



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:28 PM GMT

PDB ID : 4IFP
Title : X-ray Crystal Structure of Human NLRP1 CARD Domain
Authors : Jin, T.; Curry, J.; Smith, P.; Jiang, J.; Xiao, T.
Deposited on : 2012-12-14
Resolution : 1.99 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 (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

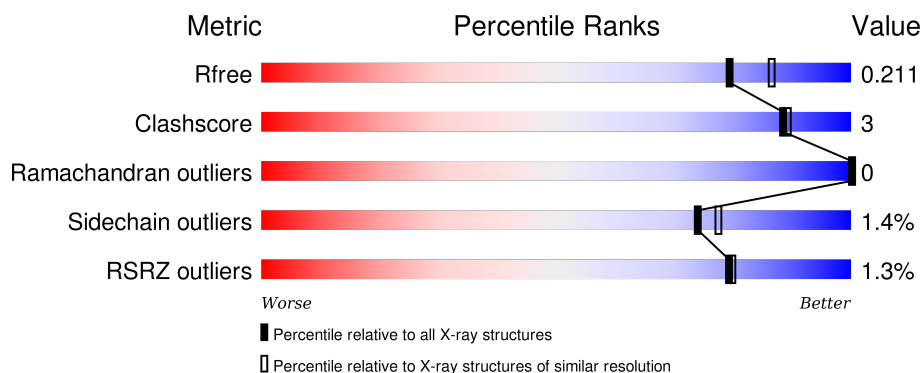
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	466	<div> <div>2%</div> <div>92%</div> <div>6% •</div> </div>
1	B	466	<div> <div>%</div> <div>89%</div> <div>8% •</div> </div>
1	C	466	<div> <div>%</div> <div>91%</div> <div>6% ••</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12414 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 Maltose-binding periplasmic protein, NACHT, LRR and PYD domains-containing protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	458	Total	C	N	O	S	0	4	0
			3596	2309	599	679	9			
1	B	458	Total	C	N	O	S	0	3	0
			3588	2304	595	680	9			
1	C	458	Total	C	N	O	S	0	5	0
			3602	2314	600	679	9			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP P0AEX9
A	83	ALA	ASP	CONFLICT	UNP P0AEX9
A	84	ALA	LYS	CONFLICT	UNP P0AEX9
A	173	ALA	GLU	CONFLICT	UNP P0AEX9
A	174	ALA	ASN	CONFLICT	UNP P0AEX9
A	240	ALA	LYS	CONFLICT	UNP P0AEX9
A	360	ALA	-	LINKER	UNP P0AEX9
A	361	ALA	-	LINKER	UNP P0AEX9
A	363	ALA	-	LINKER	UNP P0AEX9
A	364	ALA	-	LINKER	UNP P0AEX9
A	365	ALA	-	LINKER	UNP P0AEX9
A	366	GLN	-	LINKER	UNP P0AEX9
A	367	THR	-	LINKER	UNP P0AEX9
A	368	ASN	-	LINKER	UNP P0AEX9
A	369	ALA	-	LINKER	UNP P0AEX9
A	370	VAL	-	LINKER	UNP P0AEX9
A	371	ASP	-	LINKER	UNP P0AEX9
A	456	ALA	-	EXPRESSION TAG	UNP Q9C000
A	457	ALA	-	EXPRESSION TAG	UNP Q9C000
A	458	ALA	-	EXPRESSION TAG	UNP Q9C000
A	459	LEU	-	EXPRESSION TAG	UNP Q9C000
A	460	GLU	-	EXPRESSION TAG	UNP Q9C000

