



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 09:42 am BST

PDB ID : 6C72
Title : Crystal structure of a tailspike protein gp49 from *Acinetobacter baumannii* bacteriophage Fri1, a capsular polysaccharide depolymerase
Authors : Buth, S.A.; Garcon, A.; Popova, A.V.; Shneider, M.M.; Leiman, P.G.
Deposited on : 2018-01-19
Resolution : 2.40 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

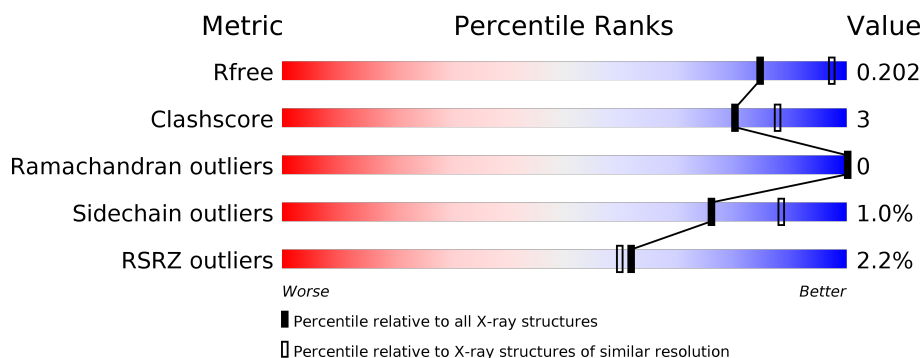
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 $\leq 5\%$. 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	597	<div> <div> <div>0%</div> <div>89%</div> <div>8%</div> <div>•</div> </div> </div>
1	B	597	<div> <div>4%</div> <div>90%</div> <div>7%</div> <div>•</div> </div>
1	C	597	<div> <div>2%</div> <div>89%</div> <div>8%</div> <div>•</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 15043 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 Particle-associated glycoside hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	579	Total	C	N	O	S	0	2	0
			4466	2821	763	867	15			
1	B	579	Total	C	N	O	S	0	3	0
			4478	2828	766	869	15			
1	C	579	Total	C	N	O	S	0	2	0
			4469	2823	765	866	15			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	187	GLY	-	expression tag	UNP A0A0H4TJ34
B	187	GLY	-	expression tag	UNP A0A0H4TJ34
C	187	GLY	-	expression tag	UNP A0A0H4TJ34

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	13	Total	Zn	0	4
			17	17		
2	A	14	Total	Zn	0	2
			16	16		
2	C	13	Total	Zn	0	2
			15	15		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	556	Total	O	0	0
			556	556		
3	B	469	Total	O	0	0
			469	469		

Continued on next page...

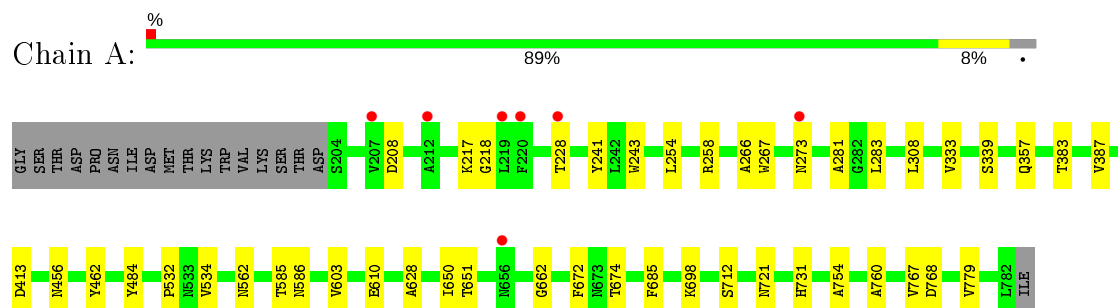
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	557	Total	O	0	0
			557	557		

