



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 27, 2016 – 03:41 PM EDT

PDB ID : 5L3F
Title : LSD1-CoREST1 in complex with polymyxin B
Authors : Speranzini, V.; Rotili, D.; Ciossani, G.; Pilotto, S.; Forgione, M.; Lucidi, A.;
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Deposited on : 2016-04-10
Resolution : 3.50 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-20027939
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-20027939

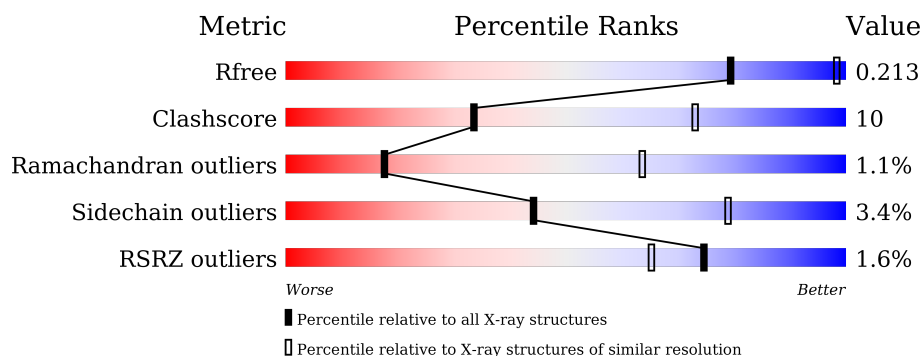
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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	1051 (3.60-3.40)
Clashscore	102246	1157 (3.60-3.40)
Ramachandran outliers	100387	1120 (3.60-3.40)
Sidechain outliers	100360	1121 (3.60-3.40)
RSRZ outliers	91569	1058 (3.60-3.40)

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	730	
2	B	178	
3	C	11	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6431 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	666	Total	C	N	O	S	0	0	0
			5217	3324	906	967	20			

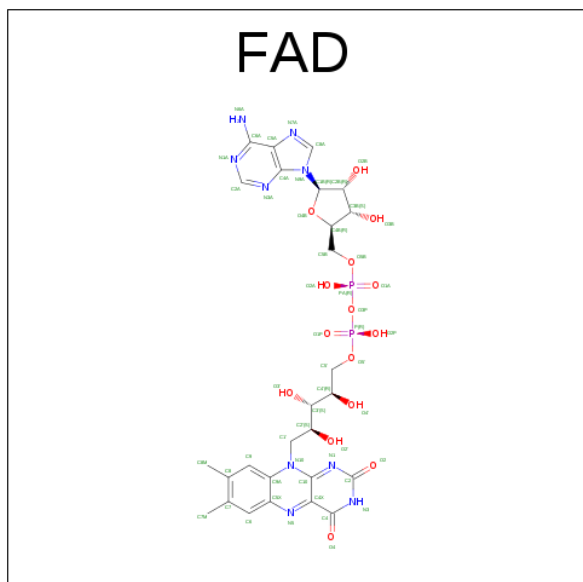
- Molecule 2 is a protein called REST corepressor 1.

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

- Molecule 3 is a protein called Polmyxin B.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	11	Total	C	N	O	15	0	0
			85	56	16	13			

