Full wwPDB X-ray Structure Validation Report ⓘ

Nov 28, 2023 – 07:16 pm GMT

PDB ID	:	1DWN
Title	:	Structure of bacteriophage PP7 from Pseudomonas aeruginosa at 3.7 A resolution
Authors	:	Tars, K.; Fridborg, K.; Bundule, M.; Liljas, L.
Deposited on	:	1999-12-09
Resolution	:	3.50 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:

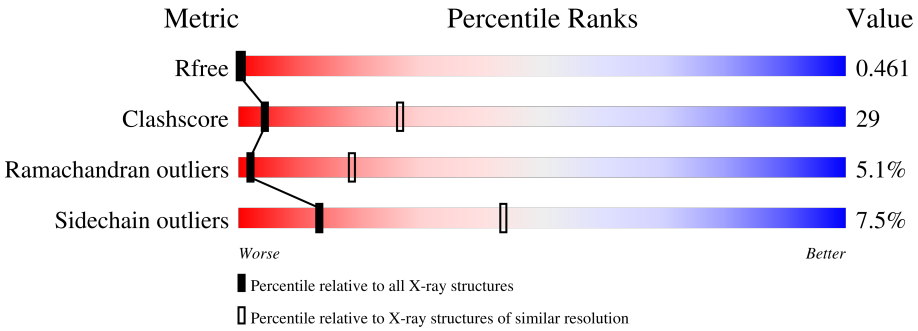
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 3.50 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	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)

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%

Mol	Chain	Length	Quality of chain
1	A	127	57% 37% 6%
1	B	127	45% 47% 8%
1	C	127	52% 43% 5%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 2904 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 PHAGE COAT PROTEIN.

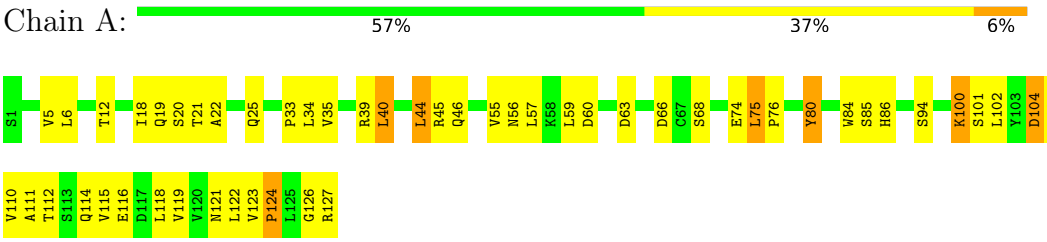
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	127	Total	C	N	O	S	0	0	0
			968	602	171	193	2			
1	B	127	Total	C	N	O	S	0	0	0
			968	602	171	193	2			
1	C	127	Total	C	N	O	S	0	0	0
			968	602	171	193	2			

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. 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. 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.

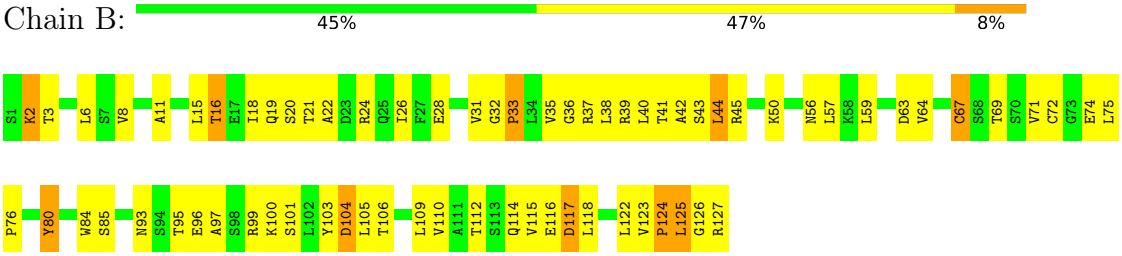
• Molecule 1: PHAGE COAT PROTEIN

Chain A:



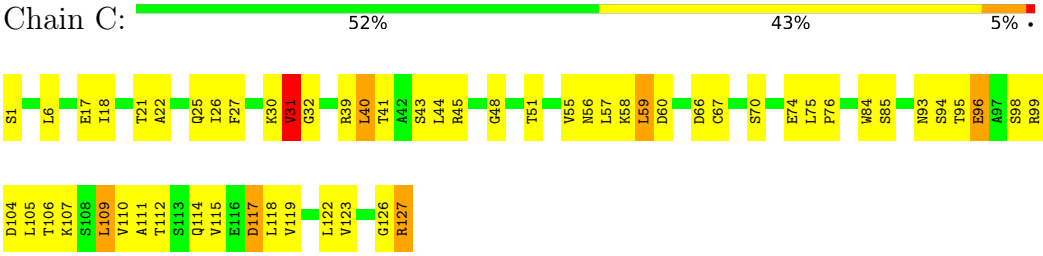
• Molecule 1: PHAGE COAT PROTEIN

Chain B:



• Molecule 1: PHAGE COAT PROTEIN

Chain C:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	285.00Å 324.00Å 380.00Å 88.40° 88.10° 87.70°	Depositor
Resolution (Å)	60.00 – 3.50 39.97 – 3.31	Depositor EDS
% Data completeness (in resolution range)	35.2 (60.00-3.50) 26.8 (39.97-3.31)	Depositor EDS
R_{merge}	0.27	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$	-	Xtriage
Refinement program	CNS 0.5	Depositor
R, R_{free}	0.288 , 0.292 0.458 , 0.461	Depositor DCC
R_{free} test set	30383 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	101.1	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.26 , 38.3	EDS
L-test for twinning[1]	$< \|L\| > = 0.42$, $< L^2 > = 0.25$	Xtriage
Estimated twinning fraction	0.028 for h,-k,-l 0.026 for -h,k,-l 0.025 for -h,-k,l	Xtriage
F_o,F_c correlation	0.65	EDS
Total number of atoms	2904	wwPDB-VP
Average B, all atoms (Å^2)	82.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.88% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]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

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	0.61	0/977	0.77	0/1328
1	B	0.56	0/977	0.79	1/1328 (0.1%)
1	C	0.58	0/977	0.76	0/1328
All	All	0.58	0/2931	0.77	1/3984 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	21	THR	N-CA-C	-5.42	96.38	111.00

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	968	0	1001	51	0
1	B	968	0	1001	65	0
1	C	968	0	1001	70	0
All	All	2904	0	3003	172	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 29.