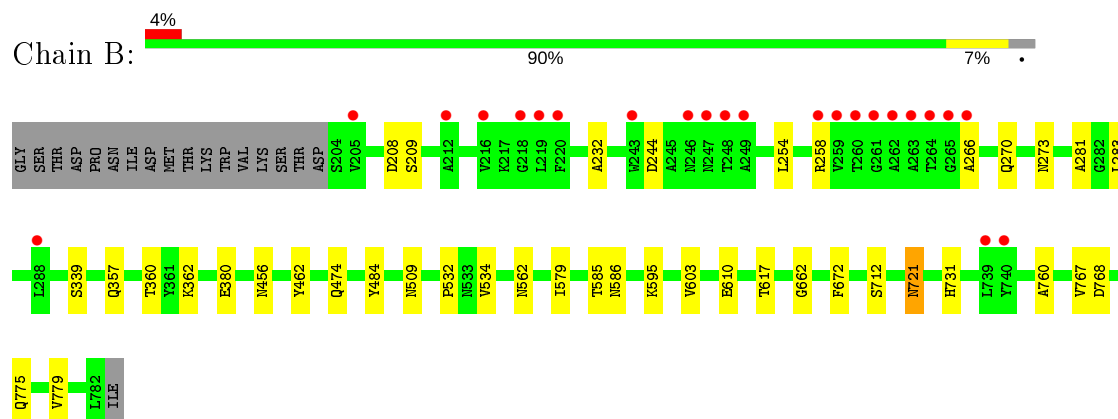
3 Residue-property plots [i](#)

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.

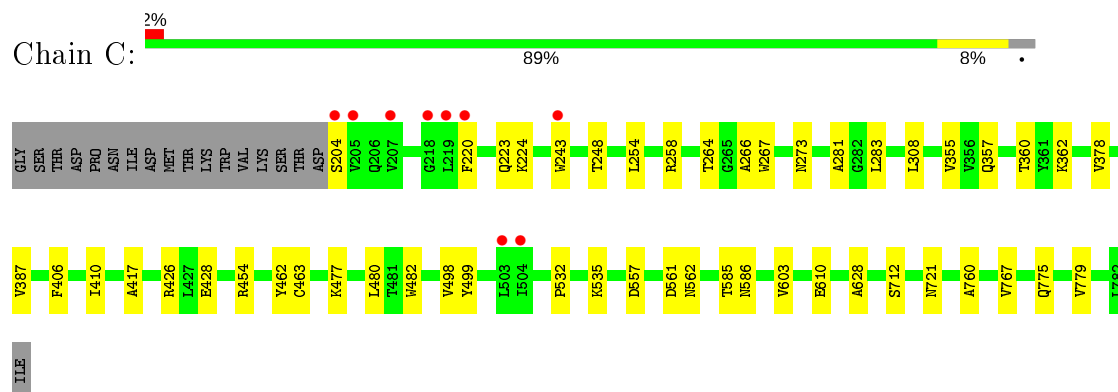
- Molecule 1: Particle-associated glycoside hydrolase



- Molecule 1: Particle-associated glycoside hydrolase



- Molecule 1: Particle-associated glycoside hydrolase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.46 Å 98.66 Å 148.70 Å 90.00° 91.81° 90.00°	Depositor
Resolution (Å)	49.33 – 2.40 49.33 – 2.40	Depositor EDS
% Data completeness (in resolution range)	97.9 (49.33-2.40) 98.3 (49.33-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.91 (at 2.39 Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.154 , 0.203 0.153 , 0.202	Depositor DCC
R_{free} test set	4107 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	31.2	Xtriage
Anisotropy	0.586	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 40.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.020 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	15043	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.75% 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, 0.333 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: ZN

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	0.39	0/4556	0.56	0/6205
1	B	0.36	0/4568	0.54	0/6220
1	C	0.40	0/4559	0.55	0/6208
All	All	0.38	0/13683	0.55	0/18633

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	4466	0	4379	27	0
1	B	4478	0	4392	23	0
1	C	4469	0	4386	26	0
2	A	16	0	0	0	0
2	B	17	0	0	0	0
2	C	15	0	0	0	0
3	A	556	0	0	4	0
3	B	469	0	0	4	1
3	C	557	0	0	3	1
All	All	15043	0	13157	71	1