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

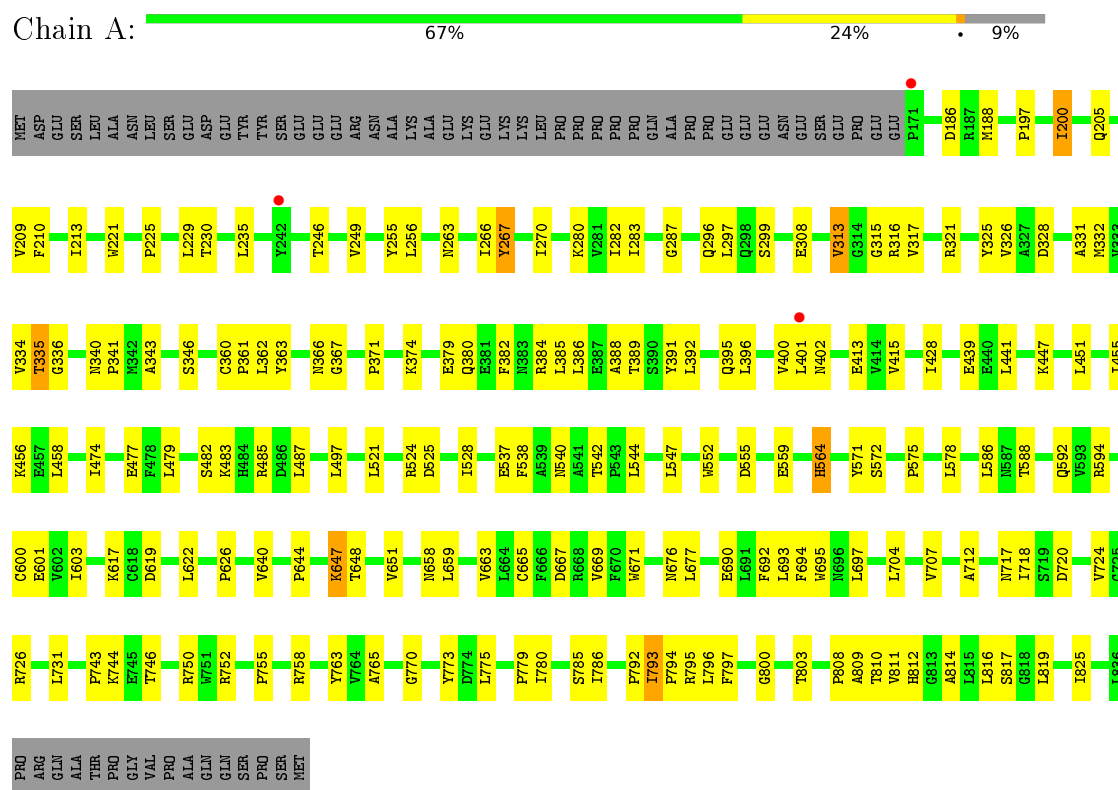


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

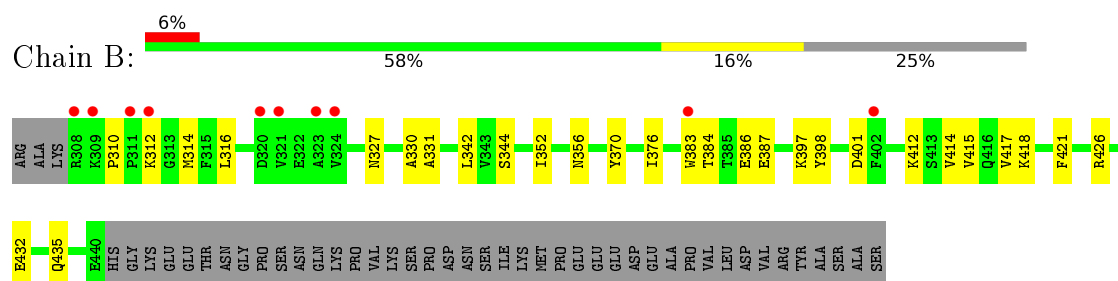
3 Residue-property plots

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: Lysine-specific histone demethylase 1A



- Molecule 2: REST corepressor 1





4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	119.20Å 179.00Å 235.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.23 – 3.50 49.23 – 3.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.23-3.50) 99.9 (49.23-3.50)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.48 (at 3.48Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.186 , 0.210 0.188 , 0.213	Depositor DCC
R_{free} test set	636 reflections (1.98%)	DCC
Wilson B-factor (Å ²)	109.9	Xtriage
Anisotropy	0.648	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 106.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6431	wwPDB-VP
Average B, all atoms (Å ²)	123.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.51% 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: 4FO, DTH, DAB, FAD, 6FH

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	0.62	0/5331	0.63	0/7232
2	B	0.45	0/1091	0.52	0/1471
3	C	2.31	1/19 (5.3%)	1.20	0/24
All	All	0.61	1/6441 (0.0%)	0.61	0/8727

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	7	PHE	CB-CG	-6.56	1.40	1.51

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	792	PRO	Peptide

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	5217	0	5252	120	0
2	B	1076	0	1091	15	0
3	C	85	0	54	5	0
4	A	53	0	29	8	0
All	All	6431	0	6426	131	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 10.

