



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:34 AM GMT

PDB ID : 3MDY  
Title : Crystal structure of the cytoplasmic domain of the bone morphogenetic protein receptor type-1B (BMPRI1B) in complex with FKBP12 and LDN-193189  
Authors : Chaikuad, A.; Sanvitale, C.; Mahajan, P.; Daga, N.; Cooper, C.; Krojer, T.; Alfano, I.; Knapp, S.; von Delft, F.; Weigelt, J.; Arrowsmith, C.H.; Edwards, A.M.; Bountra, C.; Bullock, A.; Structural Genomics Consortium (SGC)  
Deposited on : 2010-03-31  
Resolution : 2.05 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
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) : trunk26865

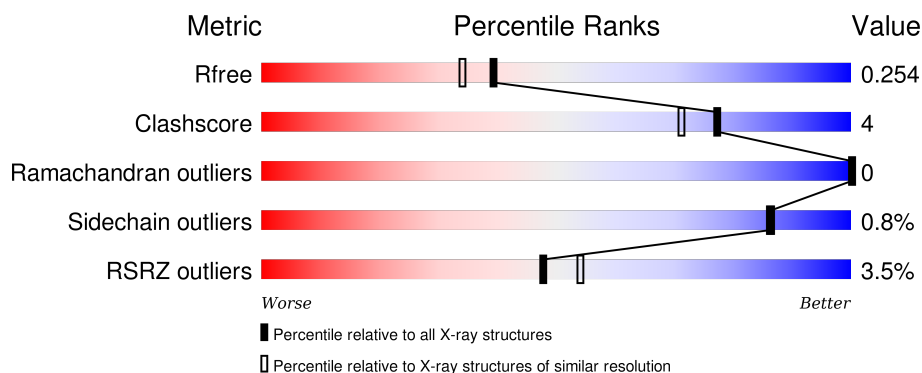
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.05 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	1192 (2.04-2.04)
Clashscore	102246	1269 (2.04-2.04)
Ramachandran outliers	100387	1258 (2.04-2.04)
Sidechain outliers	100360	1258 (2.04-2.04)
RSRZ outliers	91569	1194 (2.04-2.04)

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  $\geq 3$ , 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	337	<div> <div>4%</div> <div>87%</div> <div>8% 5%</div> </div>
1	C	337	<div> <div>3%</div> <div>88%</div> <div>7% • 5%</div> </div>
2	B	109	<div> <div>2%</div> <div>92%</div> <div>8%</div> </div>
2	D	109	<div> <div>6%</div> <div>93%</div> <div>7%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7525 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 Bone morphogenetic protein receptor type-1B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	320	Total	C	N	O	S	0	4	0
			2553	1624	443	468	18			
1	C	320	Total	C	N	O	S	0	3	0
			2532	1613	436	465	18			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	166	SER	-	EXPRESSION TAG	UNP O00238
A	167	MET	-	EXPRESSION TAG	UNP O00238
C	166	SER	-	EXPRESSION TAG	UNP O00238
C	167	MET	-	EXPRESSION TAG	UNP O00238

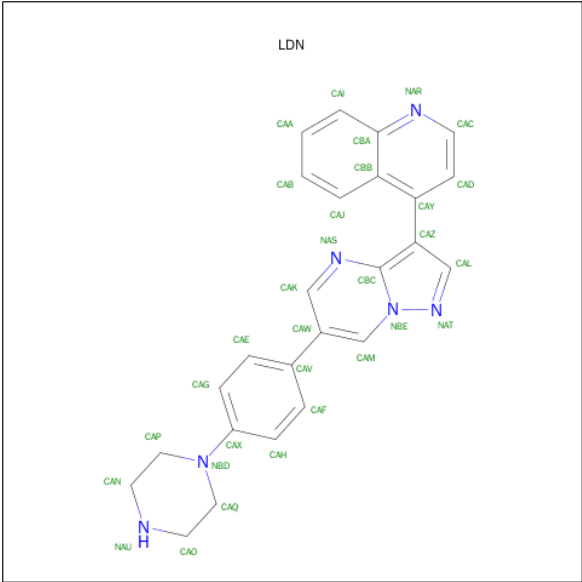
- Molecule 2 is a protein called Peptidyl-prolyl cis-trans isomerase FKBP1A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	109	Total	C	N	O	S	0	2	0
			844	536	145	158	5			
2	D	109	Total	C	N	O	S	0	1	0
			847	537	148	157	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	SER	-	EXPRESSION TAG	UNP P62942
D	0	SER	-	EXPRESSION TAG	UNP P62942

