



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:17 AM UTC

PDB ID : 3HL1 / pdb\_00003hl1  
Title : CRYSTAL STRUCTURE OF A FERRITIN LIKE PROTEIN (CC\_0557)  
FROM CAULOBACTER VIBRIOIDES AT 1.95 Å RESOLUTION  
Authors : Joint Center for Structural Genomics (JCSG)  
Deposited on : 2009-05-26  
Resolution : 1.95 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

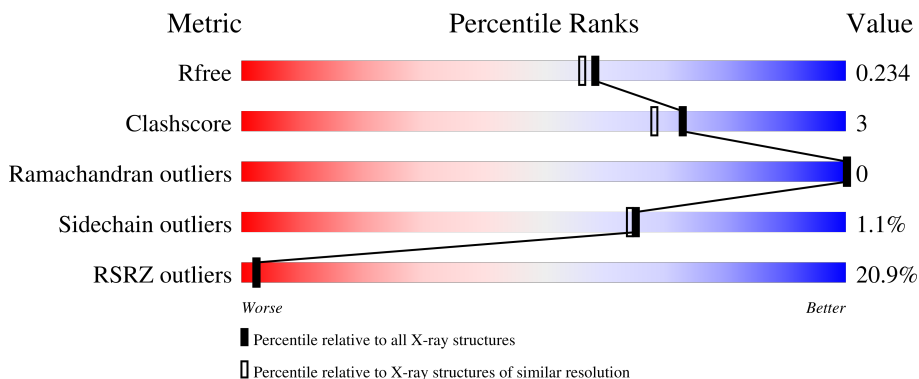
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.95 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))
$R_{free}$	180053	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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  $\geq 3$ , 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	317	
1	B	317	

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4736 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 Ferritin like protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	289	2289	1474	377	428	2	8	0	8	0
1	B	282	2186	1413	353	409	2	9	0	2	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP Q9AAP0
B	0	GLY	-	expression tag	UNP Q9AAP0

- Molecule 2 is UNKNOWN LIGAND (CCD ID: UNL) (formula: ).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 5	O 5	0	0
2	B	1	Total 1	O 1	0	0

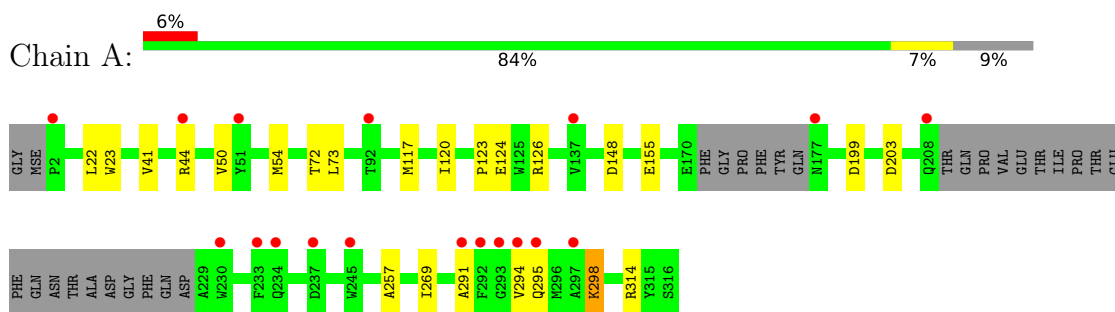
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	207	Total 208	O 208	0	1
3	B	47	Total 47	O 47	0	0

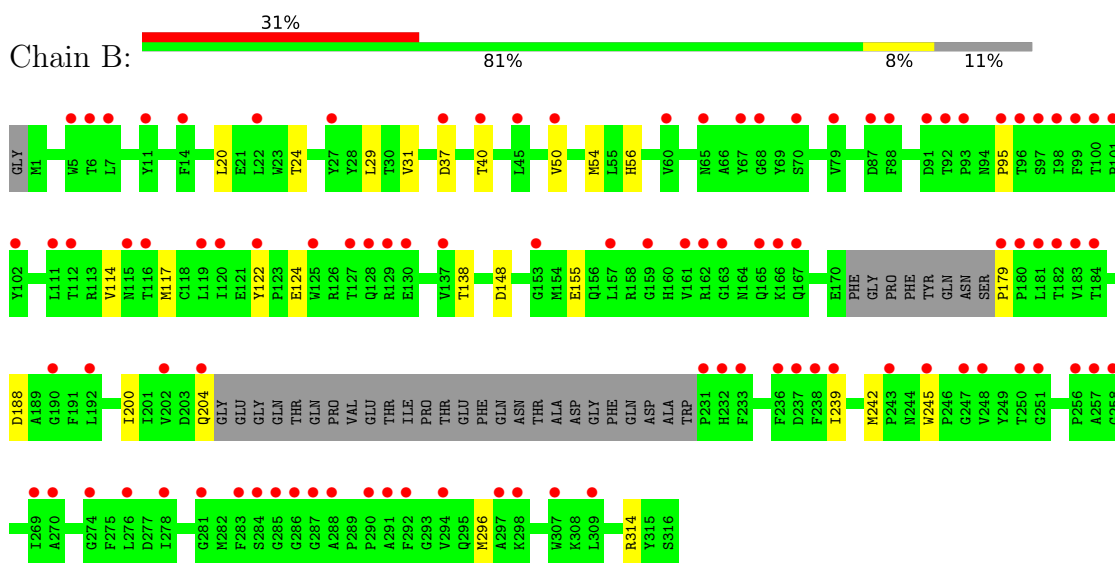
### 3 Residue-property plots [i](#)