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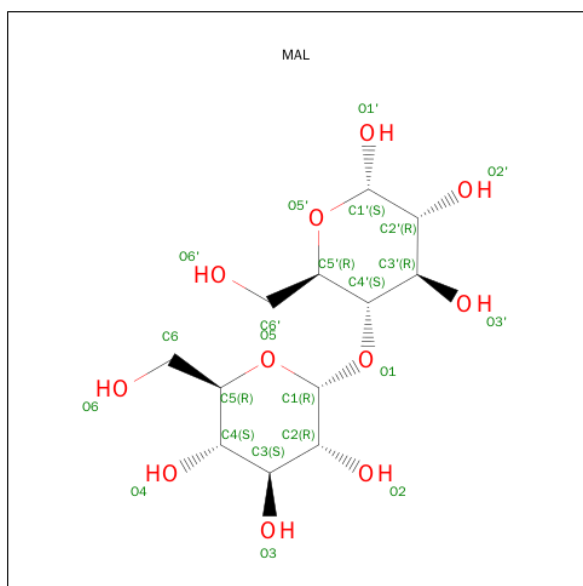
Chain	Residue	Modelled	Actual	Comment	Reference
A	461	HIS	-	EXPRESSION TAG	UNP Q9C000
A	462	HIS	-	EXPRESSION TAG	UNP Q9C000
A	463	HIS	-	EXPRESSION TAG	UNP Q9C000
A	464	HIS	-	EXPRESSION TAG	UNP Q9C000
A	465	HIS	-	EXPRESSION TAG	UNP Q9C000
A	466	HIS	-	EXPRESSION TAG	UNP Q9C000
B	1	MET	-	EXPRESSION TAG	UNP P0AEX9
B	83	ALA	ASP	CONFLICT	UNP P0AEX9
B	84	ALA	LYS	CONFLICT	UNP P0AEX9
B	173	ALA	GLU	CONFLICT	UNP P0AEX9
B	174	ALA	ASN	CONFLICT	UNP P0AEX9
B	240	ALA	LYS	CONFLICT	UNP P0AEX9
B	360	ALA	-	LINKER	UNP P0AEX9
B	361	ALA	-	LINKER	UNP P0AEX9
B	363	ALA	-	LINKER	UNP P0AEX9
B	364	ALA	-	LINKER	UNP P0AEX9
B	365	ALA	-	LINKER	UNP P0AEX9
B	366	GLN	-	LINKER	UNP P0AEX9
B	367	THR	-	LINKER	UNP P0AEX9
B	368	ASN	-	LINKER	UNP P0AEX9
B	369	ALA	-	LINKER	UNP P0AEX9
B	370	VAL	-	LINKER	UNP P0AEX9
B	371	ASP	-	LINKER	UNP P0AEX9
B	456	ALA	-	EXPRESSION TAG	UNP Q9C000
B	457	ALA	-	EXPRESSION TAG	UNP Q9C000
B	458	ALA	-	EXPRESSION TAG	UNP Q9C000
B	459	LEU	-	EXPRESSION TAG	UNP Q9C000
B	460	GLU	-	EXPRESSION TAG	UNP Q9C000
B	461	HIS	-	EXPRESSION TAG	UNP Q9C000
B	462	HIS	-	EXPRESSION TAG	UNP Q9C000
B	463	HIS	-	EXPRESSION TAG	UNP Q9C000
B	464	HIS	-	EXPRESSION TAG	UNP Q9C000
B	465	HIS	-	EXPRESSION TAG	UNP Q9C000
B	466	HIS	-	EXPRESSION TAG	UNP Q9C000
C	1	MET	-	EXPRESSION TAG	UNP P0AEX9
C	83	ALA	ASP	CONFLICT	UNP P0AEX9
C	84	ALA	LYS	CONFLICT	UNP P0AEX9
C	173	ALA	GLU	CONFLICT	UNP P0AEX9
C	174	ALA	ASN	CONFLICT	UNP P0AEX9
C	240	ALA	LYS	CONFLICT	UNP P0AEX9
C	360	ALA	-	LINKER	UNP P0AEX9
C	361	ALA	-	LINKER	UNP P0AEX9

