



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 11:39 pm GMT

PDB ID : 4UVA
Title : LSD1(KDM1A)-CoREST in complex with 1-Methyl-Tranylcypromine (1R,2S)
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Valente, S.; Villa, M.; Varasi, M.; Mercurio, C.
Deposited on : 2014-08-05
Resolution : 2.90 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

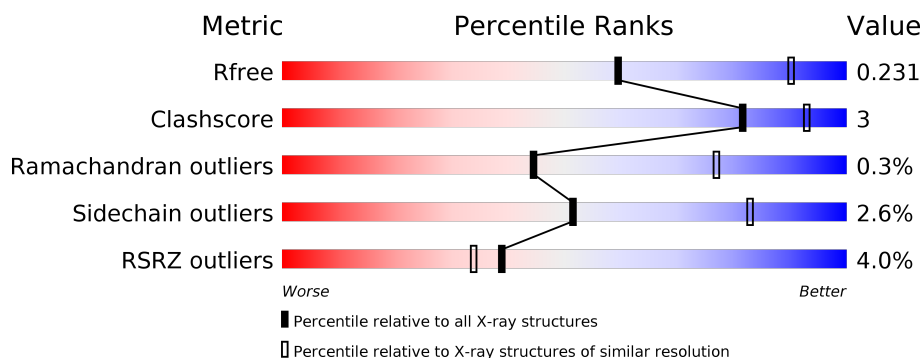
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	100719	1586 (2.90-2.90)
Clashscore	112137	1807 (2.90-2.90)
Ramachandran outliers	110173	1768 (2.90-2.90)
Sidechain outliers	110143	1770 (2.90-2.90)
RSRZ outliers	101464	1596 (2.90-2.90)

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	872	
2	B	482	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6358 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

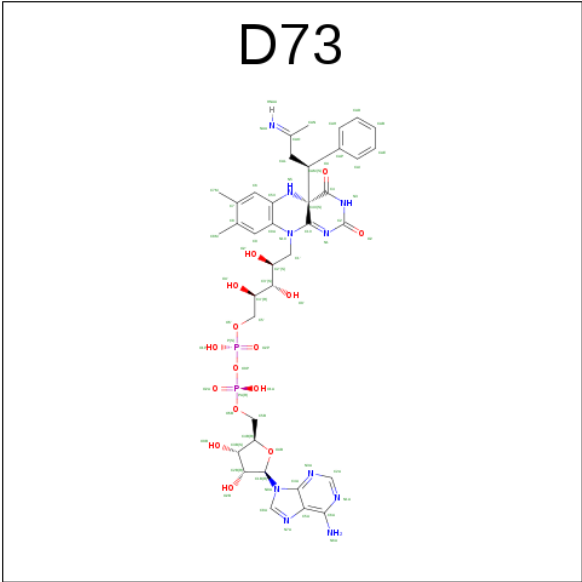
There are 5 discrepancies between the modelled and reference sequences:

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 [(2R,3S,4R,5R)-5-(6-AMINO-9H-PURIN-9-YL)-3,4-DIHYDROXYTETRAHYDROFURAN-2-YL]METHYL (2R,3S,4S)-2,3,4-TRIHYDROXY-5-[(4AS)-4A-[(1S,3E)-3-IMINO-1-PHENYLBUTYL]-7,8-DIMETHYL-2,4-DIOXO-3,4,4A,5-TETRAHYDROBENZOTRIPTERIDIN-10(2H)-YL]PENTYL DIHYDROGEN DIPHOSPHATE (three-letter code: D73) (formula: C₃₇H₄₆N₁₀O₁₅P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			64	37	10	15	2		

- Molecule 4 is water.

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

SER	GLN	SER
VAL	ALA	VAL
MET	LYS	MET
ASP	ASN	ASP
ARG	ARG	ARG
HIS	ALA	HIS
ALA	LYS	ALA
ARG	K308	ARG
LYS	K312	LYS
GLN	G313	GLN
LYS	M314	LYS
ARG	F315	ARG
GLU	L316	GLU
ARG	T332	ARG
GLU	T337	GLU
GLU	Q337	GLU
SER	Q337	SER
GLU	K346	GLU
ASP	I349	ASP
LEU	T355	LEU
GLU	L363	GLU
GLU	L372	GLU
ALA	I376	ALA
ASN	Q377	ASN
GLY	W383	GLY
ASN	F402	ASN
ASN	E440	ASN
LYS	HIS	LYS
GLU	GLY	GLU
SER	LYS	SER
LYS	GLU	LYS
LYS	GLU	LYS
GLU	THR	GLU
VAL	ASN	VAL
PRO	GLY	PRO
PRO	PRO	PRO
THR	SER	THR
GLU	ASN	GLU
THR	GLN	THR
VAL	LYS	VAL
PRO	PRO	PRO
GLN	VAL	GLN
VAL	LYS	VAL
LYS	SER	LYS
LYS	PRO	LYS
GLU	ASP	GLU
LYS	ASN	LYS
HIS	ASN	HIS
SER	SER	SER
THR	ILE	THR
	LYS	

