



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 10:04 AM UTC

PDB ID : 7CDE / pdb_00007cde
Title : Crystal structure of LSD1-CoREST in complex with PRSFLVRKR peptide
Authors : Kikuchi, M.; Kitagawa, H.; Sato, S.; Umezawa, N.; Higuchi, T.; Umehara, T.
Deposited on : 2020-06-19
Resolution : 2.68 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
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

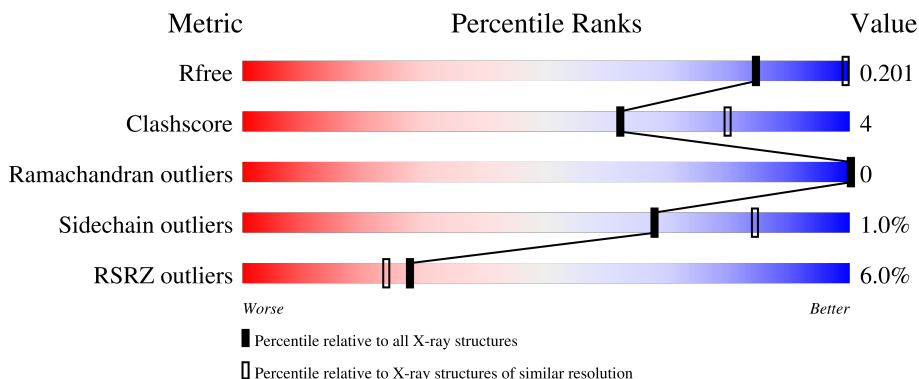
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.68 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	5070 (2.70-2.66)
Clashscore	190562	5409 (2.70-2.66)
Ramachandran outliers	187476	5324 (2.70-2.66)
Sidechain outliers	187428	5324 (2.70-2.66)
RSRZ outliers	180081	5070 (2.70-2.66)

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	 3% 89% 9%
2	B	140	 18% 83% 11% 6%
3	C	9	 22% 67% 22% 11%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6438 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	661	5167	3289	899	960	19	0	0	0

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
			Total	C	N	O	S			
2	B	132	1044	653	186	202	3	0	0	0

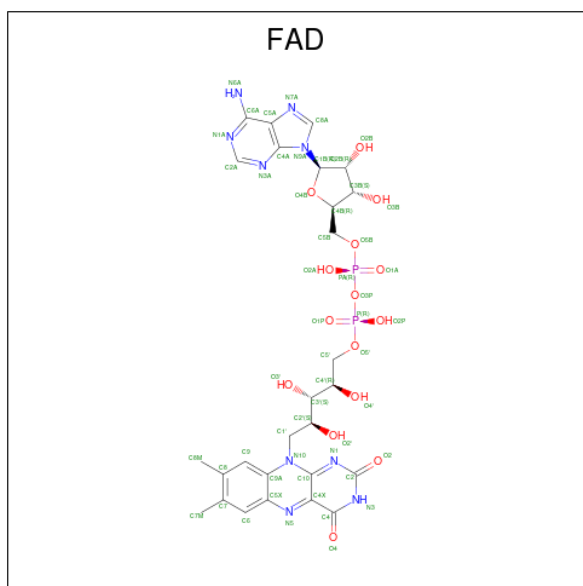
There are 7 discrepancies between the modelled and reference sequences:

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 PRO-ARG-SER-PHE-LEU-VAL-ARG-LYS-ARG.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
3	C	9	81	52	19	10	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
			Total	C	N	O	P		
4	A	1	53	27	9	15	2	0	0

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

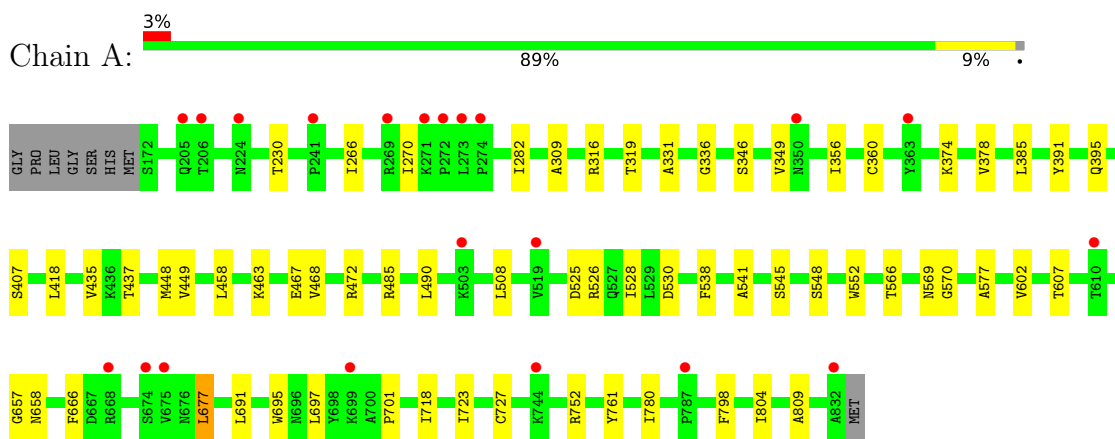
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	62	Total O 62 62	0	0
6	C	1	Total O 1 1	0	0