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Chain	Residue	Modelled	Actual	Comment	Reference
C	363	ALA	-	LINKER	UNP P0AEX9
C	364	ALA	-	LINKER	UNP P0AEX9
C	365	ALA	-	LINKER	UNP P0AEX9
C	366	GLN	-	LINKER	UNP P0AEX9
C	367	THR	-	LINKER	UNP P0AEX9
C	368	ASN	-	LINKER	UNP P0AEX9
C	369	ALA	-	LINKER	UNP P0AEX9
C	370	VAL	-	LINKER	UNP P0AEX9
C	371	ASP	-	LINKER	UNP P0AEX9
C	456	ALA	-	EXPRESSION TAG	UNP Q9C000
C	457	ALA	-	EXPRESSION TAG	UNP Q9C000
C	458	ALA	-	EXPRESSION TAG	UNP Q9C000
C	459	LEU	-	EXPRESSION TAG	UNP Q9C000
C	460	GLU	-	EXPRESSION TAG	UNP Q9C000
C	461	HIS	-	EXPRESSION TAG	UNP Q9C000
C	462	HIS	-	EXPRESSION TAG	UNP Q9C000
C	463	HIS	-	EXPRESSION TAG	UNP Q9C000
C	464	HIS	-	EXPRESSION TAG	UNP Q9C000
C	465	HIS	-	EXPRESSION TAG	UNP Q9C000
C	466	HIS	-	EXPRESSION TAG	UNP Q9C000

- Molecule 2 is SUGAR (MALTOSE) (three-letter code: MAL) (formula: C₁₂H₂₂O₁₁).



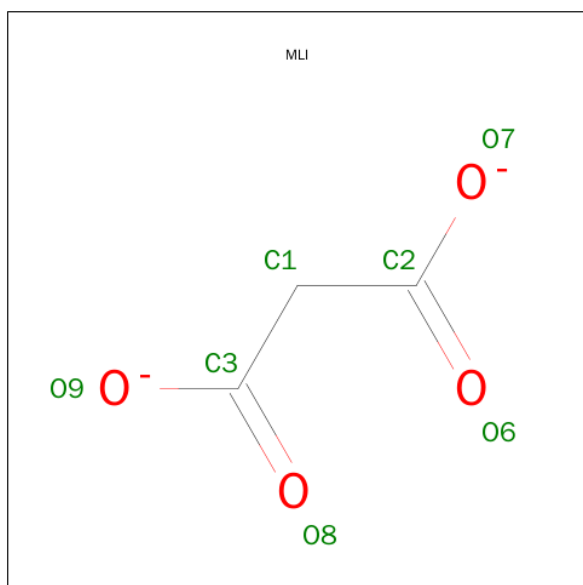
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			23	12	11		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			23	12	11		
2	C	1	Total	C	O	0	0
			23	12	11		

- Molecule 3 is MALONATE ION (three-letter code: MLI) (formula: $C_3H_2O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			7	3	4		
3	B	1	Total	C	O	0	0
			7	3	4		
3	C	1	Total	C	O	0	0
			7	3	4		

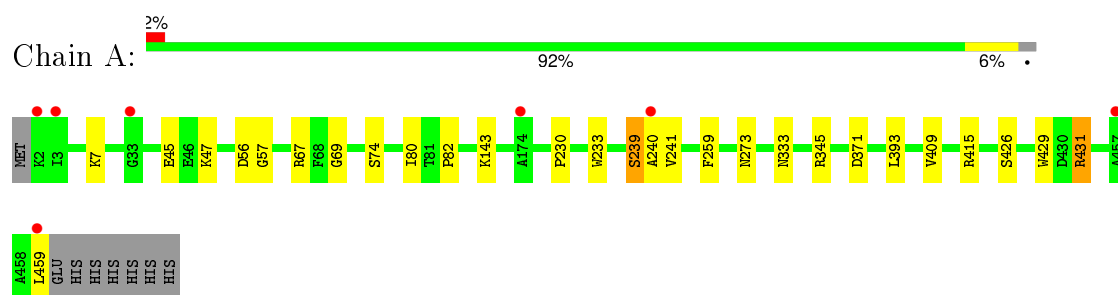
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	512	Total	O	0	0
			512	512		
4	B	522	Total	O	0	0
			522	522		
4	C	504	Total	O	0	0
			504	504		