All (131) 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:331:ALA:HA	4:A:901:FAD:N5	2.01	0.76
1:A:280:LYS:N	1:A:619:ASP:OD2	2.20	0.70
1:A:667:ASP:HB3	1:A:744:LYS:HD2	1.76	0.68
1:A:335:THR:OG1	1:A:335:THR:O	2.13	0.65
1:A:537:GLU:HG3	1:A:544:LEU:HG	1.80	0.62
1:A:800:GLY:O	1:A:803:THR:OG1	2.16	0.62
1:A:384:ARG:NH1	2:B:312:LYS:O	2.33	0.60
1:A:321:ARG:HG2	1:A:326:VAL:HG22	1.84	0.60
1:A:693:LEU:HD12	1:A:694:PHE:H	1.66	0.59
1:A:647:LYS:O	1:A:651:VAL:HG23	2.02	0.59
1:A:663:VAL:HG22	1:A:704:LEU:HD11	1.85	0.58
1:A:188:MET:SD	1:A:200:ILE:HG23	2.43	0.58
1:A:287:GLY:HA3	4:A:901:FAD:O5B	2.04	0.57
1:A:334:VAL:O	1:A:336:GLY:N	2.32	0.57
1:A:428:ILE:HG12	2:B:342:LEU:HD13	1.87	0.56
1:A:235:LEU:HD13	1:A:249:VAL:HG11	1.87	0.56
1:A:669:VAL:HG13	1:A:671:TRP:CE2	2.41	0.56
1:A:456:LYS:HG3	2:B:370:TYR:CZ	2.41	0.55
1:A:188:MET:HG2	1:A:210:PHE:HE1	1.70	0.54
1:A:221:TRP:CZ3	1:A:225:PRO:HA	2.42	0.54
1:A:266:ILE:HD11	1:A:578:LEU:HD23	1.90	0.54
1:A:559:GLU:HG2	3:C:9:DAB:HD1	1.72	0.53
1:A:197:PRO:HA	1:A:200:ILE:HD11	1.91	0.53
2:B:327:ASN:HB2	2:B:330:ALA:HB2	1.90	0.53
1:A:564:HIS:CD2	3:C:8:LEU:H	2.26	0.53
1:A:308:GLU:OE2	4:A:901:FAD:H1B	2.09	0.53
1:A:343:ALA:O	1:A:346:SER:OG	2.17	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:418:LYS:O	2:B:421:PHE:HB2	2.08	0.52
1:A:690:GLU:OE2	1:A:726:ARG:NH1	2.42	0.52
1:A:188:MET:HG2	1:A:210:PHE:CE1	2.45	0.52
1:A:693:LEU:HD12	1:A:694:PHE:N	2.25	0.51
2:B:432:GLU:O	2:B:435:GLN:HG2	2.11	0.51
1:A:385:LEU:O	1:A:388:ALA:HB3	2.10	0.51
1:A:308:GLU:OE1	4:A:901:FAD:O3B	2.29	0.51
1:A:230:THR:HG23	1:A:270:ILE:HD12	1.93	0.50
1:A:366:ASN:OD1	1:A:367:GLY:N	2.45	0.50
1:A:773:TYR:HE2	1:A:808:PRO:HB3	1.76	0.50
1:A:371:PRO:HG2	1:A:374:LYS:HB2	1.93	0.50
1:A:521:LEU:HD22	1:A:525:ASP:HB3	1.93	0.49
1:A:379:GLU:O	1:A:382:PHE:HB3	2.12	0.49
3:C:5:4FO:O	3:C:7:PHE:N	2.45	0.48
1:A:720:ASP:O	1:A:724:VAL:HG23	2.13	0.48
1:A:384:ARG:HB3	2:B:314:MET:CE	2.43	0.48
1:A:439:GLU:HG3	2:B:352:ILE:HD13	1.95	0.48
1:A:308:GLU:OE2	4:A:901:FAD:O2B	2.24	0.48