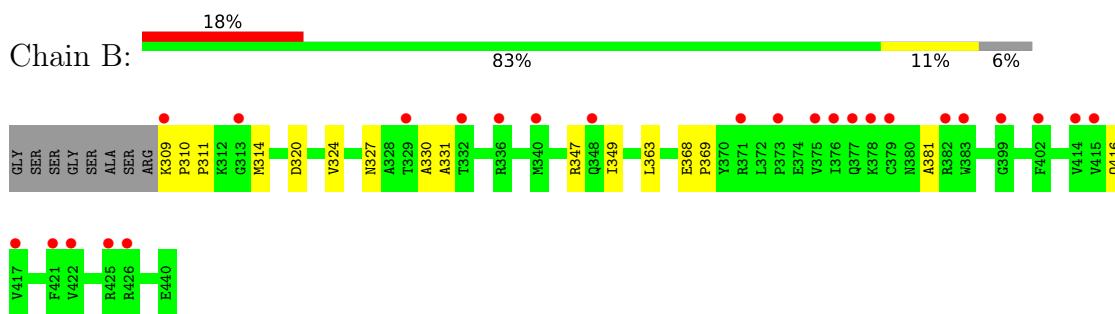
3 Residue-property plots [i](#)

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.

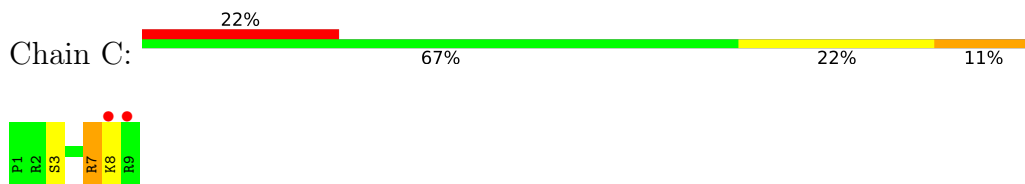
- Molecule 1: Lysine-specific histone demethylase 1A



- Molecule 2: REST corepressor 1



- Molecule 3: PRO-ARG-SER-PHE-LEU-VAL-ARG-LYS-ARG



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	121.60Å 179.94Å 232.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.00 – 2.68 45.00 – 2.68	Depositor EDS
% Data completeness (in resolution range)	100.0 (45.00-2.68) 100.0 (45.00-2.68)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 2.69Å)	Xtrriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.207 , 0.233 (Not available) , 0.201	Depositor DCC
R_{free} test set	1507 reflections (2.10%)	wwPDB-VP
Wilson B-factor (Å ²)	71.4	Xtrriage
Anisotropy	0.538	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 55.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6438	wwPDB-VP
Average B, all atoms (Å ²)	89.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.90% 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	0.97	0/5279	1.45	1/7164 (0.0%)
2	B	1.02	0/1059	1.59	0/1434
3	C	0.97	0/82	1.42	0/106
All	All	0.98	0/6420	1.47	1/8704 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	336	GLY	CA-C-O	-5.34	117.59	122.24

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	5167	0	5186	44	0
2	B	1044	0	1018	15	0
3	C	81	0	95	1	0
4	A	53	0	31	3	0
5	A	30	0	40	1	0
6	A	62	0	0	0	0
6	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6438	0	6370	52	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 4.