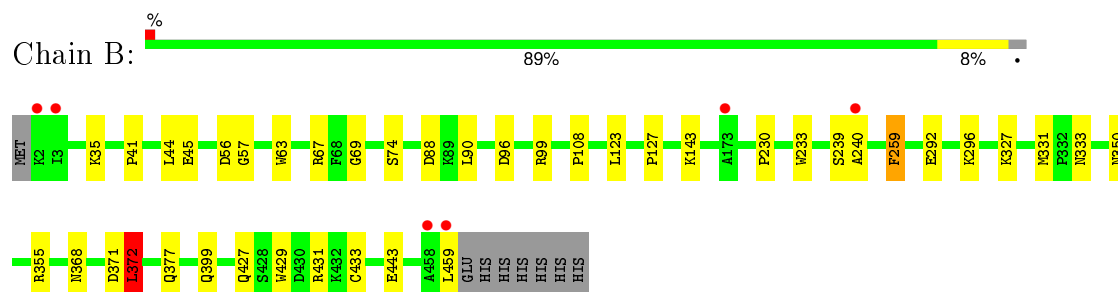
3 Residue-property plots [i](#)

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.

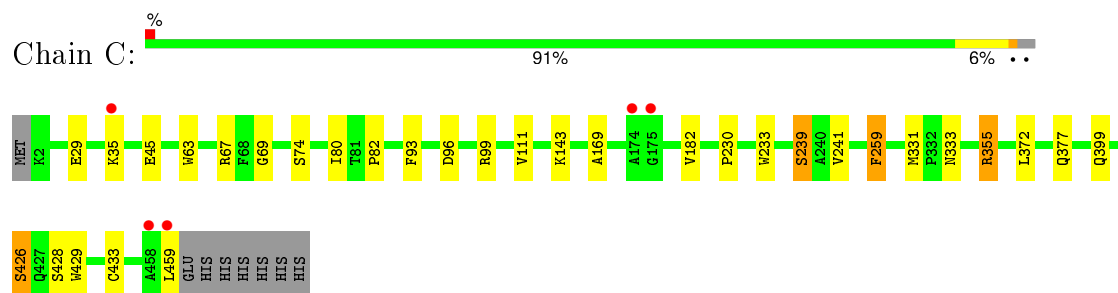
- Molecule 1: Maltose-binding periplasmic protein, NACHT, LRR and PYD domains-containing protein 1



- Molecule 1: Maltose-binding periplasmic protein, NACHT, LRR and PYD domains-containing protein 1



- Molecule 1: Maltose-binding periplasmic protein, NACHT, LRR and PYD domains-containing protein 1



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	187.01Å 108.77Å 121.27Å 90.00° 120.98° 90.00°	Depositor
Resolution (Å)	37.49 – 1.99 37.49 – 1.99	Depositor EDS
% Data completeness (in resolution range)	98.7 (37.49-1.99) 94.6 (37.49-1.99)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.83 (at 2.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1217)	Depositor
R, R_{free}	0.170 , 0.208 0.175 , 0.211	Depositor DCC
R_{free} test set	7015 reflections (5.45%)	DCC
Wilson B-factor (Å ²)	29.4	Xtriage
Anisotropy	0.147	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
Estimated twinning fraction	0.409 for $1/2^*h+3/2^*k, 1/2^*h-1/2^*k, -1/2^*h-1/2^*k-l$ 0.410 for $1/2^*h-3/2^*k, -1/2^*h-1/2^*k, -1/2^*h+1/2^*k-l$	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 139623 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	12414	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.74% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: MLI, MAL

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	0.37	0/3689	0.50	0/5008
1	B	0.37	0/3678	0.51	1/4994 (0.0%)
1	C	0.36	0/3698	0.51	0/5019
All	All	0.37	0/11065	0.51	1/15021 (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	B	372	LEU	CA-CB-CG	-5.68	102.23	115.30