1:A:773:TYR:CE2	1:A:808:PRO:HB3	2.48	0.48
1:A:644:PRO:O	1:A:648:THR:HG23	2.13	0.48
1:A:341:PRO:HG3	1:A:816:LEU:HD21	1.95	0.48
1:A:755:PRO:HA	1:A:758:ARG:NH1	2.28	0.48
1:A:552:TRP:CZ3	3:C:11:DTH:HG23	2.48	0.48
1:A:718:ILE:O	1:A:750:ARG:NH2	2.45	0.48
1:A:814:ALA:O	1:A:817:SER:N	2.46	0.47
1:A:647:LYS:HE2	1:A:647:LYS:HB2	1.51	0.47
1:A:331:ALA:HA	4:A:901:FAD:C4X	2.44	0.47
1:A:542:THR:HG21	1:A:763:TYR:CG	2.50	0.47
1:A:540:ASN:O	1:A:542:THR:HG22	2.15	0.47
1:A:308:GLU:HB3	1:A:586:LEU:HD23	1.96	0.47
1:A:770:GLY:O	1:A:773:TYR:N	2.45	0.47
1:A:209:VAL:O	1:A:213:ILE:HG13	2.15	0.47
1:A:282:ILE:HD13	1:A:282:ILE:HA	1.67	0.47
1:A:205:GLN:O	1:A:209:VAL:HG23	2.15	0.46
1:A:665:CYS:O	1:A:744:LYS:N	2.48	0.46
1:A:695:TRP:CE3	1:A:697:LEU:HD11	2.51	0.46
1:A:658:ASN:ND2	1:A:752:ARG:HB2	2.31	0.46
1:A:474:ILE:HA	1:A:474:ILE:HD12	1.76	0.46
1:A:186:ASP:N	1:A:186:ASP:OD1	2.49	0.46
1:A:380:GLN:HG2	1:A:384:ARG:HD3	1.98	0.46
2:B:383:TRP:CD2	2:B:412:LYS:HE2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:812:HIS:O	1:A:816:LEU:HG	2.16	0.45
1:A:808:PRO:O	1:A:810:THR:HG23	2.17	0.45
1:A:455:ILE:HG23	1:A:487:LEU:HD11	1.99	0.45
1:A:296:GLN:O	1:A:299:SER:HB3	2.17	0.44
1:A:360:CYS:HA	1:A:361:PRO:HD2	1.88	0.44
1:A:743:PRO:HB2	1:A:746:THR:HG23	1.99	0.44
1:A:537:GLU:CG	1:A:544:LEU:HG	2.46	0.44
1:A:626:PRO:HD3	4:A:901:FAD:H52A	1.99	0.44
1:A:386:LEU:HD23	1:A:386:LEU:HA	1.72	0.44
1:A:547:LEU:HA	1:A:547:LEU:HD23	1.83	0.44
1:A:648:THR:O	1:A:651:VAL:N	2.50	0.44
1:A:267:TYR:CD1	1:A:267:TYR:N	2.86	0.44
1:A:474:ILE:HD12	1:A:477:GLU:HB3	1.98	0.44
1:A:451:LEU:HA	1:A:451:LEU:HD12	1.71	0.43
1:A:524:ARG:O	1:A:528:ILE:HG13	2.18	0.43
1:A:283:ILE:HG12	1:A:622:LEU:HB3	2.00	0.43
1:A:458:LEU:HD23	1:A:458:LEU:HA	1.74	0.43
4:A:901:FAD:H8A	4:A:901:FAD:H2B	1.86	0.43
1:A:479:LEU:HD11	1:A:483:LYS:HE2	2.00	0.43
1:A:458:LEU:HB3	1:A:487:LEU:HD13	2.00	0.43
1:A:704:LEU:HA	1:A:704:LEU:HD12	1.72	0.43
1:A:235:LEU:HD21	1:A:246:THR:HG22	2.00	0.43
2:B:397:LYS:HD3	2:B:398:TYR:CE2	2.53	0.43
