



# Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 07:31 am BST

PDB ID : 5LFN  
Title : Crystal structure of human chondroadherin  
Authors : Ramisch, S.; Pramhed, A.; Logan, D.T.  
Deposited on : 2016-07-03  
Resolution : 2.10 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.

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

MolProbity : 4.02b-467  
Xtrriage (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

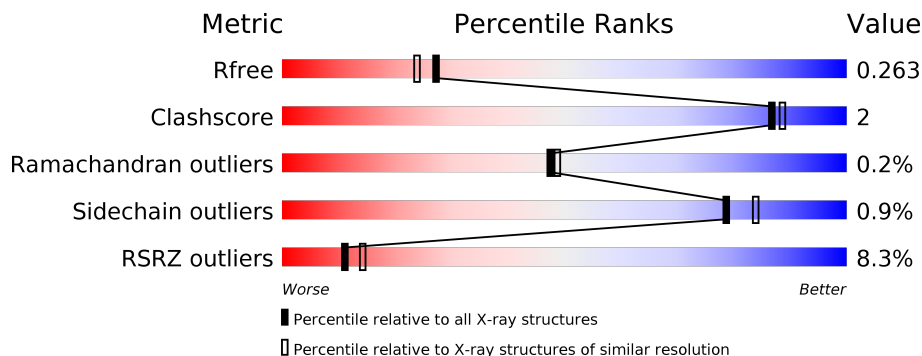
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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  $\geq 3$ , 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	337	 4% 90% 6% •
1	B	337	 10% 89% 7% ••
1	C	337	 9% 91% 5% •
1	D	337	 9% 90% 6% ••

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 10481 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 Chondroadherin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	324	2589	1640	471	468	10	0	0	0
1	B	324	2589	1640	471	468	10	0	0	0
1	C	323	2583	1637	470	467	9	0	0	0
1	D	325	2598	1646	473	469	10	0	0	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Cl	0	0
			1	1		
2	C	1	Total	Cl	0	0
			1	1		

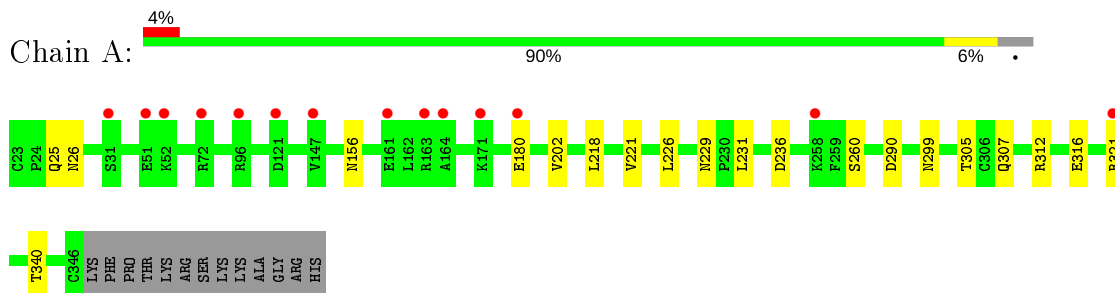
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	21	Total	O	0	0
			21	21		
3	B	32	Total	O	0	0
			32	32		
3	C	36	Total	O	0	0
			36	36		
3	D	31	Total	O	0	0
			31	31		

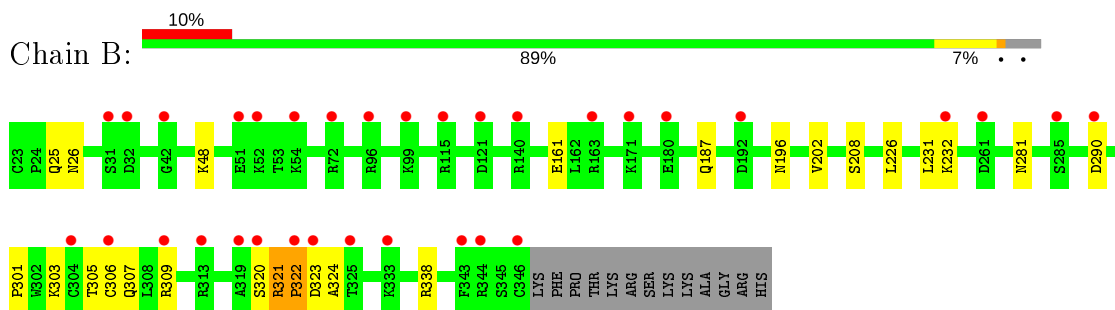
### 3 Residue-property plots [i](#)

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.