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 (71) 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:254:LEU:HD13	1:A:281:ALA:HB2	1.68	0.73
1:C:254:LEU:HD13	1:C:281:ALA:HB2	1.71	0.72
1:A:339:SER:HB2	1:C:308:LEU:HD12	1.74	0.70
1:A:768:ASP:OD2	3:A:901:HOH:O	2.09	0.69
1:B:244:ASP:OD1	3:B:901:HOH:O	2.11	0.68
1:B:258:ARG:HD2	1:B:266:ALA:HB2	1.76	0.66
1:A:273[B]:ASN:ND2	1:B:273:ASN:OD1	2.30	0.65
1:C:258:ARG:HD2	1:C:266:ALA:HB2	1.80	0.63
1:A:258:ARG:HD2	1:A:266:ALA:HB2	1.79	0.61
1:B:270:GLN:NE2	3:B:906:HOH:O	2.31	0.59
1:A:217:LYS:NZ	3:A:907:HOH:O	2.36	0.58
1:A:308:LEU:HD12	1:B:339:SER:HB2	1.86	0.57
1:C:767:VAL:HG11	1:C:779:VAL:HG11	1.87	0.56
1:A:767:VAL:HG11	1:A:779:VAL:HG11	1.87	0.55
1:C:562:ASN:HA	1:C:586:ASN:O	2.07	0.55
1:A:273[B]:ASN:OD1	1:C:273:ASN:ND2	2.38	0.55
1:B:579:ILE:HB	1:B:603:VAL:HG12	1.89	0.54
1:C:557:ASP:OD1	3:C:901:HOH:O	2.19	0.54
1:A:698:LYS:NZ	3:A:909:HOH:O	2.42	0.53
1:B:562:ASN:HA	1:B:586:ASN:O	2.10	0.51
1:B:767:VAL:HG11	1:B:779:VAL:HG11	1.91	0.51
1:B:662:GLY:HA3	1:B:672:PHE:O	2.11	0.50
1:B:360:THR:OG1	1:B:362:LYS:NZ	2.44	0.49
1:A:218:GLY:HA3	1:A:243:TRP:CG	2.47	0.49
1:C:712:SER:HA	1:C:760:ALA:HB1	1.94	0.49
1:A:241:TYR:HB3	1:A:267:TRP:HB3	1.95	0.48
1:A:562:ASN:HA	1:A:586:ASN:O	2.13	0.48
1:B:712:SER:HA	1:B:760:ALA:HB1	1.95	0.48
1:A:456:ASN:OD1	1:A:484:TYR:HB2	2.14	0.48
1:A:208:ASP:HA	1:A:228:THR:HB	1.96	0.48
1:C:426:ARG:O	1:C:454:ARG:HB2	2.14	0.48
1:A:712:SER:HA	1:A:760:ALA:HB1	1.96	0.47
1:A:532:PRO:HB2	1:A:534:VAL:HG23	1.96	0.47
1:C:477:LYS:HE3	1:C:480:LEU:HD12	1.96	0.47
1:A:685:PHE:HA	1:A:754:ALA:HB2	1.96	0.47
1:B:254:LEU:HD13	1:B:281:ALA:HB2	1.96	0.46
1:C:585:THR:HA	1:C:610:GLU:O	2.16	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:672:PHE:CE1	1:B:768:ASP:HB3	2.51	0.45
1:B:731:HIS:HE1	3:B:1245:HOH:O	1.99	0.45
1:C:248:THR:HG22	1:C:264:THR:HG22	1.98	0.45
1:A:674:THR:HA	1:A:767:VAL:O	2.16	0.45
1:C:454:ARG:O	1:C:482:TRP:HA	2.16	0.45
1:B:595:LYS:O	1:B:617:THR:HA	2.16	0.45
1:B:585:THR:HA	1:B:610:GLU:O	2.17	0.45
1:A:585:THR:HA	1:A:610:GLU:O	2.16	0.45
1:B:532:PRO:HB2	1:B:534:VAL:HG23	1.99	0.45
1:B:209:SER:HB3	1:B:232:ALA:HB2	1.98	0.44
1:B:474:GLN:HA	1:B:509:ASN:O	2.17	0.44
1:C:463:CYS:O	1:C:498:VAL:HA	2.18	0.44
1:A:383:THR:HG22	1:A:413:ASP:HB3	1.99	0.44
1:C:360:THR:OG1	1:C:362:LYS:NZ	2.52	0.43
1:A:731:HIS:HE1	3:A:1336:HOH:O	2.00	0.43
1:B:456:ASN:OD1	1:B:484:TYR:HB2	2.18	0.43
1:C:204:SER:N	3:C:927:HOH:O	2.51	0.43
1:A:333:VAL:O	1:A:387:VAL:HA	2.19	0.43
1:C:603:VAL:HG21	1:C:628:ALA:HB2	2.01	0.43
1:C:561:ASP:HA	1:C:585:THR:O	2.19	0.42
1:A:650:ILE:HG23	1:A:651:THR:HG23	2.02	0.42
1:A:662:GLY:HA3	1:A:672:PHE:O	2.19	0.42
1:A:243:TRP:HB2	1:A:267:TRP:CZ3	2.55	0.42
1:C:243:TRP:HB2	1:C:267:TRP:CZ3	2.55	0.41
1:C:535:LYS:NZ	3:C:931:HOH:O	2.53	0.41
1:C:499:TYR:HA	1:C:532:PRO:O	2.20	0.41
1:A:603:VAL:HG21	1:A:628:ALA:HB2	2.02	0.41
1:B:208:ASP:OD2	3:B:902:HOH:O	2.22	0.41
1:C:378:VAL:HB	1:C:410:ILE:HA	2.03	0.41
1:B:380:GLU:HG3	1:C:355:VAL:HG13	2.03	0.41
1:B:721:ASN:HD22	1:B:721:ASN:HA	1.65	0.40
1:C:387:VAL:O	1:C:417:ALA:HA	2.21	0.40
1:C:220:PHE:CZ	1:C:223:GLN:HG3	2.57	0.40
1:C:406:PHE:HA	1:C:428:GLU:O	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:1050:HOH:O	3:C:1224:HOH:O[2_756]	2.14	0.06

