Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 07:52 am BST

PDB ID	:	5NGJ
Title	:	Crystal structure of pb6, major tail tube protein of bacteriophage T5
Authors	:	Arnaud, C.-A.; Effantin, G.; Vives, C.; Engilberge, S.; Bacia, M.; Boulanger, P.; Girard, E.; Schoehn, G.; Breyton, C.
Deposited on	:	2017-03-17
Resolution	:	2.20 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:

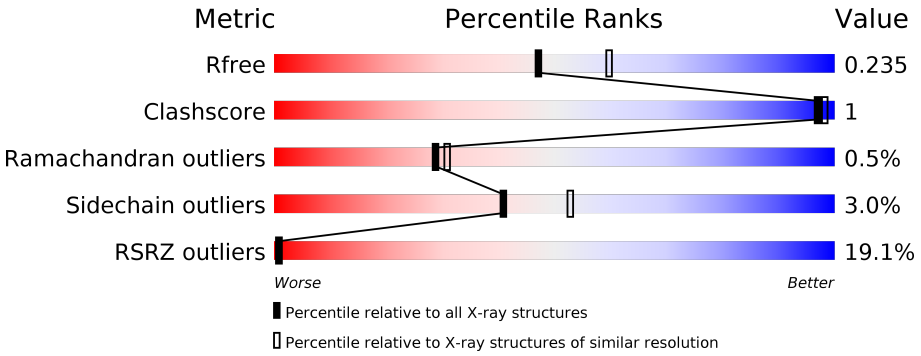
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 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	477	10% 89% . 8%
1	B	477	25% 84% 6% 9%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 13513 atoms, of which 6596 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 Tail tube protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	440	Total	C	H	N	O	S	0	1	0
			6729	2128	3347	563	682	9			
1	B	433	Total	C	H	N	O	S	0	2	1
			6551	2073	3249	552	668	9			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	465	GLU	-	expression tag	UNP Q6QGE2
A	466	ASN	-	expression tag	UNP Q6QGE2
A	467	LEU	-	expression tag	UNP Q6QGE2
A	468	TYR	-	expression tag	UNP Q6QGE2
A	469	PHE	-	expression tag	UNP Q6QGE2
A	470	GLN	-	expression tag	UNP Q6QGE2
A	471	GLY	-	expression tag	UNP Q6QGE2
A	472	HIS	-	expression tag	UNP Q6QGE2
A	473	HIS	-	expression tag	UNP Q6QGE2
A	474	HIS	-	expression tag	UNP Q6QGE2
A	475	HIS	-	expression tag	UNP Q6QGE2
A	476	HIS	-	expression tag	UNP Q6QGE2
A	477	HIS	-	expression tag	UNP Q6QGE2
B	465	GLU	-	expression tag	UNP Q6QGE2
B	466	ASN	-	expression tag	UNP Q6QGE2
B	467	LEU	-	expression tag	UNP Q6QGE2
B	468	TYR	-	expression tag	UNP Q6QGE2
B	469	PHE	-	expression tag	UNP Q6QGE2
B	470	GLN	-	expression tag	UNP Q6QGE2
B	471	GLY	-	expression tag	UNP Q6QGE2
B	472	HIS	-	expression tag	UNP Q6QGE2
B	473	HIS	-	expression tag	UNP Q6QGE2
B	474	HIS	-	expression tag	UNP Q6QGE2
B	475	HIS	-	expression tag	UNP Q6QGE2
B	476	HIS	-	expression tag	UNP Q6QGE2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	477	HIS	-	expression tag	UNP Q6QGE2

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	5	Total Cl 5 5	0	0

- Molecule 3 is water.

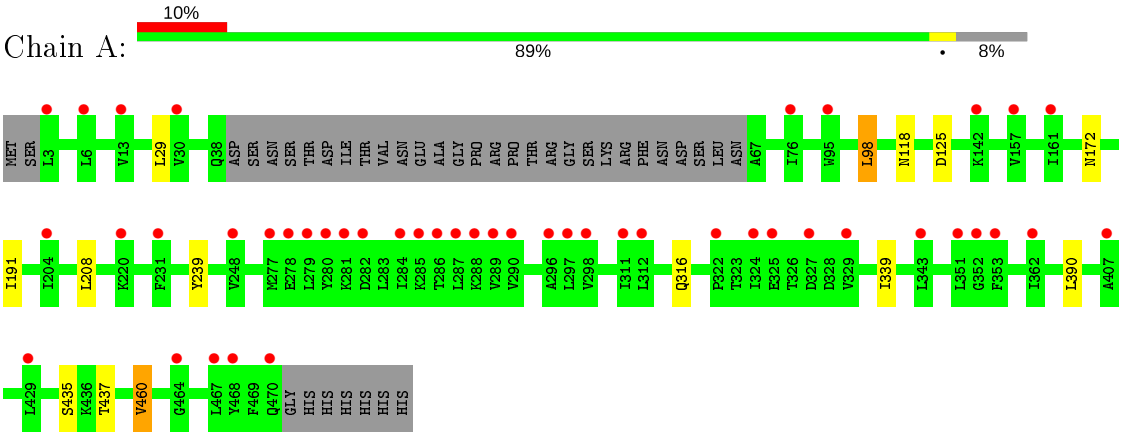
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	145	Total O 145 145	0	0
3	B	83	Total O 83 83	0	0