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	3596	0	3577	16	0
1	B	3588	0	3562	22	0
1	C	3602	0	3590	17	0
2	A	23	0	22	0	0
2	B	23	0	22	0	0
2	C	23	0	22	0	0
3	A	7	0	2	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	7	0	2	0	0
3	C	7	0	2	0	0
4	A	512	0	0	4	0
4	B	522	0	0	5	0
4	C	504	0	0	2	0
All	All	12414	0	10801	55	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 (55) 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:345:ARG:NH1	4:A:785:HOH:O	2.27	0.67
1:C:80:ILE:HG22	1:C:82:PRO:HD3	1.83	0.60
1:A:45:GLU:HB2	1:A:67:ARG:HD2	1.82	0.60
1:C:74:SER:HA	1:C:459:LEU:HD13	1.82	0.60
1:C:143:LYS:NZ	4:C:1048:HOH:O	2.33	0.60
1:A:239[A]:SER:OG	1:A:241:VAL:HG23	2.00	0.60
1:A:143:LYS:NZ	4:A:1040:HOH:O	2.34	0.58
1:B:96:ASP:OD1	1:B:99:ARG:NH1	2.34	0.56
1:A:74:SER:HA	1:A:459:LEU:HD13	1.88	0.55
1:A:7:LYS:O	1:A:273:ASN:ND2	2.41	0.54
1:B:230:PRO:HA	1:B:233:TRP:CE2	2.43	0.54
1:C:239[A]:SER:OG	1:C:241:VAL:HG23	2.09	0.53
1:B:429:TRP:HB3	1:B:433:CYS:HB2	1.91	0.53
1:A:69:GLY:HA3	1:A:333:ASN:O	2.09	0.52
1:B:74:SER:HA	1:B:459:LEU:HD13	1.91	0.52
1:C:45:GLU:HB2	1:C:67:ARG:HD2	1.92	0.52
1:B:292:GLU:HG2	1:B:296:LYS:HD3	1.92	0.51
1:B:143:LYS:NZ	4:B:723:HOH:O	2.39	0.51
1:B:69:GLY:HA3	1:B:333:ASN:O	2.11	0.50
1:A:371:ASP:HB3	1:A:431:ARG:NH2	2.27	0.49
1:C:69:GLY:HA3	1:C:333:ASN:O	2.12	0.48
1:C:96:ASP:OD1	1:C:99:ARG:NH1	2.43	0.48
1:C:230:PRO:HA	1:C:233:TRP:CE2	2.49	0.48
1:C:355:ARG:NH2	4:C:1044:HOH:O	2.47	0.47
1:B:45:GLU:HB2	1:B:67:ARG:HD2	1.97	0.47
1:A:230:PRO:HA	1:A:233:TRP:CE2	2.50	0.47
1:C:63:TRP:CD1	1:C:67:ARG:HG3	2.49	0.47
1:B:63:TRP:CD1	1:B:67:ARG:HG3	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:41:PRO:HG2	1:B:44:LEU:HD13	1.98	0.46
1:B:259:PHE:CG	1:B:331:MET:HG2	2.50	0.45
1:B:372:LEU:HD23	1:B:377:GLN:HB2	1.99	0.45
1:B:35:LYS:NZ	4:B:1100:HOH:O	2.51	0.44
1:A:80:ILE:HG22	1:A:82:PRO:HD3	1.99	0.44
1:A:47:LYS:HE3	4:A:1089:HOH:O	2.18	0.44
1:A:393:LEU:HD21	1:A:409:VAL:HG11	2.00	0.44
1:B:327:LYS:NZ	4:B:817:HOH:O	2.46	0.44
1:B:371:ASP:HB3	1:B:431:ARG:NH2	2.34	0.43
1:C:93:PHE:CZ	1:C:111:VAL:HG21	2.53	0.43
1:C:426:SER:HA	1:C:429:TRP:CD2	2.54	0.42
1:C:429:TRP:HB3	1:C:433:CYS:HB2	2.01	0.42
1:A:240:ALA:O	4:A:1056:HOH:O	2.21	0.42
1:A:426:SER:HB2	1:A:429:TRP:CE3	2.54	0.42
1:A:45:GLU:OE1	1:A:45:GLU:N	2.35	0.42
1:C:355:ARG:NH2	1:C:428:SER:OG	2.53	0.42
1:C:29:GLU:OE2	1:C:35:LYS:HD3	2.20	0.41
1:B:350:ASN:OD1	1:B:355:ARG:NH1	2.52	0.41
1:B:90:LEU:HD13	1:B:108:PRO:HG2	2.02	0.41
1:C:259:PHE:CG	1:C:331:MET:HG2	2.56	0.41
1:B:443:GLU:OE2	4:B:992:HOH:O	2.22	0.41
1:B:368:ASN:ND2	1:B:427:GLN:O	2.53	0.41
1:A:56:ASP:CG	1:A:57:GLY:H	2.24	0.41
1:B:123:LEU:HD21	1:B:127:PRO:HD3	2.01	0.41
1:B:56:ASP:OD1	1:B:57:GLY:N	2.48	0.40
1:C:169:ALA:O	1:C:182:VAL:HA	2.21	0.40
1:B:240:ALA:O	4:B:1050:HOH:O	2.22	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	460/466 (99%)	449 (98%)	11 (2%)	0	100	100
1	B	459/466 (98%)	449 (98%)	10 (2%)	0	100	100
1	C	461/466 (99%)	453 (98%)	8 (2%)	0	100	100
All	All	1380/1398 (99%)	1351 (98%)	29 (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	372/376 (99%)	367 (99%)	5 (1%)	76	79
1	B	371/376 (99%)	364 (98%)	7 (2%)	65	67
1	C	373/376 (99%)	365 (98%)	8 (2%)	61	63
All	All	1116/1128 (99%)	1096 (98%)	20 (2%)	74	69