- Molecule 3 is 4-[6-(4-PIPERAZIN-1-YLPHENYL)PYRAZOLO[1,5-A]PYRIMIDIN-3-YL]QUINOLINE (three-letter code: LDN) (formula: C<sub>25</sub>H<sub>22</sub>N<sub>6</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	N	0	0
			31	25	6		
3	C	1	Total	C	N	0	0
			31	25	6		

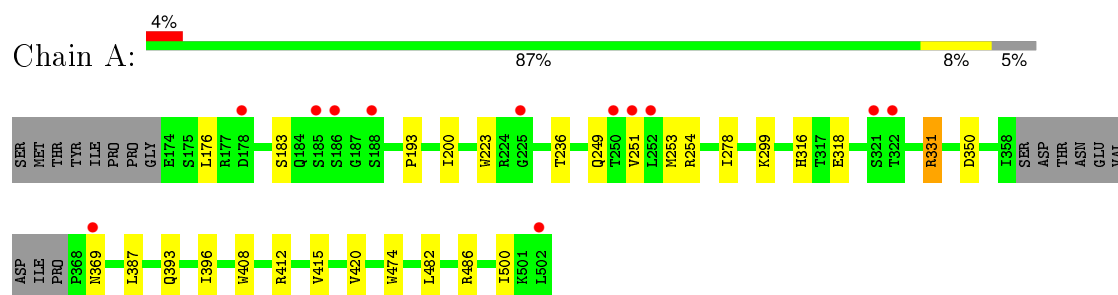
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	281	Total	O	0	0
			281	281		
4	C	284	Total	O	0	0
			284	284		
4	B	67	Total	O	0	0
			67	67		
4	D	55	Total	O	0	0
			55	55		

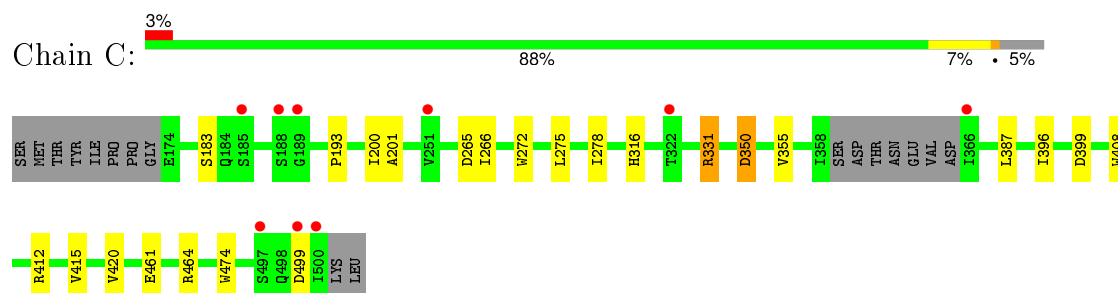
### 3 Residue-property plots [i](#)

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.

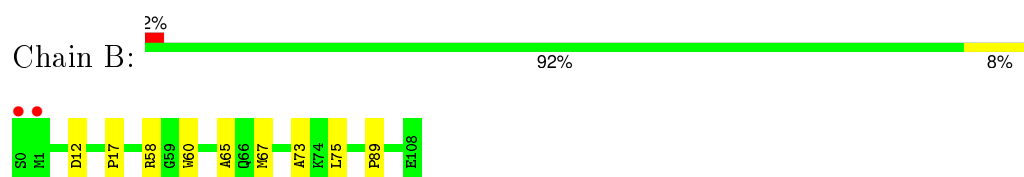
- Molecule 1: Bone morphogenetic protein receptor type-1B