All (172) 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:21:THR:HG22	1:A:22:ALA:H	1.16	1.10
1:C:67:CYS:HB2	1:C:74:GLU:HG2	1.46	0.96
1:B:40:LEU:HD23	1:B:41:THR:N	1.84	0.93
1:A:66:ASP:HB3	1:A:76:PRO:HG3	1.54	0.90
1:B:112:THR:HB	1:B:115:VAL:HG23	1.52	0.89
1:B:22:ALA:HB2	1:C:17:GLU:HG2	1.59	0.85
1:A:75:LEU:HD22	1:C:93:ASN:HD22	1.42	0.85
1:C:112:THR:HB	1:C:115:VAL:HG23	1.57	0.85
1:B:96:GLU:HA	1:B:99:ARG:NH1	1.91	0.84
1:A:112:THR:HB	1:A:115:VAL:HG23	1.63	0.81
1:A:21:THR:HG22	1:A:22:ALA:N	1.95	0.80
1:A:56:ASN:O	1:A:57:LEU:HD23	1.84	0.77
1:C:18:ILE:HD11	1:C:30:LYS:HE2	1.65	0.77
1:B:109:LEU:C	1:B:109:LEU:HD13	2.06	0.75
1:C:56:ASN:O	1:C:57:LEU:HD23	1.87	0.75
1:C:109:LEU:C	1:C:109:LEU:HD13	2.08	0.74
1:A:75:LEU:H	1:A:75:LEU:HD12	1.52	0.74
1:B:2:LYS:HZ2	1:C:1:SER:CA	2.02	0.72
1:B:28:GLU:HG3	1:B:39:ARG:HG2	1.71	0.72
1:A:109:LEU:C	1:A:109:LEU:HD13	2.09	0.71
1:C:94:SER:HB2	1:C:99:ARG:HD2	1.74	0.69
1:B:38:LEU:HD12	1:B:39:ARG:N	2.08	0.69
1:C:112:THR:HG22	1:C:114:GLN:H	1.57	0.69
1:A:57:LEU:O	1:A:85:SER:HA	1.94	0.68
1:B:43:SER:O	1:B:44:LEU:HB2	1.92	0.68
1:B:2:LYS:HZ2	1:C:1:SER:HA	1.59	0.68
1:C:95:THR:HB	1:C:98:SER:CB	2.24	0.68
1:A:112:THR:HG22	1:A:114:GLN:N	2.09	0.67
1:A:112:THR:HG22	1:A:114:GLN:H	1.60	0.67
1:A:21:THR:CG2	1:A:22:ALA:H	1.91	0.67
1:C:67:CYS:HB2	1:C:74:GLU:CG	2.21	0.66
1:C:18:ILE:HD11	1:C:30:LYS:CE	2.25	0.66
1:A:75:LEU:HD22	1:C:93:ASN:ND2	2.10	0.66
1:B:112:THR:HG22	1:B:114:GLN:H	1.61	0.65
1:B:32:GLY:O	1:B:33:PRO:O	2.14	0.65
1:C:109:LEU:HD13	1:C:110:VAL:N	2.12	0.64
1:A:46:GLN:O	1:A:46:GLN:HG3	1.98	0.63
1:A:109:LEU:HD13	1:A:110:VAL:N	2.12	0.63
1:C:57:LEU:O	1:C:85:SER:HA	1.98	0.63
1:A:66:ASP:CB	1:A:76:PRO:HG3	2.26	0.63
1:A:68:SER:HB3	1:A:74:GLU:O	1.99	0.63
1:B:43:SER:HB3	1:B:56:ASN:HB3	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:95:THR:HB	1:C:98:SER:HB2	1.81	0.62
1:C:126:GLY:O	1:C:127:ARG:HB2	2.00	0.62
1:B:36:GLY:O	1:B:37:ARG:C	2.39	0.61
1:A:75:LEU:HD12	1:A:75:LEU:N	2.14	0.61
1:B:96:GLU:HA	1:B:99:ARG:HH12	1.62	0.61
1:B:115:VAL:O	1:B:118:LEU:HB3	2.00	0.61
1:B:109:LEU:HD13	1:B:110:VAL:N	2.17	0.60
1:B:22:ALA:CB	1:C:17:GLU:HG2	2.31	0.60
1:B:40:LEU:HD23	1:B:40:LEU:C	2.22	0.60
1:C:40:LEU:HD23	1:C:58:LYS:O	2.02	0.60
1:C:31:VAL:HG22	1:C:32:GLY:H	1.67	0.60
1:C:112:THR:HG22	1:C:114:GLN:N	2.16	0.60
1:A:121:ASN:O	1:A:122:LEU:HB2	2.01	0.59
1:B:44:LEU:HD23	1:B:45:ARG:N	2.18	0.59
1:B:100:LYS:HG2	1:B:104:ASP:OD1	2.03	0.59
1:C:118:LEU:HD12	1:C:118:LEU:O	2.01	0.59
1:B:56:ASN:O	1:B:57:LEU:HD23	2.04	0.58
1:B:63:ASP:HB2	1:B:80:TYR:CE1	2.38	0.58
1:A:115:VAL:O	1:A:119:VAL:HG23	2.04	0.58
1:A:122:LEU:O	1:A:124:PRO:HD3	2.05	0.57
1:B:18:ILE:HG22	1:B:26:ILE:O	2.04	0.57
1:C:39:ARG:HB2	1:C:60:ASP:HB2	1.87	0.57
1:B:57:LEU:O	1:B:85:SER:HA	2.05	0.56
1:C:95:THR:O	1:C:98:SER:HB3	2.06	0.56
1:A:74:GLU:HG2	1:A:75:LEU:N	2.21	0.56
1:B:2:LYS:NZ	1:C:1:SER:HA	2.21	0.55
1:C:21:THR:HG22	1:C:22:ALA:N	2.21	0.55
1:A:118:LEU:HA	1:A:123:VAL:H	1.71	0.55
1:C:100:LYS:O	1:C:101:SER:C	2.45	0.55
1:C:6:LEU:HD12	1:C:6:LEU:N	2.21	0.55
1:C:55:VAL:HG12	1:C:56:ASN:N	2.22	0.54
1:B:2:LYS:NZ	1:C:1:SER:CA	2.71	0.54
1:B:112:THR:HG22	1:B:114:GLN:N	2.21	0.54
1:C:94:SER:HB2	1:C:99:ARG:CD	2.37	0.54
1:B:93:ASN:HD22	1:C:75:LEU:HD13	1.72	0.54
1:A:18:ILE:HG13	1:A:19:GLN:N	2.23	0.54
1:C:59:LEU:HD13	1:C:60:ASP:N	2.23	0.54
1:A:100:LYS:HD2	1:A:104:ASP:OD2	2.08	0.53
1:B:2:LYS:CE	1:C:1:SER:HA	2.39	0.53
1:B:40:LEU:C	1:B:40:LEU:CD2	2.77	0.53
1:C:115:VAL:O	1:C:119:VAL:HG23	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:106:THR:O	1:B:110:VAL:HG23	2.10	0.52
1:A:74:GLU:HG2	1:A:75:LEU:H	1.76	0.51
1:C:117:ASP:OD2	1:C:123:VAL:HG21	2.10	0.51
1:C:118:LEU:O	1:C:122:LEU:HA	2.11	0.51
1:B:100:LYS:O	1:B:101:SER:C	2.49	0.51