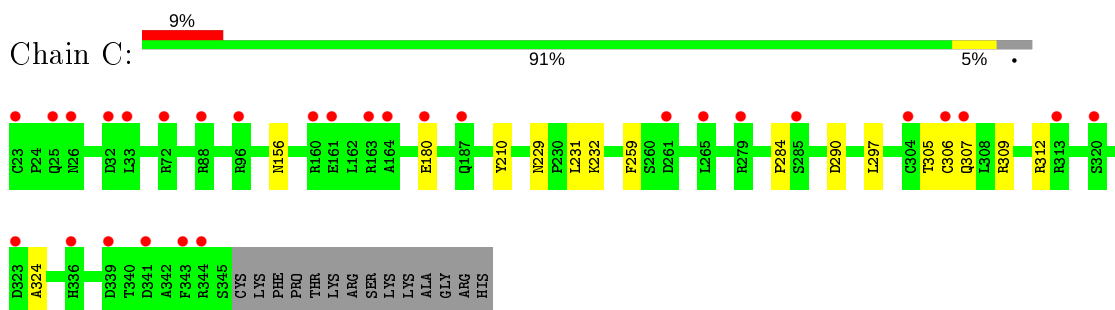
- Molecule 1: Chondroadherin



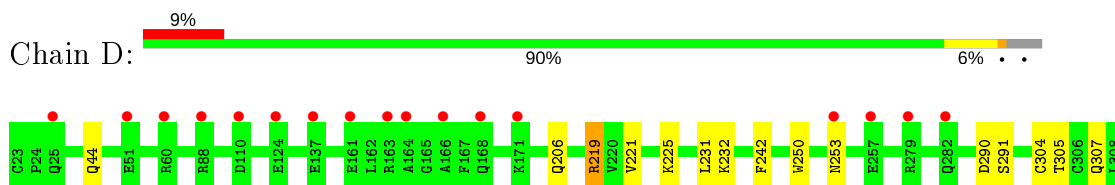
- Molecule 1: Chondroadherin

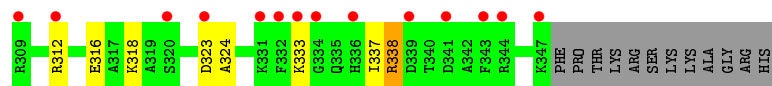


- Molecule 1: Chondroadherin



- Molecule 1: Chondroadherin





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	56.48Å 111.59Å 128.68Å 90.00° 92.22° 90.00°	Depositor
Resolution (Å)	15.00 – 2.10 28.22 – 2.10	Depositor EDS
% Data completeness (in resolution range)	95.5 (15.00-2.10) 95.8 (28.22-2.10)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.40 (at 2.10Å)	Xtrriage
Refinement program	PHENIX (1.11rc2_2531: ???)	Depositor
R, $R_{free}$	0.245 , 0.262 0.247 , 0.263	Depositor DCC
$R_{free}$ test set	4480 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	35.0	Xtrriage
Anisotropy	0.624	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 23.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	0.055 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	10481	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	53.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.00% of the height of the origin peak. No significant pseudotranslation is detected.*

<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:  
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	0.24	0/2645	0.46	0/3585
1	B	0.24	0/2645	0.45	0/3585
1	C	0.27	1/2639 (0.0%)	0.45	0/3577
1	D	0.25	0/2654	0.44	0/3596
All	All	0.25	1/10583 (0.0%)	0.45	0/14343

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	210	TYR	C-N	6.50	1.46	1.34

There are no bond angle outliers.

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	2589	0	2594	11	0
1	B	2589	0	2596	13	1
1	C	2583	0	2591	8	0
1	D	2598	0	2607	13	1
2	B	1	0	0	1	0
2	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	21	0	0	0	0
3	B	32	0	0	1	0
3	C	36	0	0	0	0
3	D	31	0	0	1	0
All	All	10481	0	10388	44	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 2.