All (52) 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)
2:B:327:ASN:HB3	2:B:330:ALA:HB2	1.66	0.77
1:A:566:THR:HG21	1:A:697:LEU:HD13	1.67	0.77
1:A:360:CYS:O	3:C:7:ARG:NH2	2.24	0.70
1:A:448:MET:HE3	2:B:363:LEU:HD13	1.73	0.69
2:B:324:VAL:HG13	2:B:331:ALA:HB2	1.80	0.63
2:B:311:PRO:HG2	2:B:314:MET:HG3	1.80	0.62
1:A:566:THR:CG2	1:A:697:LEU:HD13	2.31	0.61
1:A:435:VAL:HG12	2:B:349:ILE:HG13	1.84	0.60
1:A:526:ARG:NH1	1:A:530:ASP:OD1	2.36	0.57
2:B:381:ALA:HA	2:B:416:GLN:NE2	2.19	0.57
1:A:435:VAL:HG12	2:B:349:ILE:CG1	2.35	0.57
1:A:463:LYS:O	1:A:467:GLU:HG2	2.07	0.54
1:A:695:TRP:CE3	1:A:697:LEU:HD11	2.42	0.54
1:A:449:VAL:HA	2:B:363:LEU:HD21	1.90	0.53
2:B:381:ALA:HA	2:B:416:GLN:HE21	1.75	0.52
1:A:666:PHE:O	1:A:701:PRO:HG2	2.10	0.52
1:A:266:ILE:CD1	1:A:577:ALA:HB1	2.40	0.52
1:A:331:ALA:HA	4:A:901:FAD:C4X	2.40	0.51
1:A:374:LYS:NZ	1:A:525:ASP:OD1	2.43	0.51
1:A:437:THR:HG22	1:A:508:LEU:HD13	1.93	0.50
2:B:309:LYS:N	2:B:310:PRO:CD	2.74	0.50
2:B:327:ASN:CB	2:B:330:ALA:HB2	2.38	0.49
1:A:548:SER:O	1:A:552:TRP:HB3	2.13	0.49
1:A:391:TYR:CD1	1:A:395:GLN:HG3	2.47	0.48
1:A:331:ALA:HA	4:A:901:FAD:N5	2.28	0.47
1:A:468:VAL:O	1:A:472:ARG:NH1	2.44	0.47
2:B:368:GLU:N	2:B:369:PRO:CD	2.77	0.47
1:A:691:LEU:HD22	1:A:727:CYS:SG	2.55	0.47
1:A:677:LEU:CD2	1:A:695:TRP:CE3	2.98	0.47
1:A:526:ARG:NH2	5:A:902:GOL:H31	2.30	0.47
1:A:448:MET:HE3	2:B:363:LEU:CD1	2.43	0.46
1:A:458:LEU:HD22	1:A:490:LEU:HD12	1.96	0.46
1:A:378:VAL:HG11	1:A:528:ILE:HG22	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:718:ILE:HG22	1:A:723:ILE:HG13	1.98	0.46
1:A:385:LEU:HD23	2:B:314:MET:HE1	1.98	0.45
1:A:356:ILE:HD11	1:A:566:THR:HG22	1.98	0.45
1:A:282:ILE:HG21	1:A:602:VAL:HG21	1.97	0.45
1:A:761:TYR:CD1	1:A:809:ALA:HB1	2.51	0.45
1:A:418:LEU:HD22	2:B:320:ASP:HB3	1.98	0.44
1:A:319:THR:HG21	1:A:570:GLY:HA3	1.99	0.44
1:A:566:THR:HG21	1:A:697:LEU:HD22	1.99	0.44
1:A:804:ILE:O	1:A:804:ILE:HG23	2.18	0.44
1:A:309:ALA:O	1:A:607:THR:HG21	2.19	0.43
1:A:316:ARG:NH1	4:A:901:FAD:O1A	2.53	0.42
1:A:485:ARG:C	1:A:485:ARG:HD3	2.45	0.42
1:A:658:ASN:ND2	1:A:752:ARG:HB2	2.35	0.42
1:A:780:ILE:HG12	1:A:798:PHE:HE2	1.85	0.41
1:A:407:SER:OG	1:A:545:SER:HA	2.21	0.41
1:A:346:SER:O	1:A:349:VAL:O	2.39	0.41
1:A:541:ALA:O	1:A:657:GLY:HA3	2.19	0.41
1:A:230:THR:HG23	1:A:270:ILE:HD12	2.02	0.41
1:A:356:ILE:CG1	1:A:566:THR:HG23	2.51	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	659/669 (98%)	638 (97%)	21 (3%)	0	100	100
2	B	130/140 (93%)	124 (95%)	6 (5%)	0	100	100
3	C	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
All	All	796/818 (97%)	768 (96%)	28 (4%)	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	559/567 (99%)	556 (100%)	3 (0%)	81	91
2	B	110/121 (91%)	109 (99%)	1 (1%)	70	86
3	C	9/9 (100%)	6 (67%)	3 (33%)	0	0
All	All	678/697 (97%)	671 (99%)	7 (1%)	68	84

