Full wwPDB X-ray Structure Validation Report ⓘ

Sep 29, 2021 – 03:07 pm BST

PDB ID	:	7AIE
Title	:	Crystal structure of a truncated form of the KLC1-TPR domain ([A1-B5] fragment) - Monoclinic crystal form
Authors	:	Menetrey, J.; Llinas, P.
Deposited on	:	2020-09-27
Resolution	:	3.29 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 following versions of software and data (see references ⓘ) were used in the production of this report:

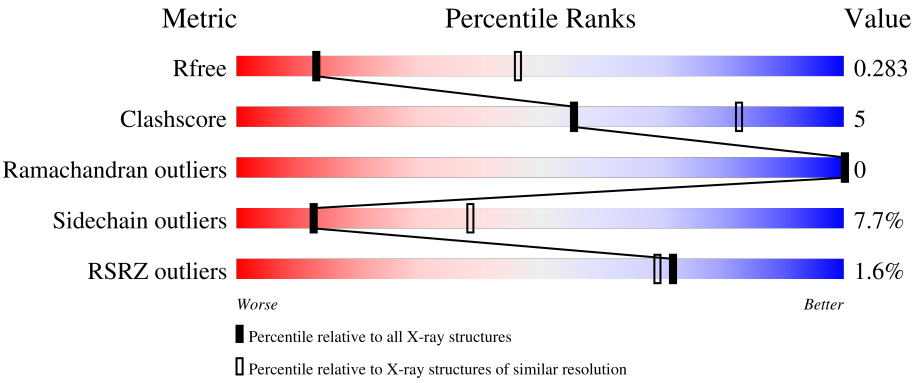
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.29 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}	130704	1177 (3.32-3.24)
Clashscore	141614	1044 (3.30-3.26)
Ramachandran outliers	138981	1026 (3.30-3.26)
Sidechain outliers	138945	1025 (3.30-3.26)
RSRZ outliers	127900	1141 (3.32-3.24)

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 <=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	255	65% 16% • 19%
1	B	255	71% 10% • 18%
1	C	255	2% 67% 14% 19%
1	D	255	2% 69% 10% • 20%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 5987 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 Kinesin light chain 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	207	Total	C	N	O	S	0	0	0
			1570	984	278	303	5			
1	B	208	Total	C	N	O	S	0	0	0
			1539	969	264	301	5			
1	C	207	Total	C	N	O	S	0	0	0
			1452	907	250	290	5			
1	D	205	Total	C	N	O	S	0	0	0
			1424	892	251	277	4			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	164	MET	-	initiating methionine	UNP Q07866
A	165	GLY	-	expression tag	UNP Q07866
A	166	SER	-	expression tag	UNP Q07866
A	167	SER	-	expression tag	UNP Q07866
A	168	HIS	-	expression tag	UNP Q07866
A	169	HIS	-	expression tag	UNP Q07866
A	170	HIS	-	expression tag	UNP Q07866
A	171	HIS	-	expression tag	UNP Q07866
A	172	HIS	-	expression tag	UNP Q07866
A	173	HIS	-	expression tag	UNP Q07866
A	174	SER	-	expression tag	UNP Q07866
A	175	SER	-	expression tag	UNP Q07866
A	176	GLY	-	expression tag	UNP Q07866
A	177	LEU	-	expression tag	UNP Q07866
A	178	VAL	-	expression tag	UNP Q07866
A	179	PRO	-	expression tag	UNP Q07866
A	180	ARG	-	expression tag	UNP Q07866
A	181	GLY	-	expression tag	UNP Q07866
A	182	SER	-	expression tag	UNP Q07866
A	183	HIS	-	expression tag	UNP Q07866
A	184	MET	-	expression tag	UNP Q07866