1:C:110:VAL:C	1:C:112:THR:H	2.14	0.51
1:B:42:ALA:HA	1:B:57:LEU:HD23	1.93	0.50
1:B:95:THR:HG22	1:B:97:ALA:H	1.74	0.50
1:C:21:THR:HG22	1:C:22:ALA:H	1.77	0.50
1:B:126:GLY:C	1:B:127:ARG:HG3	2.32	0.50
1:B:75:LEU:HB3	1:B:76:PRO:CD	2.43	0.49
1:C:44:LEU:HD12	1:C:45:ARG:N	2.28	0.49
1:B:36:GLY:HA3	1:B:64:VAL:HG11	1.93	0.49
1:B:118:LEU:O	1:B:122:LEU:N	2.45	0.49
1:A:55:VAL:HG12	1:A:56:ASN:N	2.28	0.49
1:A:44:LEU:HD23	1:A:45:ARG:N	2.27	0.49
1:C:18:ILE:HD11	1:C:30:LYS:NZ	2.28	0.49
1:C:67:CYS:CB	1:C:74:GLU:HG2	2.32	0.49
1:B:67:CYS:C	1:B:69:THR:N	2.66	0.49
1:B:67:CYS:C	1:B:69:THR:H	2.15	0.49
1:A:118:LEU:O	1:A:122:LEU:HA	2.14	0.48
1:C:112:THR:HB	1:C:115:VAL:CG2	2.38	0.48
1:B:18:ILE:HG23	1:B:19:GLN:N	2.29	0.48
1:C:99:ARG:O	1:C:102:LEU:HB3	2.14	0.48
1:A:110:VAL:C	1:A:112:THR:H	2.18	0.47
1:B:109:LEU:O	1:B:115:VAL:HG21	2.15	0.47
1:A:100:LYS:O	1:A:101:SER:C	2.52	0.47
1:A:126:GLY:O	1:A:127:ARG:HD3	2.14	0.47
1:B:3:THR:HG22	1:B:16:THR:HG23	1.97	0.46
1:C:100:LYS:HG2	1:C:104:ASP:OD2	2.15	0.46
1:B:2:LYS:NZ	1:C:1:SER:N	2.63	0.46
1:A:84:TRP:C	1:A:84:TRP:CD1	2.88	0.46
1:A:5:VAL:HG22	1:A:6:LEU:N	2.31	0.45
1:B:101:SER:O	1:B:105:LEU:HG	2.15	0.45
1:A:63:ASP:HB2	1:A:80:TYR:CE1	2.51	0.45
1:A:19:GLN:HG2	1:A:20:SER:N	2.31	0.45
1:A:59:LEU:HD22	1:A:59:LEU:HA	1.73	0.45
1:A:34:LEU:HD12	1:A:34:LEU:HA	1.62	0.45
1:A:109:LEU:C	1:A:109:LEU:CD1	2.81	0.45
1:A:115:VAL:O	1:A:118:LEU:HB3	2.17	0.45
1:A:39:ARG:HB2	1:A:60:ASP:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:55:VAL:CG1	1:C:56:ASN:N	2.81	0.44
1:A:39:ARG:HG3	1:A:39:ARG:HH11	1.83	0.44
1:B:19:GLN:O	1:B:20:SER:HB2	2.17	0.44
1:B:57:LEU:HD23	1:B:57:LEU:HA	1.79	0.44
1:A:105:LEU:O	1:A:106:THR:C	2.56	0.43
1:B:125:LEU:HD12	1:B:125:LEU:HA	1.71	0.43
1:A:6:LEU:O	1:A:12:THR:HA	2.18	0.43
1:A:40:LEU:C	1:A:40:LEU:CD2	2.86	0.43
1:B:2:LYS:HZ2	1:C:1:SER:CB	2.30	0.43
1:C:27:PHE:CD1	1:C:27:PHE:N	2.86	0.43
1:A:56:ASN:HA	1:A:86:HIS:O	2.18	0.43
1:A:115:VAL:O	1:A:116:GLU:C	2.57	0.43
1:B:116:GLU:HG3	1:B:117:ASP:N	2.34	0.43
1:B:75:LEU:HD22	1:B:76:PRO:HD3	2.01	0.43
1:B:22:ALA:HB2	1:C:17:GLU:CG	2.41	0.43
1:C:109:LEU:O	1:C:115:VAL:HG21	2.19	0.43
1:B:38:LEU:HD12	1:B:38:LEU:C	2.39	0.42
1:C:96:GLU:HA	1:C:99:ARG:CZ	2.50	0.42
1:C:109:LEU:C	1:C:109:LEU:CD1	2.81	0.42
1:C:66:ASP:OD1	1:C:76:PRO:HG3	2.20	0.42
1:A:126:GLY:O	1:A:127:ARG:CD	2.68	0.42
1:B:2:LYS:HZ2	1:C:1:SER:HB3	1.84	0.42
1:B:8:VAL:HB	1:B:11:ALA:HB3	2.00	0.42
1:B:75:LEU:HB3	1:B:76:PRO:HD2	2.01	0.42
1:C:106:THR:O	1:C:109:LEU:HB3	2.19	0.42
1:B:6:LEU:HD12	1:B:6:LEU:N	2.34	0.42
1:C:95:THR:HB	1:C:98:SER:HB3	2.00	0.42
1:C:122:LEU:HA	1:C:122:LEU:HD12	1.89	0.41
1:A:75:LEU:N	1:A:75:LEU:CD1	2.80	0.41
1:B:15:LEU:HA	1:B:15:LEU:HD23	1.69	0.41
1:B:71:VAL:HG12	1:B:71:VAL:O	2.20	0.41
1:C:84:TRP:C	1:C:84:TRP:CD1	2.94	0.41
1:C:40:LEU:CD2	1:C:41:THR:N	2.83	0.41
1:C:101:SER:O	1:C:105:LEU:HG	2.20	0.41
1:C:118:LEU:HD12	1:C:118:LEU:C	2.38	0.41
1:C:118:LEU:HA	1:C:123:VAL:H	1.85	0.41
1:C:102:LEU:O	1:C:103:TYR:C	2.58	0.41
1:A:101:SER:O	1:A:102:LEU:C	2.58	0.41
1:A:118:LEU:O	1:A:122:LEU:N	2.50	0.41
1:B:75:LEU:HD23	1:B:75:LEU:HA	1.87	0.41
1:C:110:VAL:O	1:C:112:THR:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:25:GLN:O	1:C:26:ILE:HG13	2.20	0.41
1:B:93:ASN:OD1	1:B:93:ASN:N	2.51	0.41
1:C:40:LEU:HD23	1:C:41:THR:N	2.36	0.40
1:C:94:SER:O	1:C:99:ARG:NH1	2.55	0.40
1:B:84:TRP:C	1:B:84:TRP:CD1	2.94	0.40
1:B:123:VAL:O	1:B:124:PRO:C	2.59	0.40
1:B:109:LEU:CD1	1:B:110:VAL:N	2.85	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	125/127 (98%)	97 (78%)	22 (18%)	6 (5%)	2 20
1	B	125/127 (98%)	93 (74%)	23 (18%)	9 (7%)	1 11
1	C	125/127 (98%)	102 (82%)	19 (15%)	4 (3%)	4 29
All	All	375/381 (98%)	292 (78%)	64 (17%)	19 (5%)	2 19