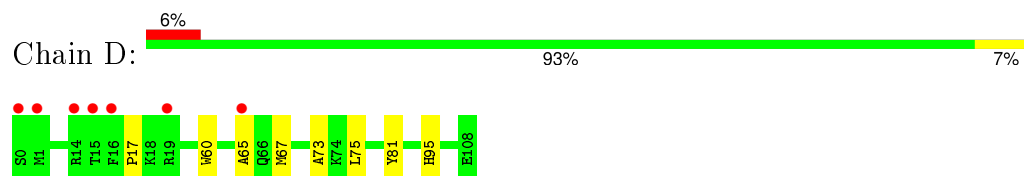
- Molecule 1: Bone morphogenetic protein receptor type-1B



- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A



- Molecule 2: Peptidyl-prolyl cis-trans isomerase FKBP1A



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	65.41Å 80.01Å 183.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.65 – 2.05 44.65 – 2.05	Depositor EDS
% Data completeness (in resolution range)	99.5 (44.65-2.05) 99.6 (44.65-2.05)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.14 (at 2.05Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.201 , 0.255 0.203 , 0.254	Depositor DCC
$R_{free}$ test set	3085 reflections (5.33%)	DCC
Wilson B-factor (Å <sup>2</sup> )	24.4	Xtriage
Anisotropy	0.773	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 43.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.55$ , $\langle L^2 \rangle = 0.39$	Xtriage
Outliers	7 of 60968 reflections (0.011%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7525	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 47.06 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.0469e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup> Intensities estimated from amplitudes.

<sup>2</sup> Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: LDN

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	0.73	0/2618	0.76	3/3531 (0.1%)
1	C	0.71	0/2595	0.79	5/3504 (0.1%)
2	B	0.64	0/869	0.64	0/1173
2	D	0.64	0/869	0.66	0/1171
All	All	0.70	0/6951	0.74	8/9379 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	499	ASP	CB-CG-OD2	7.58	125.12	118.30
1	C	399	ASP	CB-CG-OD1	6.82	124.44	118.30
1	A	254	ARG	NE-CZ-NH1	5.73	123.17	120.30
1	C	350	ASP	CB-CG-OD1	5.63	123.37	118.30
1	C	331	ARG	NE-CZ-NH1	5.58	123.09	120.30
1	C	399	ASP	CB-CG-OD2	-5.47	113.38	118.30
1	A	253	MET	CG-SD-CE	-5.41	91.54	100.20
1	A	331	ARG	NE-CZ-NH1	5.28	122.94	120.30