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	239[A]	SER
1	A	239[B]	SER
1	A	259	PHE
1	A	415	ARG
1	A	431	ARG
1	B	88[A]	ASP
1	B	88[B]	ASP
1	B	239[A]	SER
1	B	239[B]	SER
1	B	259	PHE
1	B	372	LEU
1	B	399	GLN
1	C	239[A]	SER
1	C	239[B]	SER
1	C	259	PHE

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Mol	Chain	Res	Type
1	C	355	ARG
1	C	372	LEU
1	C	377	GLN
1	C	399	GLN
1	C	426	SER

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	283	ASN

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 ⓘ

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
2	MAL	A	501	-	24,24,24	1.99	7 (29%)	35,35,35	1.06	3 (8%)
3	MLI	A	502	-	0,6,6	0.00	-	0,7,7	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MAL	B	501	-	24,24,24	1.98	8 (33%)	35,35,35	1.12	3 (8%)
3	MLI	B	502	-	0,6,6	0.00	-	0,7,7	0.00	-
2	MAL	C	501	-	24,24,24	1.98	8 (33%)	35,35,35	1.19	3 (8%)
3	MLI	C	502	-	0,6,6	0.00	-	0,7,7	0.00	-

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
2	MAL	A	501	-	-	0/8/48/48	0/2/2/2
3	MLI	A	502	-	-	0/0/4/4	0/0/0/0
2	MAL	B	501	-	-	0/8/48/48	0/2/2/2
3	MLI	B	502	-	-	0/0/4/4	0/0/0/0
2	MAL	C	501	-	-	0/8/48/48	0/2/2/2
3	MLI	C	502	-	-	0/0/4/4	0/0/0/0