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	579/597 (97%)	555 (96%)	24 (4%)	0	100	100
1	B	580/597 (97%)	555 (96%)	25 (4%)	0	100	100
1	C	579/597 (97%)	555 (96%)	24 (4%)	0	100	100
All	All	1738/1791 (97%)	1665 (96%)	73 (4%)	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	491/506 (97%)	487 (99%)	4 (1%)	81	91
1	B	492/506 (97%)	487 (99%)	5 (1%)	76	88
1	C	491/506 (97%)	485 (99%)	6 (1%)	71	85
All	All	1474/1518 (97%)	1459 (99%)	15 (1%)	76	88

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	283	LEU
1	A	357	GLN
1	A	462	TYR
1	A	721	ASN
1	B	283	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	357	GLN
1	B	462	TYR
1	B	721	ASN
1	B	775	GLN
1	C	224	LYS
1	C	283	LEU
1	C	357	GLN
1	C	462	TYR
1	C	721	ASN
1	C	775	GLN

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 48 ligands modelled in this entry, 48 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, 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	579/597 (96%)	-0.22	7 (1%) 79 77	22, 32, 59, 148	0
1	B	579/597 (96%)	0.06	23 (3%) 38 37	25, 35, 64, 131	0
1	C	579/597 (96%)	-0.09	9 (1%) 72 70	22, 32, 61, 114	0
All	All	1737/1791 (96%)	-0.08	39 (2%) 62 60	22, 33, 62, 148	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	261	GLY	5.2
1	B	220	PHE	5.0
1	B	265	GLY	4.9
1	C	219	LEU	4.8
1	B	263	ALA	4.6
1	B	262	ALA	4.2
1	B	264	THR	4.1
1	B	218	GLY	4.1
1	A	220	PHE	4.0
1	B	219	LEU	3.9
1	C	205	VAL	3.6
1	B	260	THR	3.3
1	A	219	LEU	3.3
1	B	216	VAL	3.2
1	B	259	VAL	3.0
1	B	288	LEU	2.9
1	C	220	PHE	2.8
1	A	207	VAL	2.7
1	B	243	TRP	2.7
1	B	248	THR	2.7
1	B	739	LEU	2.5
1	B	266	ALA	2.5
1	C	504	ILE	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	656	ASN	2.4
1	C	218	GLY	2.3
1	C	243	TRP	2.3
1	B	249	ALA	2.3
1	B	258	ARG	2.2
1	A	212	ALA	2.2
1	B	205	VAL	2.1
1	B	740	TYR	2.1
1	B	212	ALA	2.1
1	A	273[A]	ASN	2.1
1	C	503	LEU	2.1
1	C	204	SER	2.1
1	C	207	VAL	2.1
1	A	228	THR	2.1
1	B	246	ASN	2.1
1	B	247	ASN	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, 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	B-factors(Å ²)	Q<0.9