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: Ferritin like protein



- Molecule 1: Ferritin like protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	54.63Å 44.02Å 119.38Å 90.00° 96.17° 90.00°	Depositor
Resolution (Å)	29.42 – 1.95 29.42 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.2 (29.42-1.95) 99.2 (29.42-1.95)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.12 (at 1.95Å)	Xtrriage
Refinement program	REFMAC 5.2.0019, PHENIX	Depositor
R, $R_{free}$	0.185 , 0.232 0.190 , 0.234	Depositor DCC
$R_{free}$ test set	2079 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.5	Xtrriage
Anisotropy	0.258	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 51.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4736	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 40.76 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.6100e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: UNL

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	1.05	3/2364 (0.1%)	0.99	0/3219
1	B	0.79	0/2250	0.93	3/3067 (0.1%)
All	All	0.94	3/4614 (0.1%)	0.96	3/6286 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	117	MSE	SE-CE	-8.43	1.70	1.95
1	A	294	VAL	CA-CB	6.99	1.62	1.54
1	A	41	VAL	CA-CB	5.08	1.57	1.53

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	179	PRO	CA-C-N	7.05	126.57	119.24
1	B	179	PRO	C-N-CA	7.05	126.57	119.24
1	B	200	ILE	CB-CA-C	-5.12	105.22	112.14

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	2289	0	2213	12	0
1	B	2186	0	2099	17	0
2	A	5	0	0	1	0
2	B	1	0	0	0	0
3	A	208	0	0	2	0
3	B	47	0	0	0	0
All	All	4736	0	4312	28	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 (28) 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:54[A]:MSE:HE1	1:B:296:MSE:SE	2.10	0.99
1:B:54[A]:MSE:CE	1:B:296:MSE:SE	2.65	0.95
1:A:72:THR:HG23	3:A:408:HOH:O	1.72	0.90
1:B:114:VAL:HA	1:B:117:MSE:HE3	1.64	0.79
2:A:317:UNL:O3	2:A:317:UNL:O4	2.09	0.70
1:A:257[B]:ALA:O	3:A:401:HOH:O	2.11	0.69
1:B:95:PRO:HB3	1:B:122:TYR:CZ	2.37	0.59
1:A:123:PRO:HD2	1:A:126:ARG:HD3	1.85	0.57
1:B:29:LEU:HD21	1:B:50:VAL:HG11	1.88	0.56
1:A:22:LEU:HD22	1:A:73:LEU:HD22	1.88	0.56
1:A:50[A]:VAL:CG1	1:A:54[A]:MSE:HE3	2.38	0.54
1:B:54[A]:MSE:HE2	1:B:296:MSE:SE	2.58	0.54
1:A:199:ASP:OD2	1:B:155:GLU:OE2	2.26	0.53
1:A:203:ASP:OD2	1:B:188:ASP:OD2	2.27	0.51
1:B:20:LEU:O	1:B:24:THR:HG23	2.12	0.50
1:A:269:ILE:HD11	1:A:314[A]:ARG:HE	1.75	0.49
1:B:56:HIS:NE2	1:B:204:GLN:OE1	2.44	0.48
1:B:114:VAL:HG21	1:B:245:TRP:CH2	2.48	0.48
1:A:298:LYS:NZ	1:A:298:LYS:HB3	2.31	0.46
1:B:31:VAL:HG11	1:B:117:MSE:HE1	1.98	0.46
1:A:291:ALA:O	1:A:295:GLN:CB	2.66	0.43
1:B:239:ILE:HG23	1:B:242:MSE:CE	2.48	0.43
1:A:23:TRP:HZ3	1:A:120:ILE:HD11	1.84	0.43
1:B:37:ASP:HB3	1:B:40:THR:HG23	2.00	0.43
1:B:239:ILE:O	1:B:242:MSE:HE2	2.19	0.43
1:B:124:GLU:OE2	1:B:148:ASP:OD2	2.37	0.42
1:B:242:MSE:HE3	1:B:245:TRP:CD1	2.56	0.41
1:A:124:GLU:OE2	1:A:148:ASP:OD2	2.40	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	291/317 (92%)	285 (98%)	6 (2%)	0	100	100
1	B	278/317 (88%)	273 (98%)	5 (2%)	0	100	100
All	All	569/634 (90%)	558 (98%)	11 (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	242/255 (95%)	238 (98%)	4 (2%)	53	49
1	B	229/255 (90%)	227 (99%)	2 (1%)	70	70
All	All	471/510 (92%)	465 (99%)	6 (1%)	65	58