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 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.

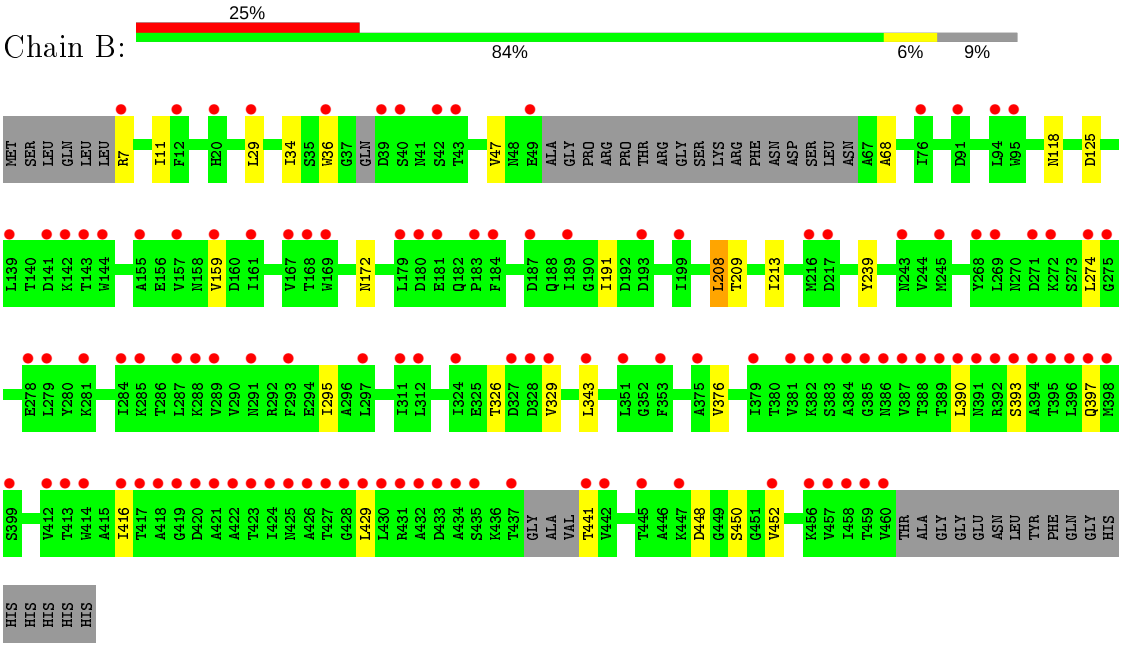
- Molecule 1: Tail tube protein

Chain A:



- Molecule 1: Tail tube protein

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	76.79Å 115.08Å 83.37Å 90.00° 111.88° 90.00°	Depositor
Resolution (Å)	44.00 – 2.20 57.32 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.7 (44.00-2.20) 99.7 (57.32-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.73 (at 2.20Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.205 , 0.235 0.209 , 0.235	Depositor DCC
R_{free} test set	3400 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	56.8	Xtriage
Anisotropy	0.495	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 71.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	13513	wwPDB-VP
Average B, all atoms (Å^2)	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.42% 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: CL

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	0.52	0/3442	0.71	2/4685 (0.0%)
1	B	0.46	0/3362	0.69	1/4575 (0.0%)
All	All	0.49	0/6804	0.70	3/9260 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	208	LEU	CD1-CG-CD2	5.57	127.21	110.50
1	A	98	LEU	CA-CB-CG	5.24	127.35	115.30
1	A	208	LEU	CD1-CG-CD2	5.03	125.59	110.50

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	3382	3347	3347	3	0
1	B	3302	3249	3221	9	0
2	A	5	0	0	0	0
3	A	145	0	0	0	0
3	B	83	0	0	0	0
All	All	6917	6596	6568	12	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 1.

