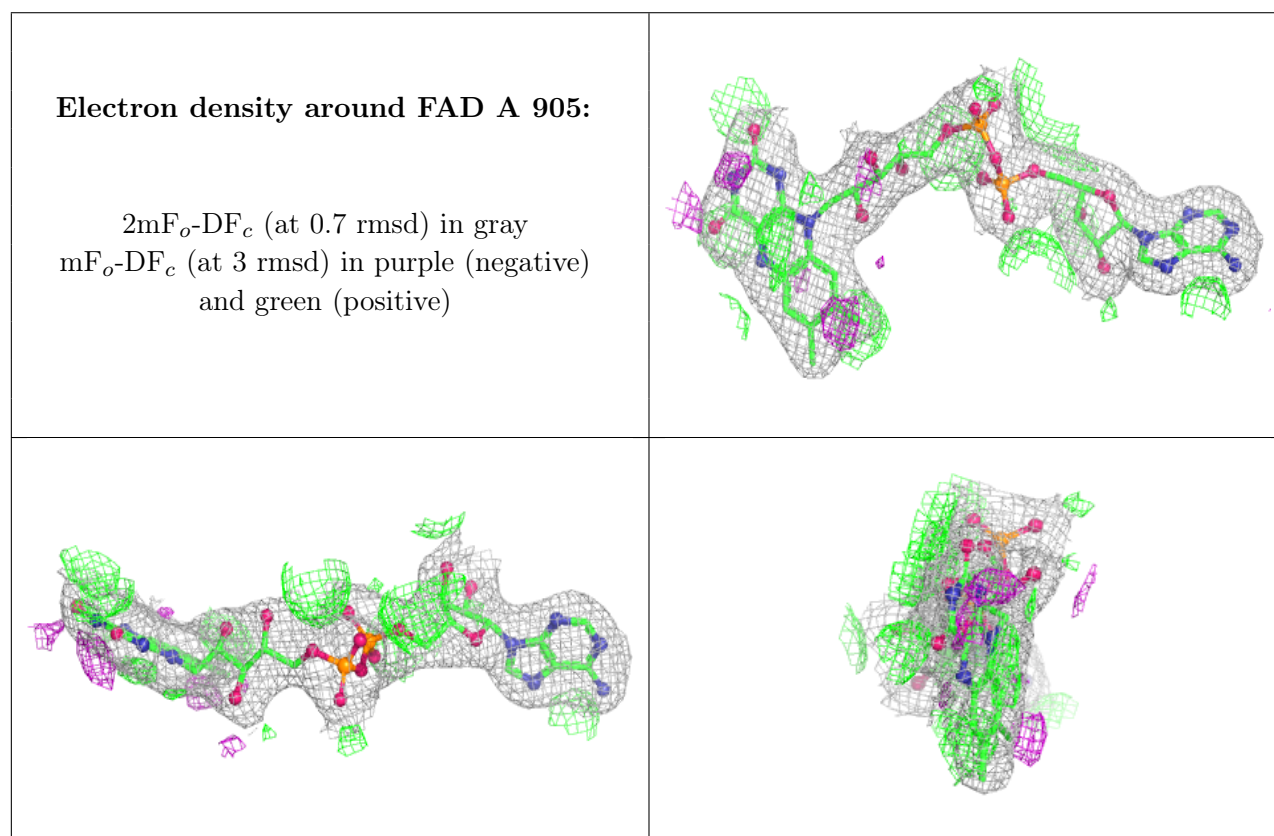
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	GOL	A	902	6/6	0.70	0.26	68,79,84,84	0
4	GOL	A	903	6/6	0.83	0.30	57,63,68,73	0
4	GOL	A	904	6/6	0.90	0.17	52,57,70,70	0
4	GOL	A	901	6/6	0.95	0.12	60,64,66,69	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	FAD	A	905	53/53	0.97	0.07	34,42,51,53	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.