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Chain	Residue	Modelled	Actual	Comment	Reference
B	164	MET	-	initiating methionine	UNP Q07866
B	165	GLY	-	expression tag	UNP Q07866
B	166	SER	-	expression tag	UNP Q07866
B	167	SER	-	expression tag	UNP Q07866
B	168	HIS	-	expression tag	UNP Q07866
B	169	HIS	-	expression tag	UNP Q07866
B	170	HIS	-	expression tag	UNP Q07866
B	171	HIS	-	expression tag	UNP Q07866
B	172	HIS	-	expression tag	UNP Q07866
B	173	HIS	-	expression tag	UNP Q07866
B	174	SER	-	expression tag	UNP Q07866
B	175	SER	-	expression tag	UNP Q07866
B	176	GLY	-	expression tag	UNP Q07866
B	177	LEU	-	expression tag	UNP Q07866
B	178	VAL	-	expression tag	UNP Q07866
B	179	PRO	-	expression tag	UNP Q07866
B	180	ARG	-	expression tag	UNP Q07866
B	181	GLY	-	expression tag	UNP Q07866
B	182	SER	-	expression tag	UNP Q07866
B	183	HIS	-	expression tag	UNP Q07866
B	184	MET	-	expression tag	UNP Q07866
C	164	MET	-	initiating methionine	UNP Q07866
C	165	GLY	-	expression tag	UNP Q07866
C	166	SER	-	expression tag	UNP Q07866
C	167	SER	-	expression tag	UNP Q07866
C	168	HIS	-	expression tag	UNP Q07866
C	169	HIS	-	expression tag	UNP Q07866
C	170	HIS	-	expression tag	UNP Q07866
C	171	HIS	-	expression tag	UNP Q07866
C	172	HIS	-	expression tag	UNP Q07866
C	173	HIS	-	expression tag	UNP Q07866
C	174	SER	-	expression tag	UNP Q07866
C	175	SER	-	expression tag	UNP Q07866
C	176	GLY	-	expression tag	UNP Q07866
C	177	LEU	-	expression tag	UNP Q07866
C	178	VAL	-	expression tag	UNP Q07866
C	179	PRO	-	expression tag	UNP Q07866
C	180	ARG	-	expression tag	UNP Q07866
C	181	GLY	-	expression tag	UNP Q07866
C	182	SER	-	expression tag	UNP Q07866
C	183	HIS	-	expression tag	UNP Q07866
C	184	MET	-	expression tag	UNP Q07866

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Chain	Residue	Modelled	Actual	Comment	Reference
D	164	MET	-	initiating methionine	UNP Q07866
D	165	GLY	-	expression tag	UNP Q07866
D	166	SER	-	expression tag	UNP Q07866
D	167	SER	-	expression tag	UNP Q07866
D	168	HIS	-	expression tag	UNP Q07866
D	169	HIS	-	expression tag	UNP Q07866
D	170	HIS	-	expression tag	UNP Q07866
D	171	HIS	-	expression tag	UNP Q07866
D	172	HIS	-	expression tag	UNP Q07866
D	173	HIS	-	expression tag	UNP Q07866
D	174	SER	-	expression tag	UNP Q07866
D	175	SER	-	expression tag	UNP Q07866
D	176	GLY	-	expression tag	UNP Q07866
D	177	LEU	-	expression tag	UNP Q07866
D	178	VAL	-	expression tag	UNP Q07866
D	179	PRO	-	expression tag	UNP Q07866
D	180	ARG	-	expression tag	UNP Q07866
D	181	GLY	-	expression tag	UNP Q07866
D	182	SER	-	expression tag	UNP Q07866
D	183	HIS	-	expression tag	UNP Q07866
D	184	MET	-	expression tag	UNP Q07866

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

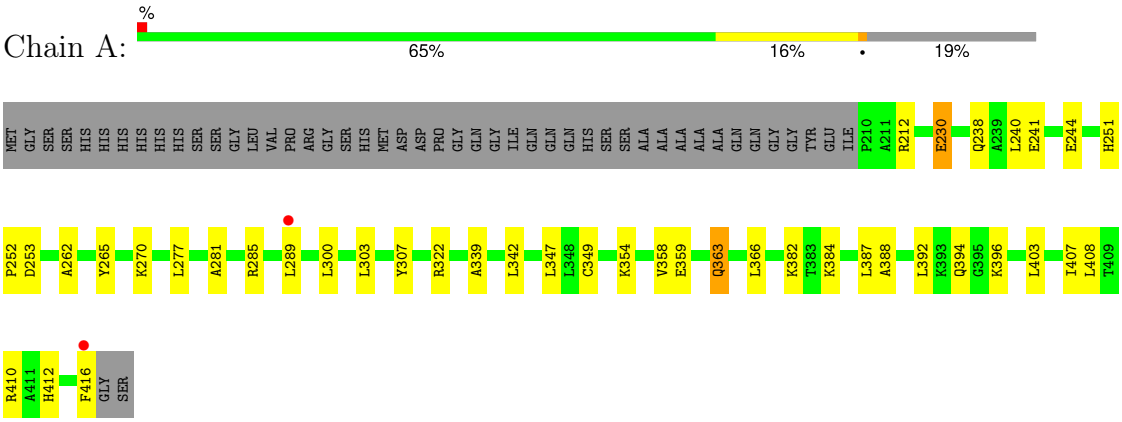
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Mg 1 1	0	0
2	B	1	Total Mg 1 1	0	0

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.