All (12) 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:B:376:VAL:HG12	1:B:452:VAL:HG11	1.67	0.76
1:B:213:ILE:HG22	1:B:295:ILE:HG22	1.82	0.61
1:B:376:VAL:CG1	1:B:452:VAL:HG11	2.32	0.60
1:B:159:VAL:HG12	1:B:159:VAL:O	2.11	0.51
1:B:450:SER:OG	1:B:452:VAL:HG12	2.12	0.49
1:A:390:LEU:O	1:A:460:VAL:HA	2.13	0.48
1:A:172:ASN:HB2	1:A:239:TYR:CE2	2.50	0.47
1:A:316:GLN:HG2	1:A:339:ILE:O	2.17	0.45
1:B:36:TRP:CZ2	1:B:68:ALA:HB3	2.52	0.45
1:B:172:ASN:HB2	1:B:239:TYR:CE2	2.52	0.44
1:B:159:VAL:HG13	1:B:209:THR:HG21	2.02	0.42
1:B:11:ILE:HD11	1:B:34:ILE:HG21	2.01	0.42

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	437/477 (92%)	423 (97%)	14 (3%)	0	100 100
1	B	427/477 (90%)	406 (95%)	17 (4%)	4 (1%)	17 16
All	All	864/954 (91%)	829 (96%)	31 (4%)	4 (0%)	29 31

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	448	ASP
1	B	393	SER

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Mol	Chain	Res	Type
1	B	329	VAL
1	B	47	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	374/406 (92%)	366 (98%)	8 (2%)	53	67
1	B	362/406 (89%)	348 (96%)	14 (4%)	32	41
All	All	736/812 (91%)	714 (97%)	22 (3%)	41	53

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	LEU
1	A	98	LEU
1	A	118	ASN
1	A	125	ASP
1	A	191	ILE
1	A	435	SER
1	A	437	THR
1	A	460	VAL
1	B	7	ARG
1	B	29	LEU
1	B	118	ASN
1	B	125	ASP
1	B	191	ILE
1	B	208	LEU
1	B	274	LEU
1	B	326	THR
1	B	343	LEU
1	B	390	LEU
1	B	397	GLN
1	B	416	ILE
1	B	429	LEU

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Mol	Chain	Res	Type
1	B	441	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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

Of 5 ligands modelled in this entry, 5 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

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^{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	440/477 (92%)	0.84	47 (10%)	6	5	49, 70, 112, 149	0
1	B	433/477 (90%)	1.45	120 (27%)	0	0	57, 86, 178, 285	0
All	All	873/954 (91%)	1.15	167 (19%)	1	1	49, 76, 139, 285	0

All (167) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	389	THR	13.7
1	B	458	ILE	10.8
1	B	426	ALA	8.4
1	B	429	LEU	7.5
1	B	394	ALA	7.3
1	B	387	VAL	7.3
1	B	433	ASP	6.6
1	B	329	VAL	6.4
1	B	418	ALA	6.1
1	B	396	LEU	6.0
1	B	419	GLY	5.7
1	B	420	ASP	5.7
1	B	391	ASN	5.7
1	B	36	TRP	5.6
1	B	328	ASP	5.3
1	B	424	ILE	5.3
1	B	430	LEU	5.2
1	B	423	THR	5.2
1	B	383	SER	5.2
1	B	324	ILE	5.1
1	B	385	GLY	5.0
1	B	398	MET	4.9
1	B	460	VAL	4.9
1	B	456	LYS	4.6

