



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 15, 2025 – 12:35 PM EDT

PDB ID : 9EAE / pdb\_00009eae  
Title : Structure of Citrobacter BubCD(D104A)-BubB  
Authors : Ye, Q.; Corbett, K.D.  
Deposited on : 2024-11-10  
Resolution : 2.53 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 Phenix2.0rc1  
Xtriage (Phenix) : 2.0rc1  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.006 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.45.1

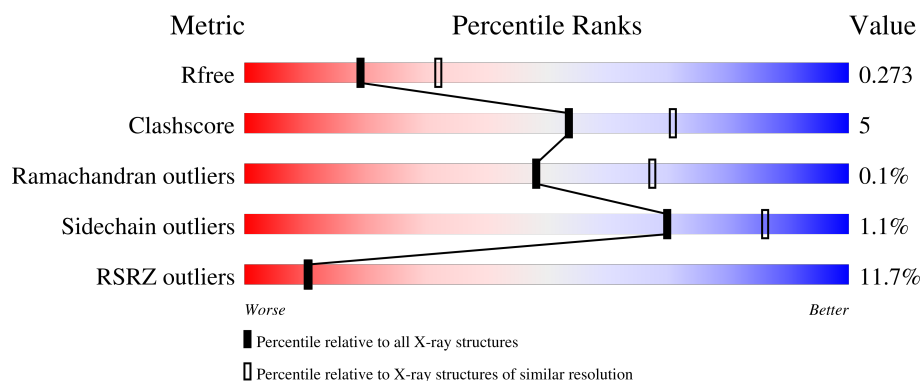
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.53 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))
$R_{free}$	164625	6935 (2.54-2.50)
Clashscore	180529	7778 (2.54-2.50)
Ramachandran outliers	177936	7674 (2.54-2.50)
Sidechain outliers	177891	7676 (2.54-2.50)
RSRZ outliers	164620	6935 (2.54-2.50)

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	458	<div> <div>7%</div> <div>91%</div> <div>8%</div> </div>
1	B	458	<div> <div>18%</div> <div>85%</div> <div>14%</div> </div>
2	C	133	<div> <div>7%</div> <div>84%</div> <div>12%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NA	B	601	-	-	-	X

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 16268 atoms, of which 8002 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 Citrobacter BubCD.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	453	Total	C	H	N	O	S	0	0	0
			7016	2223	3494	602	680	17			
1	B	455	Total	C	H	N	O	S	0	0	0
			7063	2236	3517	606	687	17			

- Molecule 2 is a protein called Citrobacter BubB.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	C	128	Total	C	H	N	O	S	0	0	0
			2031	660	991	181	193	6			

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Na	0	0
			1	1		
3	B	1	Total	Na	0	0
			1	1		

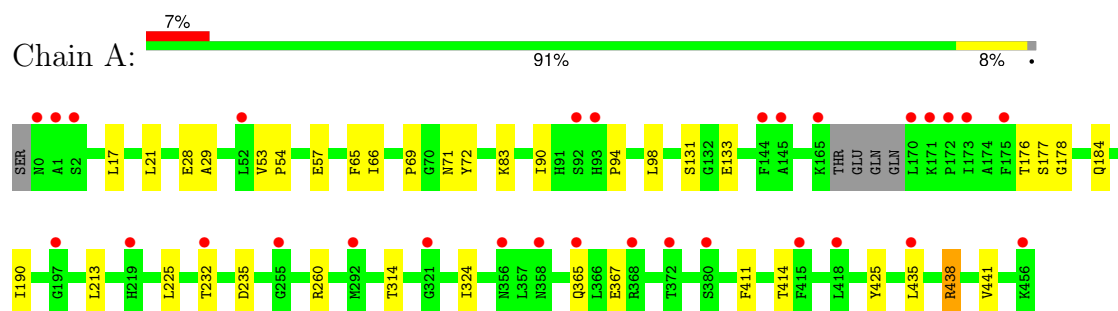
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	106	Total	O	0	0
			106	106		
4	B	36	Total	O	0	0
			36	36		
4	C	14	Total	O	0	0
			14	14		