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	538	PHE
1	A	569	ASN
1	A	677	LEU
2	B	347	ARG
3	C	3	SER
3	C	7	ARG
3	C	8	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	191	GLN
1	A	680	HIS
1	A	791	GLN
1	A	828	GLN
2	B	348	GLN

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](#)

6 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	GOL	A	905	-	5,5,5	0.14	0	5,5,5	0.40	0
4	FAD	A	901	-	58,58,58	0.57	0	85,89,89	0.71	0
5	GOL	A	906	-	5,5,5	0.08	0	5,5,5	0.27	0
5	GOL	A	903	-	5,5,5	0.09	0	5,5,5	0.25	0
5	GOL	A	902	-	5,5,5	0.07	0	5,5,5	0.30	0
5	GOL	A	904	-	5,5,5	0.12	0	5,5,5	0.32	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	GOL	A	905	-	-	1/4/4/4	-
4	FAD	A	901	-	-	0/34/50/50	0/6/6/6
5	GOL	A	906	-	-	0/4/4/4	-
5	GOL	A	903	-	-	1/4/4/4	-
5	GOL	A	902	-	-	0/4/4/4	-
5	GOL	A	904	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	905	GOL	C1-C2-C3-O3
5	A	903	GOL	O2-C2-C3-O3

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	901	FAD	3	0
5	A	902	GOL	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	661/669 (98%)	0.34	21 (3%) 50 45	51, 82, 118, 145	0
2	B	132/140 (94%)	1.24	25 (18%) 3 2	79, 117, 142, 153	0
3	C	9/9 (100%)	1.14	2 (22%) 2 1	71, 74, 134, 157	0
All	All	802/818 (98%)	0.50	48 (5%) 27 24	51, 89, 129, 157	0

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	832	ALA	7.3
2	B	309	LYS	4.4
2	B	376	ILE	4.3
2	B	375	VAL	4.0
2	B	379	CYS	3.7
2	B	415	VAL	3.7
2	B	426	ARG	3.5
3	C	9	ARG	3.5
2	B	414	VAL	3.4
1	A	269	ARG	3.3
2	B	348	GLN	3.3
2	B	340	MET	3.1
1	A	272	PRO	3.1
2	B	425	ARG	3.1
2	B	399	GLY	3.1
2	B	422	VAL	3.0
1	A	271	LYS	3.0
2	B	421	PHE	3.0
2	B	402	PHE	2.9
2	B	383	TRP	2.8
1	A	273	LEU	2.8
1	A	241	PRO	2.8
2	B	313	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
2	B	382	ARG	2.8
1	A	274	PRO	2.7
1	A	610	THR	2.7
2	B	336	ARG	2.7
2	B	377	GLN	2.5
1	A	519	VAL	2.5
2	B	371	ARG	2.5
2	B	373	PRO	2.5
2	B	329	THR	2.4
3	C	8	LYS	2.3
1	A	699	LYS	2.3
1	A	350	ASN	2.3
2	B	378	LYS	2.2
1	A	744	LYS	2.2
1	A	206	THR	2.2
1	A	503	LYS	2.2
1	A	224	ASN	2.1
1	A	675	VAL	2.1
1	A	674	SER	2.1
1	A	205	GLN	2.1
2	B	332	THR	2.0
1	A	363	TYR	2.0
1	A	668	ARG	2.0
1	A	787	PRO	2.0
2	B	417	VAL	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(\AA^2)	Q<0.9
5	GOL	A	903	6/6	0.78	0.24	135,138,141,145	0
5	GOL	A	904	6/6	0.85	0.30	118,126,131,132	0
5	GOL	A	905	6/6	0.93	0.18	86,91,98,99	0
5	GOL	A	902	6/6	0.95	0.12	80,82,84,86	0
5	GOL	A	906	6/6	0.96	0.16	99,107,108,112	0
4	FAD	A	901	53/53	0.98	0.07	48,62,69,71	0

6.5 Other polymers [i](#)

There are no such residues in this entry.