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Mol	Chain	Res	Type	RSRZ
1	A	329	VAL	4.6
1	B	434	ALA	4.5
1	B	189	ILE	4.5
1	B	144	TRP	4.4
1	B	397	GLN	4.4
1	B	459	THR	4.3
1	B	382	LYS	4.3
1	B	395	THR	4.3
1	B	441	THR	4.3
1	A	327	ASP	4.3
1	A	278	GLU	4.3
1	A	290	VAL	4.3
1	A	279	LEU	4.2
1	B	431	ARG	4.2
1	A	281	LYS	4.2
1	B	435	SER	4.2
1	A	289	VAL	4.2
1	B	425	ASN	4.2
1	B	183	PRO	4.1
1	B	442	VAL	4.1
1	A	325	GLU	4.1
1	B	384	ALA	4.0
1	B	421	ALA	4.0
1	B	414	TRP	4.0
1	B	39	ASP	3.9
1	B	432	ALA	3.8
1	B	281	LYS	3.7
1	A	470	GLN	3.7
1	A	95	TRP	3.7
1	B	392	ARG	3.6
1	B	375	ALA	3.6
1	A	324	ILE	3.6
1	B	40	SER	3.5
1	B	216	MET	3.5
1	B	452	VAL	3.5
1	A	285	LYS	3.5
1	B	390	LEU	3.5
1	A	277	MET	3.4
1	B	285	LYS	3.4
1	B	379	ILE	3.4
1	B	457	VAL	3.4
1	B	159	VAL	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	343	LEU	3.3
1	B	422	ALA	3.3
1	B	217	ASP	3.3
1	B	327	ASP	3.3
1	A	468	TYR	3.3
1	B	437	THR	3.2
1	B	381	VAL	3.2
1	B	268	TYR	3.1
1	B	288	LYS	3.1
1	B	181	GLU	3.1
1	A	464	GLY	3.1
1	B	287	LEU	2.9
1	B	428	GLY	2.9
1	B	416	ILE	2.9
1	B	417	THR	2.9
1	A	297	LEU	2.9
1	B	179	LEU	2.9
1	B	427	THR	2.9
1	B	399	SER	2.8
1	B	143	THR	2.8
1	B	95	TRP	2.8
1	B	279	LEU	2.7
1	B	49	GLU	2.7
1	B	180	ASP	2.7
1	A	298	VAL	2.7
1	B	393	SER	2.7
1	B	291	ASN	2.7
1	A	3	LEU	2.7
1	A	287	LEU	2.7
1	B	269	LEU	2.7
1	B	43	THR	2.6
1	B	12	PHE	2.6
1	B	412	VAL	2.6
1	B	386	ASN	2.6
1	A	312	LEU	2.6
1	A	351	LEU	2.6
1	B	184	PHE	2.5
1	B	289	VAL	2.5
1	B	91	ASP	2.5
1	B	169	TRP	2.5
1	B	245	MET	2.5
1	B	413	THR	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	311	ILE	2.5
1	B	284	ILE	2.4
1	A	322	PRO	2.4
1	B	141	ASP	2.4
1	B	278	GLU	2.4
1	A	284	ILE	2.4
1	B	161	ILE	2.4
1	B	157	VAL	2.4
1	B	388	THR	2.4
1	B	243	ASN	2.4
1	B	199	ILE	2.3
1	A	296	ALA	2.3
1	B	139	LEU	2.3
1	B	142	LYS	2.3
1	B	353	PHE	2.3
1	A	343	LEU	2.3
1	B	94	LEU	2.3
1	B	7	ARG	2.3
1	B	20	HIS	2.3
1	B	293	PHE	2.3
1	A	282	ASP	2.3
1	A	280	TYR	2.2
1	A	286	THR	2.2
1	A	6	LEU	2.2
1	A	142	LYS	2.2
1	A	13	VAL	2.2
1	B	311	ILE	2.2
1	A	30	VAL	2.2
1	A	353	PHE	2.2
1	A	161	ILE	2.2
1	B	445	THR	2.2
1	A	204	ILE	2.2
1	A	288	LYS	2.2
1	A	429	LEU	2.2
1	B	274	LEU	2.2
1	B	297	LEU	2.2
1	B	187	ASP	2.2
1	A	407	ALA	2.2
1	B	272	LYS	2.2
1	B	447	LYS	2.1
1	B	193	ASP	2.1
1	A	248	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	220	LYS	2.1
1	A	362	ILE	2.1
1	B	76	ILE	2.1
1	B	29	LEU	2.1
1	B	168	THR	2.1
1	A	231	PHE	2.1
1	B	271	ASP	2.1
1	A	157	VAL	2.1
1	B	275	GLY	2.1
1	B	312	LEU	2.1
1	B	351	LEU	2.1
1	A	76	ILE	2.0
1	A	352	GLY	2.0
1	A	467	LEU	2.0
1	B	167	VAL	2.0
1	B	42	SER	2.0
1	B	155	ALA	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. 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	CL	A	503	1/1	0.29	0.18	107,107,107,107	0
2	CL	A	505	1/1	0.86	0.35	91,91,91,91	1
2	CL	A	501	1/1	0.90	0.15	56,56,56,56	1
2	CL	A	504	1/1	0.90	0.25	92,92,92,92	0
2	CL	A	502	1/1	0.96	0.29	50,50,50,50	1

6.5 Other polymers (i)

There are no such residues in this entry.