1:A:572:SER:O	1:A:575:PRO:HD2	2.18	0.43
1:A:555:ASP:N	1:A:555:ASP:OD1	2.43	0.43
1:A:564:HIS:HD2	3:C:8:LEU:HB2	1.82	0.43
2:B:384:THR:OG1	2:B:386:GLU:HB3	2.19	0.43
1:A:600:CYS:SG	1:A:795:ARG:HB3	2.58	0.43
1:A:362:LEU:C	1:A:363:TYR:CD1	2.92	0.43
1:A:447:LYS:HD2	1:A:497:LEU:HD21	2.01	0.43
1:A:594:ARG:HA	1:A:640:VAL:O	2.19	0.43
1:A:780:ILE:HB	1:A:796:LEU:HB3	2.01	0.43
1:A:296:GLN:HG3	1:A:819:LEU:HD22	2.01	0.43
1:A:200:ILE:HG13	1:A:200:ILE:H	1.31	0.43
1:A:592:GLN:HB3	1:A:603:ILE:HD12	2.00	0.42
1:A:315:GLY:O	1:A:317:VAL:N	2.52	0.42
1:A:391:TYR:CD1	1:A:395:GLN:HG3	2.54	0.42
1:A:386:LEU:O	1:A:389:THR:OG1	2.23	0.42
2:B:414:VAL:O	2:B:417:VAL:HB	2.19	0.42
1:A:325:TYR:CE2	1:A:665:CYS:HB3	2.55	0.42
2:B:310:PRO:HB3	2:B:316:LEU:HD12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:255:TYR:CD2	1:A:256:LEU:HD23	2.55	0.42
1:A:731:LEU:HA	1:A:731:LEU:HD23	1.85	0.42
1:A:487:LEU:HD12	1:A:487:LEU:HA	1.79	0.41
1:A:707:VAL:HG12	1:A:712:ALA:HA	2.02	0.41
1:A:694:PHE:HA	1:A:704:LEU:O	2.20	0.41
1:A:786:ILE:H	1:A:786:ILE:HD12	1.85	0.41
1:A:676:ASN:HA	1:A:676:ASN:HD22	1.71	0.41
1:A:361:PRO:HB2	1:A:363:TYR:CE1	2.56	0.41
1:A:797:PHE:CE1	1:A:825:ILE:HG12	2.56	0.41
1:A:229:LEU:N	1:A:263:ASN:OD1	2.34	0.41
1:A:385:LEU:HD23	1:A:415:VAL:CG1	2.51	0.41
1:A:340:ASN:HA	1:A:341:PRO:HD2	1.87	0.41
1:A:392:LEU:O	1:A:396:LEU:HB2	2.20	0.41
1:A:441:LEU:HD23	2:B:356:ASN:HD22	1.85	0.41
1:A:763:TYR:HE1	1:A:765:ALA:HA	1.86	0.41
1:A:332:MET:HE2	1:A:332:MET:HB3	1.76	0.41
1:A:775:LEU:HA	1:A:775:LEU:HD23	1.85	0.40
1:A:601:GLU:OE1	1:A:617:LYS:HE3	2.22	0.40
1:A:779:PRO:HB3	1:A:797:PHE:CD2	2.57	0.40
2:B:384:THR:HG23	2:B:387:GLU:OE1	2.21	0.40
1:A:297:LEU:HD23	1:A:297:LEU:HA	1.76	0.40
1:A:793:ILE:HA	1:A:794:PRO:HD3	1.86	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	664/730 (91%)	604 (91%)	53 (8%)	7 (1%)	17	63
2	B	131/178 (74%)	126 (96%)	3 (2%)	2 (2%)	13	56
3	C	2/11 (18%)	1 (50%)	1 (50%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	797/919 (87%)	731 (92%)	57 (7%)	9 (1%)	17	63