All (44) 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)
2:B:401:CL:CL	3:B:531:HOH:O	2.26	0.89
1:B:303:LYS:O	1:B:307:GLN:NE2	2.15	0.80
1:B:305:THR:OG1	1:B:307:GLN:OE1	2.01	0.78
1:A:305:THR:OG1	1:A:307:GLN:OE1	2.01	0.77
1:D:305:THR:OG1	1:D:307:GLN:OE1	2.02	0.76
1:B:323:ASP:OD2	1:B:338:ARG:N	2.20	0.75
1:C:305:THR:OG1	1:C:307:GLN:OE1	2.06	0.73
1:B:161:GLU:OE2	1:B:187:GLN:NE2	2.24	0.71
1:B:281:ASN:ND2	1:B:301:PRO:O	2.24	0.71
1:D:312:ARG:NH1	1:D:316:GLU:OE2	2.26	0.68
1:B:306:CYS:O	1:B:309:ARG:NH1	2.26	0.68
1:D:323:ASP:OD2	1:D:338:ARG:N	2.29	0.66
1:A:299:ASN:ND2	1:D:253:ASN:OD1	2.34	0.60
1:C:156:ASN:ND2	1:C:180:GLU:OE1	2.33	0.60
1:A:156:ASN:ND2	1:A:180:GLU:OE1	2.35	0.58
1:D:318:LYS:O	1:D:338:ARG:NH2	2.39	0.56
1:B:323:ASP:OD1	1:B:324:ALA:N	2.42	0.53
1:B:321:ARG:O	1:B:322:PRO:O	2.29	0.50
1:A:312:ARG:NH1	1:A:340:THR:O	2.44	0.50
1:A:321:ARG:NH1	1:D:333:LYS:O	2.47	0.48
1:B:202:VAL:O	1:B:202:VAL:HG22	2.14	0.47
1:D:221:VAL:HG12	1:D:242:PHE:CG	2.50	0.47
1:A:218:LEU:HB3	1:A:221:VAL:CG2	2.46	0.46
1:D:323:ASP:OD1	1:D:324:ALA:N	2.49	0.45
1:B:231:LEU:O	1:B:232:LYS:HB2	2.18	0.44
1:B:202:VAL:HG13	1:B:226:LEU:HD23	2.00	0.43
1:C:229:ASN:O	1:C:231:LEU:N	2.52	0.43
1:D:312:ARG:CZ	1:D:316:GLU:OE2	2.66	0.43
1:B:208:SER:O	1:B:232:LYS:NZ	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:ASP:OD1	1:A:260:SER:OG	2.30	0.43
1:D:291:SER:OG	3:D:401:HOH:O	2.22	0.42
1:D:304:CYS:SG	1:D:337:ILE:HG12	2.58	0.42
1:A:229:ASN:O	1:A:231:LEU:N	2.52	0.42
1:C:231:LEU:O	1:C:232:LYS:HB2	2.19	0.42
1:A:312:ARG:NE	1:A:316:GLU:OE2	2.52	0.42
1:C:306:CYS:O	1:C:309:ARG:NH1	2.51	0.42
1:C:312:ARG:HG2	1:C:312:ARG:HH11	1.85	0.42
1:A:202:VAL:CG1	1:A:226:LEU:HD23	2.50	0.41
1:D:225:LYS:HA	1:D:250:TRP:HB2	2.02	0.41
1:D:231:LEU:O	1:D:232:LYS:HB2	2.21	0.41
1:C:259:PHE:HB2	1:C:284:PRO:HD3	2.03	0.41
1:C:297:LEU:HD12	1:C:324:ALA:HB2	2.01	0.41
1:B:25:GLN:O	1:B:26:ASN:HB2	2.21	0.40
1:A:25:GLN:O	1:A:26:ASN:HB2	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)
1:B:196:ASN:OD1	1:D:219:ARG:NH2[2_546]	1.99	0.21

## 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	322/337 (96%)	302 (94%)	20 (6%)	0	100 100
1	B	322/337 (96%)	300 (93%)	20 (6%)	2 (1%)	25 21
1	C	321/337 (95%)	300 (94%)	21 (6%)	0	100 100
1	D	323/337 (96%)	301 (93%)	22 (7%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1288/1348 (96%)	1203 (93%)	83 (6%)	2 (0%)	47	49

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	322	PRO
1	B	320	SER

### 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	286/297 (96%)	285 (100%)	1 (0%)	92	95
1	B	286/297 (96%)	283 (99%)	3 (1%)	76	82
1	C	285/297 (96%)	284 (100%)	1 (0%)	91	94
1	D	287/297 (97%)	282 (98%)	5 (2%)	60	67
All	All	1144/1188 (96%)	1134 (99%)	10 (1%)	78	84

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	290	ASP
1	B	48	LYS
1	B	290	ASP
1	B	321	ARG
1	C	290	ASP
1	D	44	GLN
1	D	206	GLN
1	D	219	ARG
1	D	290	ASP
1	D	338	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	28	HIS
1	B	30	HIS