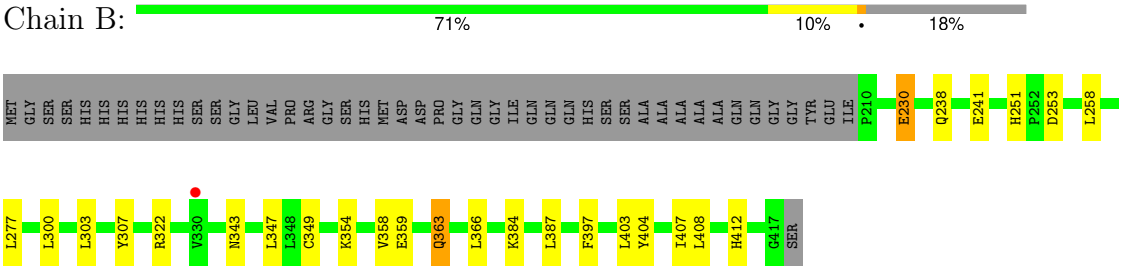
• Molecule 1: Kinesin light chain 1

Chain A:



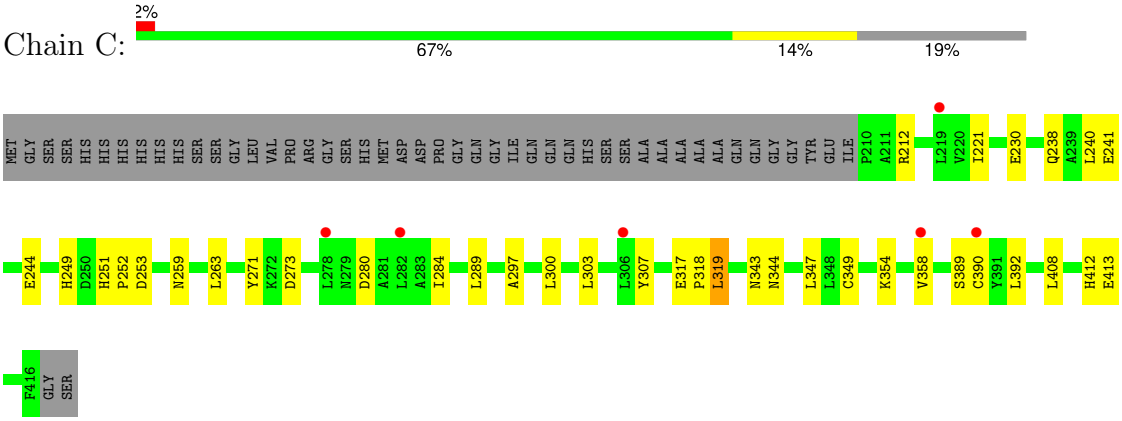
• Molecule 1: Kinesin light chain 1

Chain B:



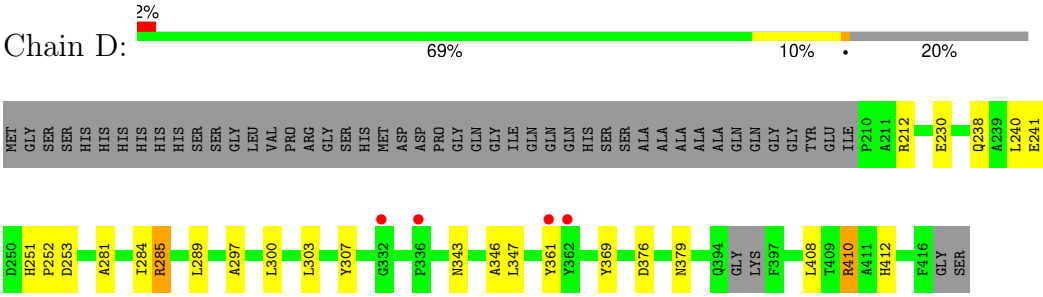
• Molecule 1: Kinesin light chain 1

Chain C:



• Molecule 1: Kinesin light chain 1

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	71.49Å 72.71Å 110.87Å 90.00° 90.05° 90.00°	Depositor
Resolution (Å)	46.33 – 3.29 46.33 – 3.29	Depositor EDS
% Data completeness (in resolution range)	98.7 (46.33-3.29) 98.7 (46.33-3.29)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.97 (at 3.25Å)	Xtriage
Refinement program	BUSTER 2.10.3 (6-FEB-2020)	Depositor
R, R_{free}	0.201 , 0.250 0.233 , 0.283	Depositor DCC
R_{free} test set	867 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	97.3	Xtriage
Anisotropy	0.627	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.026 for -k,-h,-l 0.024 for k,h,-l 0.148 for h,-k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	5987	wwPDB-VP
Average B, all atoms (Å^2)	116.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.51% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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: MG

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	0.45	0/1597	0.57	0/2176
1	B	0.43	0/1567	0.54	0/2145
1	C	0.43	0/1476	0.56	0/2031
1	D	0.41	0/1449	0.52	0/1994
All	All	0.43	0/6089	0.55	0/8346

There are no bond length outliers.