MET
PRO
GLU
GLU
GLU
ASP
GLU
ALA
PRO
VAL
LEU
ASP
VAL
ARG
TYR
ALA
SER
SER

4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	118.97Å 179.91Å 234.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	90.12 – 2.90 89.95 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.4 (90.12-2.90) 99.4 (89.95-2.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.55 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.7.0027	Depositor
R, R_{free}	0.220 , 0.232 0.218 , 0.231	Depositor DCC
R_{free} test set	1092 reflections (2.00%)	DCC
Wilson B-factor (Å ²)	72.4	Xtriage
Anisotropy	0.176	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 44.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6358	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.95% 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: D73

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	0.43	3/5331 (0.1%)	0.48	0/7232
2	B	0.39	0/1091	0.45	0/1471
All	All	0.42	3/6422 (0.0%)	0.48	0/8703

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	431	TRP	CD2-CE2	5.07	1.47	1.41
1	A	646	TRP	CD2-CE2	5.05	1.47	1.41
1	A	695	TRP	CD2-CE2	5.01	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 [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	38	0
2	B	1076	0	1091	8	0
3	A	64	0	42	1	0
4	A	1	0	0	0	0
All	All	6358	0	6385	38	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 (38) 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:384:ARG:HB3	2:B:314:MET:HE1	1.77	0.66
1:A:384:ARG:HB3	2:B:314:MET:CE	2.27	0.64
1:A:548:SER:O	1:A:552:TRP:HB3	1.99	0.62
1:A:435:VAL:HG13	2:B:349:ILE:HG13	1.84	0.59
1:A:374:LYS:HE3	1:A:525:ASP:OD1	2.04	0.57
1:A:566:THR:HG21	1:A:697:LEU:HD13	1.88	0.56
1:A:419:GLN:HE22	2:B:315:PHE:H	1.54	0.55
1:A:435:VAL:CG1	2:B:349:ILE:HG13	2.39	0.52
1:A:353:LEU:HB3	1:A:565:LEU:HD22	1.92	0.51
1:A:364:GLU:HA	1:A:681:VAL:HB	1.93	0.50
1:A:484:HIS:CD2	2:B:372:LEU:HD13	2.46	0.49
1:A:435:VAL:O	1:A:439:GLU:HB2	2.11	0.49
1:A:801:GLU:HG2	1:A:809:ALA:H	1.78	0.49
1:A:801:GLU:CG	1:A:809:ALA:HA	2.42	0.48
1:A:442:LYS:HE3	2:B:355:THR:HG21	1.96	0.48
1:A:627:LEU:HD22	1:A:654:MET:HE2	1.96	0.48
1:A:761:TYR:CD1	1:A:809:ALA:HB1	2.49	0.47
1:A:463:LYS:O	1:A:467:GLU:HG2	2.14	0.47
1:A:695:TRP:CE3	1:A:697:LEU:HD11	2.50	0.46
1:A:760:SER:HB2	3:A:900:D73:H8MB	1.97	0.46
1:A:537:GLU:HG3	1:A:544:LEU:HG	1.98	0.46
1:A:601:GLU:HA	1:A:616:TYR:O	2.17	0.44
1:A:662:VAL:HB	1:A:705:ALA:HB3	2.00	0.44
1:A:501:GLN:O	1:A:505:GLU:HB2	2.18	0.43
1:A:720:ASP:O	1:A:724:VAL:HG23	2.17	0.43
1:A:537:GLU:CG	1:A:544:LEU:HG	2.49	0.43
1:A:384:ARG:HB3	2:B:314:MET:HE3	2.01	0.43
1:A:592:GLN:HB3	1:A:603:ILE:HD12	2.01	0.43
1:A:801:GLU:HG2	1:A:809:ALA:N	2.34	0.43
1:A:662:VAL:HG13	1:A:748:VAL:HG22	2.00	0.43
1:A:625:LEU:HD22	1:A:629:VAL:HG11	2.01	0.42
1:A:594:ARG:HG2	1:A:640:VAL:HB	2.02	0.42
1:A:209:VAL:HG13	1:A:242:TYR:HD1	1.84	0.42
1:A:716:GLU:HG2	1:A:750:ARG:HG2	2.02	0.41
1:A:661:LYS:HD3	1:A:704:LEU:HD21	2.03	0.41
1:A:199:ILE:HD11	1:A:248:LEU:HD13	2.03	0.41
1:A:458:LEU:HB3	1:A:487:LEU:HD13	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:694:PHE:HA	1:A:704:LEU:O	2.21	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%)	641 (96%)	21 (3%)	2 (0%)	44	77
2	B	131/482 (27%)	125 (95%)	6 (5%)	0	100	100
All	All	795/1354 (59%)	766 (96%)	27 (3%)	2 (0%)	44	77