### 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 carbohydrates 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<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	324/337 (96%)	0.50	14 (4%) 35 41	28, 49, 82, 125	0
1	B	324/337 (96%)	0.62	33 (10%) 6 8	30, 54, 95, 150	0
1	C	323/337 (95%)	0.52	29 (8%) 9 12	28, 50, 82, 118	0
1	D	325/337 (96%)	0.60	31 (9%) 8 10	27, 48, 87, 125	0
All	All	1296/1348 (96%)	0.56	107 (8%) 11 14	27, 50, 87, 150	0

All (107) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	344	ARG	8.7
1	B	320	SER	6.6
1	D	164	ALA	6.2
1	D	163	ARG	5.6
1	D	331	LYS	5.5
1	D	161	GLU	5.2
1	A	52	LYS	5.0
1	D	334	GLY	4.7
1	B	115	ARG	4.7
1	B	140	ARG	4.7
1	C	160	ARG	4.6
1	A	31	SER	4.2
1	D	332	PHE	4.1
1	D	257	GLU	4.0
1	B	51	GLU	3.9
1	B	96	ARG	3.8
1	B	31	SER	3.8
1	A	96	ARG	3.8
1	D	341	ASP	3.7
1	C	164	ALA	3.7
1	D	339	ASP	3.7

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	C	32	ASP	3.7
1	C	261	ASP	3.7
1	A	321	ARG	3.7
1	D	333	LYS	3.6
1	B	99	LYS	3.5
1	C	344	ARG	3.5
1	C	180	GLU	3.5
1	A	51	GLU	3.4
1	A	164	ALA	3.4
1	D	88	ARG	3.4
1	B	72	ARG	3.3
1	B	163	ARG	3.3
1	D	253	ASN	3.2
1	C	341	ASP	3.2
1	C	23	CYS	3.2
1	C	96	ARG	3.1
1	D	320	SER	3.1
1	B	171	LYS	3.1
1	C	163	ARG	3.1
1	C	306	CYS	3.1
1	C	320	SER	3.1
1	D	323	ASP	3.1
1	C	307	GLN	3.0
1	C	304	CYS	2.9
1	A	171	LYS	2.9
1	B	322	PRO	2.9
1	D	282	GLN	2.9
1	D	343	PHE	2.8
1	D	336	HIS	2.8
1	C	25	GLN	2.8
1	D	312	ARG	2.8
1	B	261	ASP	2.8
1	C	187	GLN	2.8
1	B	32	ASP	2.7
1	D	279	ARG	2.7
1	C	313	ARG	2.7
1	B	333	LYS	2.7
1	B	309	ARG	2.7
1	D	110	ASP	2.6
1	A	72	ARG	2.6
1	B	42	GLY	2.6
1	D	60	ARG	2.6

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	313	ARG	2.5
1	B	344	ARG	2.5
1	C	279	ARG	2.5
1	B	343	PHE	2.5
1	B	180	GLU	2.5
1	B	306	CYS	2.5
1	C	339	ASP	2.5
1	B	319	ALA	2.5
1	D	51	GLU	2.5
1	C	343	PHE	2.5
1	C	323	ASP	2.4
1	D	347	LYS	2.4
1	B	121	ASP	2.4
1	C	26	ASN	2.4
1	B	304	CYS	2.4
1	A	180	GLU	2.4
1	A	147	VAL	2.3
1	C	336	HIS	2.3
1	C	265	LEU	2.3
1	B	285	SER	2.3
1	C	161	GLU	2.3
1	A	258	LYS	2.3
1	D	171	LYS	2.3
1	A	161	GLU	2.3
1	A	163	ARG	2.2
1	B	54	LYS	2.2
1	D	137	GLU	2.2
1	C	72	ARG	2.2
1	C	88	ARG	2.2
1	D	309	ARG	2.2
1	D	166	ALA	2.2
1	D	124	GLU	2.2
1	D	25	GLN	2.1
1	A	121	ASP	2.1
1	C	285	SER	2.1
1	B	290	ASP	2.1
1	B	52	LYS	2.1
1	B	323	ASP	2.0
1	B	346	CYS	2.0
1	C	33	LEU	2.0
1	B	325	THR	2.0
1	B	192	ASP	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	232	LYS	2.0
1	D	168	GLN	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<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	CL	C	401	1/1	0.92	0.10	83,83,83,83	0
2	CL	B	401	1/1	0.96	0.04	61,61,61,61	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.