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	MAL	C6'-C5'	-4.30	1.36	1.51
2	B	501	MAL	C6'-C5'	-4.22	1.36	1.51
2	C	501	MAL	C6'-C5'	-4.20	1.37	1.51
2	B	501	MAL	C3'-C2'	-3.96	1.42	1.52
2	A	501	MAL	C3'-C2'	-3.89	1.42	1.52
2	C	501	MAL	C3'-C2'	-3.84	1.42	1.52
2	C	501	MAL	C1'-C2'	-3.58	1.46	1.52
2	A	501	MAL	C1'-C2'	-3.46	1.46	1.52
2	B	501	MAL	C1'-C2'	-3.42	1.46	1.52
2	B	501	MAL	O1-C1	-2.11	1.35	1.41
2	C	501	MAL	O1-C1	-2.09	1.36	1.41
2	B	501	MAL	O3'-C3'	2.16	1.48	1.43
2	A	501	MAL	O3'-C3'	2.26	1.48	1.43
2	C	501	MAL	O3'-C3'	2.41	1.48	1.43
2	A	501	MAL	O5-C1	2.68	1.48	1.41
2	C	501	MAL	O5-C1	2.72	1.48	1.41
2	B	501	MAL	O5-C1	2.78	1.49	1.41
2	B	501	MAL	O5'-C5'	2.80	1.51	1.44
2	B	501	MAL	O2'-C2'	2.91	1.49	1.43
2	C	501	MAL	O5'-C5'	2.91	1.51	1.44
2	C	501	MAL	O2'-C2'	2.95	1.50	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	MAL	O2'-C2'	2.97	1.50	1.43
2	A	501	MAL	O5'-C5'	3.03	1.51	1.44

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	MAL	C2'-C3'-C4'	2.31	114.67	109.60
2	A	501	MAL	C2'-C3'-C4'	2.41	114.90	109.60
2	B	501	MAL	O5'-C1'-C2'	2.45	113.70	109.80
2	A	501	MAL	O5'-C1'-C2'	2.48	113.76	109.80
2	C	501	MAL	C2'-C3'-C4'	2.50	115.09	109.60
2	C	501	MAL	O5'-C1'-C2'	2.82	114.29	109.80
2	A	501	MAL	C1'-C2'-C3'	2.96	114.83	110.43
2	B	501	MAL	C1'-C2'-C3'	3.38	115.45	110.43
2	C	501	MAL	C1'-C2'-C3'	3.54	115.70	110.43

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 [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	458/466 (98%)	-0.13	7 (1%) 76 77	16, 28, 52, 80	0
1	B	458/466 (98%)	-0.09	6 (1%) 79 80	16, 29, 53, 79	0
1	C	458/466 (98%)	-0.10	5 (1%) 82 83	17, 29, 53, 75	0
All	All	1374/1398 (98%)	-0.11	18 (1%) 79 80	16, 29, 52, 80	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	459	LEU	4.9
1	A	2	LYS	4.0
1	B	459	LEU	3.9
1	B	458	ALA	3.8
1	A	459	LEU	3.4
1	A	174	ALA	3.0
1	C	174	ALA	2.8
1	A	240	ALA	2.7
1	A	457	ALA	2.6
1	B	240	ALA	2.6
1	B	173	ALA	2.6
1	B	2	LYS	2.5
1	C	175	GLY	2.5
1	A	33	GLY	2.2
1	C	35	LYS	2.1
1	B	3	ILE	2.1
1	C	458	ALA	2.1
1	A	3	ILE	2.0

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

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(\AA^2)	Q<0.9
2	MAL	C	501	23/23	0.97	0.08	-0.79	18,22,27,31	0
2	MAL	B	501	23/23	0.97	0.08	-0.89	17,22,29,32	0
2	MAL	A	501	23/23	0.97	0.08	-1.14	17,22,28,30	0
3	MLI	A	502	7/7	0.95	0.12	-	28,31,47,57	0
3	MLI	B	502	7/7	0.95	0.13	-	28,30,50,61	0
3	MLI	C	502	7/7	0.94	0.15	-	29,32,54,64	0

6.5 Other polymers [i](#)

There are no such residues in this entry.