### 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.

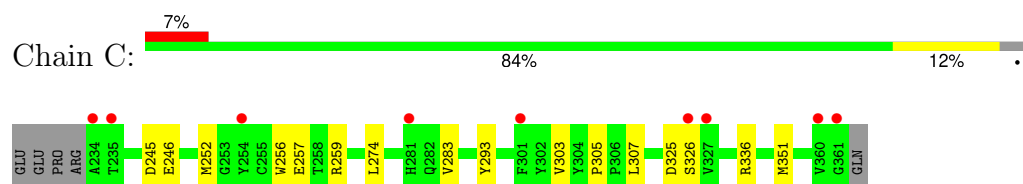
#### • Molecule 1: Citrobacter BubCD



#### • Molecule 1: Citrobacter BubCD



#### • Molecule 2: Citrobacter BubB



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	135.35Å 135.35Å 172.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.35 – 2.53 49.35 – 2.53	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.35-2.53) 100.0 (49.35-2.53)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.02 (at 2.52Å)	Xtriage
Refinement program	PHENIX 1.21.1_5286	Depositor
R, $R_{free}$	0.246 , 0.271 0.248 , 0.273	Depositor DCC
$R_{free}$ test set	2779 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	66.2	Xtriage
Anisotropy	0.463	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 50.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	16268	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	94.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.71% 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

### 5.1 Standard geometry

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

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	0.13	0/3585	0.28	0/4851
1	B	0.13	0/3610	0.30	0/4886
2	C	0.12	0/1069	0.31	0/1460
All	All	0.13	0/8264	0.29	0/11197

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	3
All	All	0	4

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	438	ARG	Sidechain
1	B	135	ARG	Sidechain
1	B	137	ARG	Sidechain
1	B	6	ARG	Sidechain

## 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	3522	3494	3493	25	0
1	B	3546	3517	3513	44	0
2	C	1040	991	991	9	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	106	0	0	2	0
4	B	36	0	0	2	0
4	C	14	0	0	0	0
All	All	8266	8002	7997	77	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 5.