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	31	VAL
1	B	33	PRO
1	A	94	SER
1	B	44	LEU
1	B	72	CYS
1	C	31	VAL
1	C	111	ALA
1	A	25	GLN
1	A	33	PRO
1	A	100	LYS

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Mol	Chain	Res	Type
1	B	74	GLU
1	B	103	TYR
1	B	104	ASP
1	C	48	GLY
1	C	107	LYS
1	A	104	ASP
1	A	111	ALA
1	B	50	LYS
1	B	124	PRO

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	111/112 (99%)	105 (95%)	6 (5%)	22 55
1	B	111/112 (99%)	102 (92%)	9 (8%)	11 41
1	C	111/112 (99%)	101 (91%)	10 (9%)	9 37
All	All	333/336 (99%)	308 (92%)	25 (8%)	13 43

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	VAL
1	A	40	LEU
1	A	44	LEU
1	A	75	LEU
1	A	80	TYR
1	A	124	PRO
1	B	2	LYS
1	B	16	THR
1	B	24	ARG
1	B	35	VAL
1	B	59	LEU
1	B	67	CYS
1	B	80	TYR

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Mol	Chain	Res	Type
1	B	117	ASP
1	B	125	LEU
1	C	31	VAL
1	C	40	LEU
1	C	43	SER
1	C	51	THR
1	C	59	LEU
1	C	70	SER
1	C	96	GLU
1	C	109	LEU
1	C	117	ASP
1	C	127	ARG

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

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)

There are no ligands in this entry.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.