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	316	ARG
1	A	402	ASN
1	A	401	LEU
1	A	809	ALA
1	A	785	SER
2	B	331	ALA
2	B	401	ASP
1	A	793	ILE
1	A	313	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	566/623 (91%)	547 (97%)	19 (3%)	44	79
2	B	117/156 (75%)	113 (97%)	4 (3%)	44	79
3	C	2/2 (100%)	2 (100%)	0	100	100
All	All	685/781 (88%)	662 (97%)	23 (3%)	44	79

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	200	ILE
1	A	267	TYR
1	A	313	VAL
1	A	328	ASP
1	A	335	THR
1	A	400	VAL
1	A	413	GLU

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Mol	Chain	Res	Type
1	A	482	SER
1	A	485	ARG
1	A	538	PHE
1	A	564	HIS
1	A	571	TYR
1	A	588	THR
1	A	647	LYS
1	A	659	LEU
1	A	677	LEU
1	A	692	PHE
1	A	717	ASN
1	A	811	VAL
2	B	344	SER
2	B	376	ILE
2	B	415	VAL
2	B	426	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	383	ASN
1	A	632	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

8 non-standard protein/DNA/RNA residues 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
3	DAB	C	10	3	4,6,7	0.55	0	3,6,8	1.25	1 (33%)
3	DTH	C	11	3	5,6,7	0.52	0	5,7,9	1.84	1 (20%)
3	4FO	C	2	3	4,6,7	0.49	0	3,6,8	1.07	0
3	DTH	C	3	3	5,6,7	0.54	0	5,7,9	1.14	1 (20%)
3	4FO	C	4	3	4,6,7	0.49	0	3,6,8	1.12	0
3	4FO	C	5	3	4,6,7	0.43	0	3,6,8	1.39	1 (33%)
3	DAB	C	6	3	4,6,7	0.58	0	3,6,8	1.00	0
3	DAB	C	9	3	4,6,7	0.41	0	3,6,8	1.04	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
3	DAB	C	10	3	-	0/3/5/7	0/0/0/0
3	DTH	C	11	3	-	0/4/6/8	0/0/0/0
3	4FO	C	2	3	-	0/3/5/7	0/0/0/0
3	DTH	C	3	3	-	0/4/6/8	0/0/0/0
3	4FO	C	4	3	-	0/3/5/7	0/0/0/0
3	4FO	C	5	3	-	0/3/5/7	0/0/0/0
3	DAB	C	6	3	-	0/3/5/7	0/0/0/0
3	DAB	C	9	3	-	0/3/5/7	0/0/0/0

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	11	DTH	O-C-CA	-3.29	116.71	125.69
3	C	5	4FO	O-C-CA	-2.35	119.43	125.72
3	C	3	DTH	O-C-CA	-2.16	119.78	125.69
3	C	10	DAB	O-C-CA	-2.14	119.98	125.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	11	DTH	1	0
3	C	5	4FO	1	0
3	C	9	DAB	1	0

5.5 Carbohydrates

There are no carbohydrates 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	901	-	52,58,58	3.75	20 (38%)	52,89,89	2.71	15 (28%)