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	2553	0	2565	21	0
1	C	2532	0	2530	13	0
2	B	844	0	835	10	0
2	D	847	0	847	9	0
3	A	31	0	22	0	0
3	C	31	0	22	0	0
4	A	281	0	0	6	0
4	B	67	0	0	0	0
4	C	284	0	0	0	0
4	D	55	0	0	1	0
All	All	7525	0	6821	50	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 (50) 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:67[B]:MET:CE	2:B:75:LEU:HD11	2.09	0.83
2:D:67[B]:MET:CE	2:D:75:LEU:HD11	2.11	0.80
2:D:67[B]:MET:HE3	2:D:75:LEU:HD11	1.64	0.79
2:B:67[B]:MET:CE	2:B:73:ALA:HB3	2.15	0.77
2:D:67[B]:MET:CE	2:D:73:ALA:HB3	2.17	0.75
2:B:67[B]:MET:HE3	2:B:75:LEU:HD11	1.68	0.73
2:D:67[B]:MET:HE1	2:D:73:ALA:HB3	1.72	0.70
2:B:67[B]:MET:HE2	2:B:73:ALA:HB3	1.75	0.67
2:B:67[B]:MET:HE1	2:B:75:LEU:HD11	1.77	0.67
1:A:318:GLU:OE1	4:A:670:HOH:O	2.16	0.63
2:B:67[B]:MET:HE1	2:B:73:ALA:HB3	1.80	0.63
2:D:67[B]:MET:HE1	2:D:75:LEU:HD11	1.85	0.58
1:C:408:TRP:CZ2	1:C:412:ARG:HD2	2.39	0.57
2:D:67[B]:MET:HE2	2:D:73:ALA:HB3	1.88	0.56
1:A:316:HIS:CD2	1:A:396:ILE:HD12	2.40	0.56
1:C:316:HIS:CG	1:C:396:ILE:HD12	2.41	0.56
1:A:408:TRP:CZ2	1:A:412:ARG:HD2	2.41	0.55
1:A:316:HIS:CG	1:A:396:ILE:HD12	2.44	0.53
1:A:176:LEU:HD11	1:A:223:TRP:CZ3	2.43	0.53
1:A:393:GLN:HG3	4:A:521:HOH:O	2.09	0.52
1:A:299:LYS:HG3	1:A:500:ILE:HG23	1.91	0.52
1:A:316:HIS:CD2	1:A:396:ILE:CD1	2.92	0.52
1:A:251:VAL:HA	4:A:662:HOH:O	2.10	0.51
1:C:316:HIS:CD2	1:C:396:ILE:CD1	2.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:17:PRO:HG2	2:D:65:ALA:HA	1.94	0.49
2:B:17:PRO:HG2	2:B:65:ALA:HA	1.95	0.49
1:A:176:LEU:HD11	1:A:223:TRP:HZ3	1.77	0.49
1:C:201:ALA:HB2	1:C:265:ASP:HB3	1.95	0.48
1:A:387:LEU:HD23	1:A:387:LEU:C	2.34	0.48
1:A:249:GLN:NE2	2:B:89:PRO:O	2.47	0.48
1:A:331:ARG:NH2	1:A:369:ASN:O	2.46	0.47
1:C:183:SER:CB	1:C:193:PRO:HD3	2.45	0.47
1:A:393:GLN:HG2	4:A:620:HOH:O	2.15	0.47
1:C:316:HIS:CD2	1:C:396:ILE:HD12	2.50	0.46
1:C:415:VAL:HG22	1:C:420:VAL:HB	1.98	0.46
1:A:183:SER:CB	1:A:193:PRO:HD3	2.46	0.46
1:C:200:ILE:HG21	1:C:278:ILE:HD13	1.98	0.46
1:A:236:THR:HG21	2:D:81:TYR:CE1	2.52	0.45
1:A:415:VAL:HG22	1:A:420:VAL:HB	1.99	0.45
1:A:500:ILE:HA	4:A:713:HOH:O	2.17	0.43
1:C:387:LEU:HD23	1:C:387:LEU:C	2.38	0.43
1:C:331:ARG:HD2	1:C:355:VAL:HG12	1.99	0.43
1:A:482:LEU:HD22	1:A:486[B]:ARG:HG2	2.00	0.43
1:C:272:TRP:CZ2	2:B:58:ARG:HA	2.53	0.43
2:D:95:HIS:ND1	4:D:474:HOH:O	2.37	0.42
1:A:393:GLN:CG	4:A:521:HOH:O	2.66	0.42
1:C:461:GLU:HA	1:C:464:ARG:HD3	2.02	0.41
1:C:266:ILE:HG12	1:C:275:LEU:HD23	2.01	0.41
1:A:200:ILE:HG21	1:A:278:ILE:HD13	2.03	0.41
2:B:12:ASP:OD1	2:B:12:ASP:C	2.59	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	320/337 (95%)	314 (98%)	6 (2%)	0	100	100
1	C	319/337 (95%)	310 (97%)	9 (3%)	0	100	100
2	B	109/109 (100%)	106 (97%)	3 (3%)	0	100	100
2	D	108/109 (99%)	105 (97%)	3 (3%)	0	100	100
All	All	856/892 (96%)	835 (98%)	21 (2%)	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	279/298 (94%)	277 (99%)	2 (1%)	88	88
1	C	275/298 (92%)	273 (99%)	2 (1%)	88	88
2	B	90/91 (99%)	89 (99%)	1 (1%)	80	79
2	D	91/91 (100%)	90 (99%)	1 (1%)	80	79
All	All	735/778 (94%)	729 (99%)	6 (1%)	86	86

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	350	ASP
1	A	474	TRP
1	C	350	ASP
1	C	474	TRP
2	B	60	TRP
2	D	60	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	393	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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