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	801	GLU
1	A	468	VAL

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%)	552 (98%)	14 (2%)	53	83
2	B	117/395 (30%)	113 (97%)	4 (3%)	42	76
All	All	683/1106 (62%)	665 (97%)	18 (3%)	51	83

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	429	GLU
1	A	438	GLN
1	A	458	LEU
1	A	469	LYS
1	A	492	LYS
1	A	538	PHE
1	A	556	ASP
1	A	557	ASP
1	A	571	TYR
1	A	624	THR
1	A	645	GLU
1	A	659	LEU
1	A	684	THR
1	A	704	LEU
2	B	312	LYS
2	B	316	LEU
2	B	332	THR
2	B	337	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	380	GLN
1	A	395	GLN
1	A	410	GLN
1	A	419	GLN
1	A	438	GLN
1	A	484	HIS
1	A	532	HIS
1	A	742	GLN
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 [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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	$\# Z > 2$
3	D73	A	900	-	61,70,70	2.37	9 (14%)	64,107,107	1.57	8 (12%)

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	D73	A	900	-	-	0/40/97/97	0/7/7/7

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	900	D73	C4X-C4	-12.19	1.49	1.54
3	A	900	D73	CAP-CAM	-6.67	1.41	1.51
3	A	900	D73	C5X-N5	-2.29	1.35	1.38
3	A	900	D73	CAO-NAA	2.38	1.33	1.27
3	A	900	D73	CAN-CAO	2.44	1.53	1.49
3	A	900	D73	C5A-C4A	3.21	1.47	1.40
3	A	900	D73	C8-C7	3.46	1.49	1.41
3	A	900	D73	C10-N10	3.47	1.42	1.36
3	A	900	D73	C5X-C9A	8.02	1.49	1.40

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	900	D73	N3A-C2A-N1A	-6.76	122.97	128.86
3	A	900	D73	CAL-CAM-CAP	-4.14	107.83	112.54
3	A	900	D73	O4-C4-C4X	-2.97	118.02	123.64
3	A	900	D73	C4A-C5A-N7A	-2.72	106.78	109.41
3	A	900	D73	C9A-N10-C10	-2.28	115.95	119.95
3	A	900	D73	C1B-N9A-C4A	-2.03	123.13	126.64
3	A	900	D73	C2A-N1A-C6A	2.06	122.38	118.77
3	A	900	D73	CAM-C4X-C10	6.23	120.50	108.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	900	D73	1	0

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%)	0.66	23 (3%) 44 38	43, 72, 110, 141	0
2	B	133/482 (27%)	0.79	9 (6%) 18 13	65, 103, 127, 144	0
All	All	799/1354 (59%)	0.68	32 (4%) 39 34	43, 79, 115, 144	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	740	VAL	3.2
1	A	174	VAL	3.1
1	A	669	VAL	3.1
1	A	739	ALA	3.0
2	B	402	PHE	3.0
1	A	212	PHE	2.8
1	A	504	LEU	2.7
1	A	242	TYR	2.6
1	A	325	TYR	2.6
1	A	508	LEU	2.6
2	B	312	LYS	2.5
2	B	308	ARG	2.5
1	A	836	LEU	2.5
2	B	376	ILE	2.5
1	A	273	LEU	2.4
1	A	171	PRO	2.4
1	A	172	SER	2.4
1	A	437	THR	2.4
1	A	377	MET	2.3
1	A	668	ARG	2.3
2	B	349	ILE	2.2
1	A	438	GLN	2.2
2	B	363	LEU	2.2
1	A	398	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	480	VAL	2.2
2	B	383	TRP	2.2
2	B	377	GLN	2.1
1	A	436	LYS	2.1
1	A	408	LEU	2.1
2	B	346	LYS	2.1
1	A	435	VAL	2.1
1	A	380	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 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(Å ²)	Q<0.9
3	D73	A	900	64/64	0.97	0.25	0.04	43,58,79,82	0

6.5 Other polymers [i](#)

There are no such residues in this entry.