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44[A]	ARG
1	A	44[B]	ARG
1	A	155	GLU
1	A	298	LYS
1	B	138	THR

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Mol	Chain	Res	Type
1	B	314	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	164	ASN
1	B	12	GLN
1	B	47	GLN
1	B	160	HIS
1	B	164	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are unknown - 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	282/317 (88%)	0.54	18 (6%) 25 29	14, 33, 56, 77	7 (2%)
1	B	274/317 (86%)	1.81	98 (35%) 1 0	28, 40, 54, 74	1 (0%)
All	All	556/634 (87%)	1.17	116 (20%) 2 2	14, 38, 56, 77	8 (1%)

All (116) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	97	SER	6.5
1	A	294	VAL	6.5
1	B	115	ASN	5.5
1	B	101	PRO	5.1
1	B	102	TYR	4.9
1	B	127	THR	4.6
1	B	119	LEU	4.3
1	B	99	PHE	4.2
1	B	233	PHE	4.1
1	B	247	GLY	4.1
1	B	111	LEU	4.1
1	B	125	TRP	4.0
1	B	122	TYR	4.0
1	B	116	THR	3.9
1	B	294	VAL	3.9
1	B	257	ALA	3.9
1	B	250	THR	3.7
1	B	232	HIS	3.7
1	B	278	ILE	3.7
1	A	293	GLY	3.6
1	B	286	GLY	3.6
1	B	92	THR	3.5
1	B	292	PHE	3.5
1	B	288	ALA	3.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	309	LEU	3.5
1	A	295	GLN	3.4
1	B	159	GLY	3.3
1	B	98	ILE	3.3
1	B	112	THR	3.1
1	B	297	ALA	3.1
1	B	239	ILE	3.1
1	B	204	GLN	3.1
1	A	297	ALA	3.1
1	B	298	LYS	3.1
1	B	93	PRO	3.1
1	A	230	TRP	3.0
1	B	281	GLY	3.0
1	A	291	ALA	3.0
1	A	2	PRO	3.0
1	B	248	VAL	3.0
1	B	283	PHE	3.0
1	B	243	PRO	3.0
1	A	177	ASN	2.9
1	B	120	ILE	2.9
1	B	7	LEU	2.9
1	B	68	GLY	2.9
1	B	95	PRO	2.9
1	B	79	VAL	2.9
1	B	251	GLY	2.9
1	B	183	VAL	2.8
1	B	276	LEU	2.8
1	B	40	THR	2.8
1	B	11	TYR	2.8
1	A	233	PHE	2.8
1	B	238	PHE	2.8
1	B	258	GLY	2.8
1	B	100	THR	2.7
1	B	291	ALA	2.7
1	B	274	GLY	2.7
1	A	292	PHE	2.7
1	B	245	TRP	2.7
1	B	27	TYR	2.7
1	A	234	GLN	2.7
1	B	237	ASP	2.6
1	B	182	THR	2.6
1	B	70	SER	2.6

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	181	LEU	2.6
1	B	161	VAL	2.6
1	B	166	LYS	2.6
1	B	231	PRO	2.6
1	B	163	GLY	2.6
1	B	88	PHE	2.5
1	A	245	TRP	2.5
1	B	236	PHE	2.5
1	B	285	GLY	2.5
1	A	208	GLN	2.5
1	B	167	GLN	2.5
1	B	202	VAL	2.5
1	A	237	ASP	2.5
1	B	6	THR	2.5
1	B	153	GLY	2.4
1	B	128	GLN	2.4
1	B	87	ASP	2.4
1	B	45	LEU	2.4
1	B	269	ILE	2.4
1	B	270	ALA	2.4
1	B	307	TRP	2.4
1	B	192	LEU	2.4
1	B	91	ASP	2.4
1	B	130	GLU	2.3
1	A	51	TYR	2.2
1	B	129	ARG	2.2
1	A	137	VAL	2.2
1	B	60	VAL	2.2
1	B	137	VAL	2.2
1	B	290	PRO	2.2
1	B	14	PHE	2.1
1	A	92	THR	2.1
1	B	96	THR	2.1
1	B	284[A]	SER	2.1
1	B	287	GLY	2.1
1	B	5	TRP	2.1
1	A	44[A]	ARG	2.1
1	B	22	LEU	2.1
1	B	37	ASP	2.1
1	B	65	ASN	2.1
1	B	256	PRO	2.1
1	B	157	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	67	TYR	2.0
1	B	184	THR	2.0
1	B	179	PRO	2.0
1	B	180	PRO	2.0
1	B	162	ARG	2.0
1	B	165	GLN	2.0
1	B	190	GLY	2.0
1	B	50	VAL	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 oligosaccharides 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	UNL	A	317	5/-	0.89	0.13	36,43,45,49	0
2	UNL	B	317	1/-	0.90	0.17	54,54,54,54	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.