2 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	$\# Z  > 2$
3	LDN	A	1	-	31,36,36	1.21	3 (9%)	40,51,51	2.16	8 (20%)
3	LDN	C	1	-	31,36,36	1.13	4 (12%)	40,51,51	2.13	8 (20%)

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	LDN	A	1	-	-	0/11/20/20	0/6/6/6
3	LDN	C	1	-	-	0/11/20/20	0/6/6/6

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1	LDN	CAZ-CAY	-2.82	1.42	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1	LDN	CAZ-CAY	-2.60	1.43	1.49
3	A	1	LDN	CAV-CAW	-2.04	1.43	1.49
3	C	1	LDN	CAV-CAW	-2.02	1.43	1.49
3	C	1	LDN	CBC-NAS	2.02	1.38	1.35
3	C	1	LDN	CAK-NAS	3.00	1.36	1.31
3	A	1	LDN	CAP-NBD	3.75	1.52	1.46

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1	LDN	CAW-CAK-NAS	-2.94	121.75	125.46
3	C	1	LDN	CAW-CAK-NAS	-2.85	121.86	125.46
3	A	1	LDN	CAN-CAP-NBD	2.27	116.27	110.70
3	A	1	LDN	CAC-CAD-CAY	2.37	121.84	119.98
3	C	1	LDN	CAC-CAD-CAY	2.56	122.00	119.98
3	C	1	LDN	CAO-NAU-CAN	2.70	119.29	110.33
3	A	1	LDN	CAZ-CAY-CBB	2.77	125.38	121.44
3	C	1	LDN	CAK-NAS-CBC	3.29	121.22	116.86
3	C	1	LDN	CAZ-CAY-CBB	3.71	126.73	121.44
3	A	1	LDN	CAK-NAS-CBC	4.02	122.18	116.86
3	C	1	LDN	CAQ-NBD-CAP	4.16	120.33	111.59
3	A	1	LDN	CAY-CBB-CBA	4.75	119.94	117.46
3	A	1	LDN	CAQ-NBD-CAP	5.56	123.27	111.59
3	C	1	LDN	CAY-CBB-CBA	5.65	120.42	117.46
3	C	1	LDN	CAL-NAT-NBE	7.41	109.28	103.70
3	A	1	LDN	CAL-NAT-NBE	8.08	109.78	103.70

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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 ⓘ

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	320/337 (94%)	0.05	12 (3%) 44 50	11, 26, 66, 91	0
1	C	320/337 (94%)	0.01	9 (2%) 56 63	11, 26, 61, 89	0
2	B	109/109 (100%)	0.09	2 (1%) 71 76	17, 38, 71, 78	0
2	D	109/109 (100%)	0.44	7 (6%) 23 26	19, 41, 77, 89	0
All	All	858/892 (96%)	0.09	30 (3%) 48 54	11, 30, 68, 91	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	188	SER	6.5
1	C	188	SER	6.0
2	D	0	SER	5.8
2	D	1	MET	5.5
1	C	500	ILE	5.5
1	C	251	VAL	5.3
1	A	322	THR	5.2
1	A	251	VAL	4.6
2	B	1	MET	4.4
2	B	0	SER	4.1
1	A	185	SER	3.9
1	A	502	LEU	3.6
1	C	499	ASP	3.5
1	C	366	ILE	3.3
1	C	322	THR	2.9
1	C	189	GLY	2.8
1	A	186	SER	2.6
1	C	185	SER	2.6
1	A	252	LEU	2.4
1	A	369	ASN	2.3
1	A	321	SER	2.2

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Mol	Chain	Res	Type	RSRZ
2	D	65	ALA	2.2
1	A	250	THR	2.2
1	A	178	ASP	2.1
1	A	225	GLY	2.1
2	D	16	PHE	2.1
2	D	15	THR	2.1
2	D	19	ARG	2.1
1	C	497	SER	2.1
2	D	14	ARG	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	LDN	C	1	31/31	0.96	0.10	-0.34	7,15,28,40	0
3	LDN	A	1	31/31	0.96	0.10	-0.44	11,17,28,33	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.