2	ZN	B	812[B]	1/1	0.86	0.09	69,69,69,69	1
2	ZN	B	812[A]	1/1	0.86	0.09	76,76,76,76	1
2	ZN	B	804	1/1	0.91	0.10	92,92,92,92	0
2	ZN	C	811[A]	1/1	0.92	0.07	72,72,72,72	1
2	ZN	C	811[B]	1/1	0.92	0.07	77,77,77,77	1
2	ZN	B	807	1/1	0.93	0.06	93,93,93,93	0
2	ZN	A	812[B]	1/1	0.93	0.08	69,69,69,69	1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	ZN	A	812[A]	1/1	0.93	0.08	61,61,61,61	1
2	ZN	C	813	1/1	0.94	0.07	81,81,81,81	0
2	ZN	C	805	1/1	0.95	0.08	86,86,86,86	0
2	ZN	B	809[B]	1/1	0.96	0.19	61,61,61,61	1
2	ZN	A	807	1/1	0.96	0.04	86,86,86,86	0
2	ZN	B	809[A]	1/1	0.96	0.19	52,52,52,52	1
2	ZN	B	810	1/1	0.96	0.09	83,83,83,83	0
2	ZN	C	808	1/1	0.96	0.10	83,83,83,83	0
2	ZN	A	810[B]	1/1	0.97	0.06	44,44,44,44	1
2	ZN	A	809	1/1	0.97	0.03	74,74,74,74	0
2	ZN	C	810	1/1	0.97	0.05	76,76,76,76	0
2	ZN	B	813[A]	1/1	0.97	0.13	52,52,52,52	1
2	ZN	B	805	1/1	0.97	0.05	82,82,82,82	0
2	ZN	B	806	1/1	0.97	0.10	78,78,78,78	0
2	ZN	A	810[A]	1/1	0.97	0.06	56,56,56,56	1
2	ZN	B	813[B]	1/1	0.97	0.13	120,120,120,120	1
2	ZN	C	804	1/1	0.98	0.04	90,90,90,90	0
2	ZN	A	802	1/1	0.98	0.04	76,76,76,76	0
2	ZN	B	811	1/1	0.98	0.03	69,69,69,69	0
2	ZN	A	808	1/1	0.98	0.05	68,68,68,68	0
2	ZN	C	809[A]	1/1	0.98	0.30	56,56,56,56	1
2	ZN	C	809[B]	1/1	0.98	0.30	62,62,62,62	1
2	ZN	A	811	1/1	0.99	0.09	66,66,66,66	0
2	ZN	C	803	1/1	0.99	0.10	49,49,49,49	0
2	ZN	C	802	1/1	0.99	0.07	54,54,54,54	0
2	ZN	C	806	1/1	0.99	0.05	73,73,73,73	0
2	ZN	C	807	1/1	0.99	0.10	79,79,79,79	0
2	ZN	A	813	1/1	0.99	0.16	63,63,63,63	0
2	ZN	A	803	1/1	0.99	0.08	66,66,66,66	0
2	ZN	A	804	1/1	0.99	0.06	40,40,40,40	0
2	ZN	B	802	1/1	0.99	0.04	68,68,68,68	0
2	ZN	A	814	1/1	0.99	0.05	59,59,59,59	0
2	ZN	B	808[A]	1/1	0.99	0.20	67,67,67,67	1
2	ZN	B	808[B]	1/1	0.99	0.20	48,48,48,48	1
2	ZN	B	801	1/1	0.99	0.10	37,37,37,37	0
2	ZN	A	801	1/1	1.00	0.07	35,35,35,35	0
2	ZN	C	801	1/1	1.00	0.09	40,40,40,40	0
2	ZN	B	803	1/1	1.00	0.09	49,49,49,49	0
2	ZN	A	805	1/1	1.00	0.07	38,38,38,38	0
2	ZN	A	806	1/1	1.00	0.05	53,53,53,53	0
2	ZN	C	812	1/1	1.00	0.05	42,42,42,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.