There are no bond angle outliers.

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	1570	0	1481	22	0
1	B	1539	0	1407	15	0
1	C	1452	0	1262	14	0
1	D	1424	0	1209	11	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
All	All	5987	0	5359	58	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 5.

All (58) 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:D:249:HIS:CD2	1:D:284:ILE:HD11	2.26	0.70
1:A:349:CYS:HB3	1:A:354:LYS:HB2	1.74	0.70
1:B:349:CYS:HB3	1:B:354:LYS:HB2	1.76	0.68
1:C:249:HIS:CD2	1:C:284:ILE:HD11	2.30	0.66
1:A:281:ALA:O	1:A:285:ARG:HG3	1.98	0.63
1:D:249:HIS:NE2	1:D:284:ILE:HD11	2.14	0.63
1:D:281:ALA:O	1:D:285:ARG:HG3	2.02	0.60
1:A:354:LYS:O	1:A:358:VAL:HG23	2.03	0.59
1:B:258:LEU:HD22	1:B:277:LEU:HD22	1.86	0.57
1:B:354:LYS:O	1:B:358:VAL:HG23	2.05	0.56
1:C:303:LEU:HD22	1:C:307:TYR:HE2	1.72	0.54
1:D:346:ALA:HB2	1:D:361:TYR:HB2	1.89	0.53
1:A:416:PHE:HB3	1:C:221:ILE:HD12	1.92	0.52
1:D:376:ASP:CB	1:D:410:ARG:HH22	2.22	0.52
1:A:394:GLN:OE1	1:A:396:LYS:HD2	2.10	0.52
1:C:252:PRO:HB3	1:C:289:LEU:HD21	1.93	0.51
1:D:252:PRO:HB3	1:D:289:LEU:HD21	1.93	0.51
1:C:280:ASP:O	1:C:284:ILE:HG12	2.11	0.50
1:B:359:GLU:O	1:B:363:GLN:HB2	2.12	0.50
1:A:252:PRO:HB3	1:A:289:LEU:HD21	1.94	0.49
1:C:354:LYS:O	1:C:358:VAL:HG23	2.11	0.49
1:D:303:LEU:HD22	1:D:307:TYR:HE2	1.78	0.49
1:A:230:GLU:H	1:A:230:GLU:HG3	1.32	0.49
1:A:251:HIS:CD2	1:A:253:ASP:H	2.31	0.48
1:A:388:ALA:HB1	1:B:397:PHE:HZ	1.78	0.48
1:A:303:LEU:HD22	1:A:307:TYR:HE2	1.77	0.48
1:B:303:LEU:HD22	1:B:307:TYR:HE2	1.77	0.48
1:C:251:HIS:CD2	1:C:253:ASP:H	2.32	0.47
1:C:389:SER:HA	1:C:392:LEU:HG	1.95	0.47
1:C:300:LEU:HD23	1:C:319:LEU:HD23	1.96	0.47
1:A:388:ALA:HB1	1:B:397:PHE:CZ	2.49	0.47
1:D:251:HIS:CD2	1:D:253:ASP:H	2.33	0.47
1:A:300:LEU:HD13	1:A:322:ARG:HG2	1.97	0.46
1:D:240:LEU:O	1:D:244:GLU:HG2	2.15	0.46
1:C:240:LEU:O	1:C:244:GLU:HG2	2.14	0.46
1:B:230:GLU:H	1:B:230:GLU:HG3	1.36	0.46
1:C:317:GLU:N	1:C:318:PRO:HD2	2.31	0.46
1:B:366:LEU:HD11	1:B:384:LYS:HG3	1.98	0.46
1:B:251:HIS:CD2	1:B:253:ASP:H	2.34	0.46
1:A:359:GLU:O	1:A:363:GLN:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:300:LEU:HD13	1:B:322:ARG:HG2	1.97	0.45
1:A:366:LEU:HD11	1:A:384:LYS:HG3	1.99	0.45
1:D:369:TYR:CE2	1:D:379:ASN:HB3	2.51	0.44
1:C:349:CYS:HB2	1:C:358:VAL:HG22	1.98	0.44
1:B:258:LEU:CD2	1:B:277:LEU:HD22	2.48	0.44
1:B:384:LYS:HB3	1:B:407:ILE:HD11	1.98	0.44
1:B:387:LEU:HD23	1:B:403:LEU:HD11	2.00	0.43
1:A:392:LEU:HB3	1:B:404:TYR:HD2	1.83	0.43
1:A:265:TYR:HB3	1:A:270:LYS:HB2	2.02	0.42
1:A:262:ALA:HB2	1:A:277:LEU:HB2	2.02	0.42
1:A:300:LEU:CD1	1:A:322:ARG:HG2	2.50	0.41
1:A:384:LYS:HB3	1:A:407:ILE:HD11	2.01	0.41
1:D:297:ALA:HA	1:D:300:LEU:HD12	2.02	0.41
1:A:387:LEU:HD23	1:A:403:LEU:HD11	2.03	0.41
1:A:240:LEU:O	1:A:244:GLU:HG2	2.19	0.41
1:C:297:ALA:HA	1:C:300:LEU:HD12	2.02	0.40
1:A:339:ALA:HA	1:A:342:LEU:HD12	2.02	0.40
1:C:259:ASN:O	1:C:263:LEU:HG	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	205/255 (80%)	201 (98%)	4 (2%)	0	100	100
1	B	206/255 (81%)	203 (98%)	3 (2%)	0	100	100
1	C	205/255 (80%)	202 (98%)	3 (2%)	0	100	100
1	D	201/255 (79%)	199 (99%)	2 (1%)	0	100	100
All	All	817/1020 (80%)	805 (98%)	12 (2%)	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	153/210 (73%)	143 (94%)	10 (6%)	17 46
1	B	145/210 (69%)	137 (94%)	8 (6%)	21 52
1	C	127/210 (60%)	113 (89%)	14 (11%)	6 24
1	D	117/210 (56%)	107 (92%)	10 (8%)	10 35
All	All	542/840 (64%)	500 (92%)	42 (8%)	13 38