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	901	-	-	0/30/50/50	0/6/6/6

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	901	FAD	C2B-C1B	-15.70	1.28	1.53
4	A	901	FAD	O4B-C4B	-6.02	1.31	1.45
4	A	901	FAD	O2'-C2'	-3.97	1.34	1.43
4	A	901	FAD	O3B-C3B	-3.48	1.34	1.43
4	A	901	FAD	C6-C5X	-2.51	1.37	1.41
4	A	901	FAD	C5A-C4A	-2.43	1.35	1.40
4	A	901	FAD	C1'-N10	-2.15	1.46	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	901	FAD	C4A-N3A	2.11	1.38	1.35
4	A	901	FAD	C6A-N6A	2.75	1.45	1.34
4	A	901	FAD	C2A-N3A	2.83	1.37	1.32
4	A	901	FAD	C4-C4X	3.56	1.48	1.41
4	A	901	FAD	C10-N10	3.60	1.43	1.39
4	A	901	FAD	C2-N3	3.78	1.46	1.38
4	A	901	FAD	C4X-N5	3.81	1.39	1.33
4	A	901	FAD	C2-N1	4.71	1.48	1.38
4	A	901	FAD	C4-N3	4.76	1.41	1.33
4	A	901	FAD	C10-N1	5.27	1.44	1.35
4	A	901	FAD	C9A-N10	5.55	1.46	1.38
4	A	901	FAD	C5X-N5	6.30	1.45	1.35
4	A	901	FAD	O4B-C1B	12.59	1.59	1.41

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	901	FAD	N3A-C2A-N1A	-12.31	119.20	128.87
4	A	901	FAD	N6A-C6A-N1A	-6.60	107.44	118.52
4	A	901	FAD	N3-C2-N1	-4.02	120.92	127.69
4	A	901	FAD	C4B-O4B-C1B	-3.77	105.65	109.64
4	A	901	FAD	C7M-C7-C6	-3.26	111.12	120.33
4	A	901	FAD	C4X-C4-N3	-3.07	119.52	123.52
4	A	901	FAD	C4-C4X-N5	-2.31	115.89	118.70
4	A	901	FAD	C8M-C8-C7	-2.13	116.15	120.73
4	A	901	FAD	O4'-C4'-C3'	2.36	115.04	108.96
4	A	901	FAD	C4X-N5-C5X	2.38	119.53	116.72
4	A	901	FAD	C6-C5X-C9A	2.89	122.30	119.11
4	A	901	FAD	C5X-C9A-N10	3.59	120.27	117.58
4	A	901	FAD	C7M-C7-C8	3.95	129.23	120.73
4	A	901	FAD	C4-C4X-C10	4.20	122.63	119.94
4	A	901	FAD	C4-N3-C2	4.76	119.13	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	901	FAD	8	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	666/730 (91%)	-0.18	3 (0%) 91 88	76, 110, 162, 239	0
2	B	133/178 (74%)	0.30	10 (7%) 17 14	113, 153, 208, 294	0
3	C	2/11 (18%)	-0.56	0 100 100	176, 176, 176, 182	0
All	All	801/919 (87%)	-0.10	13 (1%) 74 65	76, 117, 178, 294	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	171	PRO	4.1
2	B	323	ALA	3.4
2	B	308	ARG	3.3
2	B	312	LYS	3.2
2	B	324	VAL	2.7
2	B	309	LYS	2.4
1	A	401	LEU	2.2
2	B	311	PRO	2.2
2	B	320	ASP	2.1
2	B	321	VAL	2.1
2	B	402	PHE	2.1
1	A	242	TYR	2.0
2	B	383	TRP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
3	DAB	C	9	7/8	0.78	0.36	-	183,185,190,191	0
3	DAB	C	10	7/8	0.90	0.33	-	177,185,193,197	0
3	DTH	C	3	7/8	0.87	0.22	-	188,192,195,198	0
3	4FO	C	2	7/8	0.71	0.44	-	186,187,189,189	5
3	DAB	C	6	7/8	0.90	0.29	-	187,188,190,196	0
3	DTH	C	11	7/8	0.89	0.30	-	195,196,197,198	0
3	4FO	C	5	7/8	0.78	0.27	-	190,193,198,199	0
3	4FO	C	4	7/8	0.90	0.21	-	189,194,197,197	0

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
4	FAD	A	901	53/53	0.95	0.24	-0.20	60,86,99,109	0

6.5 Other polymers [i](#)

There are no such residues in this entry.