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	212	ARG
1	A	230	GLU
1	A	238	GLN
1	A	241	GLU
1	A	347	LEU
1	A	363	GLN
1	A	382	LYS
1	A	408	LEU
1	A	410	ARG
1	A	412	HIS
1	B	230	GLU
1	B	238	GLN
1	B	241	GLU
1	B	343	ASN
1	B	347	LEU
1	B	363	GLN
1	B	408	LEU
1	B	412	HIS
1	C	212	ARG
1	C	230	GLU
1	C	238	GLN
1	C	241	GLU
1	C	271	TYR
1	C	273	ASP

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Mol	Chain	Res	Type
1	C	319	LEU
1	C	343	ASN
1	C	344	ASN
1	C	347	LEU
1	C	390	CYS
1	C	408	LEU
1	C	412	HIS
1	C	413	GLU
1	D	212	ARG
1	D	230	GLU
1	D	238	GLN
1	D	241	GLU
1	D	285	ARG
1	D	343	ASN
1	D	347	LEU
1	D	408	LEU
1	D	410	ARG
1	D	412	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	251	HIS
1	A	259	ASN
1	A	302	ASN
1	B	259	ASN
1	B	302	ASN
1	B	343	ASN
1	C	269	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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, 95^{th} 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	207/255 (81%)	0.28	2 (0%)	82	82	85, 105, 136, 155	0
1	B	208/255 (81%)	0.23	1 (0%)	91	91	85, 107, 137, 147	0
1	C	207/255 (81%)	0.14	6 (2%)	51	50	89, 121, 149, 155	0
1	D	205/255 (80%)	0.13	4 (1%)	65	63	82, 125, 158, 166	0
All	All	827/1020 (81%)	0.19	13 (1%)	72	69	82, 112, 153, 166	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	336	PRO	2.9
1	A	289	LEU	2.6
1	C	306	LEU	2.5
1	C	282	LEU	2.5
1	A	416	PHE	2.5
1	C	219	LEU	2.4
1	D	332	GLY	2.2
1	D	362	TYR	2.2
1	D	361	TYR	2.2
1	C	390	CYS	2.1
1	B	330	VAL	2.1
1	C	358	VAL	2.1
1	C	278	LEU	2.1

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 monosaccharides 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, 95^{th} 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(Å^2)	Q<0.9
2	MG	B	501	1/1	0.59	0.37	81,81,81,81	0
2	MG	A	501	1/1	0.73	0.29	62,62,62,62	0

6.5 Other polymers (i)

There are no such residues in this entry.