All (77) 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:131:SER:OG	1:A:133:GLU:OE1	1.99	0.79
1:B:30:ALA:HB3	1:B:53:VAL:HG21	1.70	0.74
2:C:325:ASP:O	2:C:326:SER:OG	2.10	0.67
1:A:83:LYS:NZ	4:A:702:HOH:O	2.30	0.65
1:A:53:VAL:HG13	1:A:72:TYR:CD2	2.34	0.63
2:C:245:ASP:OD2	2:C:293:TYR:OH	2.12	0.62
1:B:6:ARG:HG3	1:B:6:ARG:HH11	1.65	0.61
1:A:232:THR:HG21	4:A:761:HOH:O	2.00	0.60
1:B:51:ILE:HD12	1:B:75:LYS:HE3	1.82	0.60
1:B:119:VAL:HG23	1:B:123:HIS:CE1	2.40	0.57
1:A:57:GLU:OE1	1:A:72:TYR:OH	2.14	0.57
1:B:88:ILE:HD13	1:B:124:GLY:C	2.30	0.57
1:B:30:ALA:HB1	4:B:705:HOH:O	2.06	0.56
1:A:411:PHE:CZ	1:B:421:VAL:HG21	2.42	0.55
1:B:395:GLU:OE1	1:B:404:ARG:NH2	2.36	0.54
1:B:75:LYS:O	1:B:79:VAL:HG23	2.08	0.54
2:C:252:MET:HE3	2:C:252:MET:HA	1.90	0.53
1:B:193:VAL:HG12	1:B:193:VAL:O	2.09	0.53
1:B:50:LEU:HD12	1:B:51:ILE:N	2.23	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:254:ARG:CZ	1:B:258:ILE:HD13	2.39	0.52
2:C:336:ARG:HD3	2:C:351:MET:HE3	1.91	0.52
1:B:232:THR:HG21	4:B:725:HOH:O	2.09	0.51
2:C:274:LEU:HD13	2:C:307:LEU:HD21	1.92	0.51
2:C:336:ARG:CD	2:C:351:MET:HE3	2.41	0.50
1:A:232:THR:HG23	1:A:235:ASP:H	1.76	0.50
1:B:176:THR:HG22	1:B:177:SER:N	2.27	0.50
1:B:53:VAL:HG12	1:B:72:TYR:CD2	2.47	0.49
1:B:21:LEU:HA	1:B:29:ALA:HB3	1.94	0.48
1:A:17:LEU:HD21	1:A:90:ILE:HG21	1.96	0.48
1:A:21:LEU:HA	1:A:29:ALA:HB3	1.97	0.47
1:A:414:THR:HG23	1:A:425:TYR:CE1	2.50	0.47
1:A:28:GLU:OE2	1:A:94:PRO:HB2	2.14	0.46
1:B:98:LEU:C	1:B:98:LEU:HD12	2.39	0.46
1:B:15:THR:HG22	1:B:19:LYS:HE3	1.97	0.46
2:C:283:VAL:HG12	2:C:305:PRO:HD2	1.96	0.46
1:A:54:PRO:HD2	1:A:72:TYR:CE2	2.51	0.46
1:B:366:LEU:HD23	1:B:371:ILE:HG13	1.98	0.46
2:C:257:GLU:OE2	2:C:259:ARG:NH2	2.49	0.46
2:C:246:GLU:HG2	2:C:256:TRP:CH2	2.50	0.45
1:B:6:ARG:HH11	1:B:6:ARG:CG	2.28	0.45
1:A:213:LEU:HD22	1:A:260:ARG:HD3	1.98	0.45
1:B:362:TYR:CE2	1:B:366:LEU:HD11	2.52	0.45
1:B:4:GLY:HA3	1:B:149:GLU:OE1	2.17	0.45
1:B:281:LEU:HD13	1:B:303:ILE:HG21	1.97	0.45
1:A:69:PRO:HB2	1:A:71:ASN:OD1	2.16	0.45
1:B:92:SER:O	1:B:127:ILE:HG23	2.17	0.45
1:B:222:LYS:HA	1:B:225:LEU:HD12	1.98	0.44
1:B:229:LEU:O	1:B:230:ASN:HB2	2.16	0.44
1:A:28:GLU:OE1	1:A:66:ILE:HG22	2.18	0.43
1:A:314:THR:HG22	1:A:324:ILE:HD13	1.99	0.43
1:B:374:VAL:HG13	1:B:376:GLU:HG2	2.00	0.43
1:B:20:HIS:ND1	1:B:52:LEU:HD22	2.32	0.43
1:A:176:THR:HG22	1:A:178:GLY:H	1.83	0.43
1:B:87:ILE:HG21	1:B:115:LEU:HD22	2.01	0.43
1:B:95:GLY:HA3	1:B:127:ILE:HD11	2.01	0.43
1:B:428:GLU:HA	1:B:431:ILE:HD12	2.00	0.43
1:B:90:ILE:HD13	1:B:126:ALA:HB3	2.00	0.43
1:B:140:ARG:HH22	1:B:146:GLU:CD	2.27	0.43
1:B:17:LEU:HG	1:B:21:LEU:HD23	2.00	0.43
1:A:438:ARG:O	1:A:441:VAL:HG22	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:65:PHE:CE2	1:A:98:LEU:HD23	2.55	0.42
1:A:176:THR:CG2	1:A:177:SER:N	2.82	0.42
1:B:273:LEU:CD2	1:B:447:LEU:HD21	2.50	0.42
1:B:452:GLU:OE1	1:B:452:GLU:N	2.45	0.42
1:B:6:ARG:HG3	1:B:6:ARG:NH1	2.33	0.42
1:A:225:LEU:HD21	1:A:232:THR:C	2.46	0.41
1:B:77:ILE:HD11	1:B:115:LEU:HA	2.02	0.41
1:A:232:THR:HG22	1:A:235:ASP:CG	2.45	0.41
1:B:20:HIS:CD2	1:B:20:HIS:C	2.99	0.41
1:B:232:THR:HG22	1:B:235:ASP:CG	2.45	0.41
1:B:372:THR:HG22	1:B:372:THR:O	2.20	0.41
1:B:176:THR:CG2	1:B:177:SER:N	2.84	0.41
1:A:190:ILE:HD12	1:A:190:ILE:N	2.35	0.41
1:A:435:LEU:HD12	1:A:435:LEU:HA	1.97	0.41
1:B:199:ILE:HD13	1:B:386:MET:HG3	2.03	0.40
1:B:447:LEU:HD12	1:B:447:LEU:HA	1.97	0.40
1:A:57:GLU:OE1	1:A:72:TYR:CZ	2.75	0.40

There are no symmetry-related clashes.

## 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	449/458 (98%)	434 (97%)	15 (3%)	0	100	100
1	B	453/458 (99%)	435 (96%)	17 (4%)	1 (0%)	44	62
2	C	126/133 (95%)	122 (97%)	4 (3%)	0	100	100
All	All	1028/1049 (98%)	991 (96%)	36 (4%)	1 (0%)	48	67

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	94	PRO

### 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	379/387 (98%)	376 (99%)	3 (1%)	79	91
1	B	383/387 (99%)	377 (98%)	6 (2%)	58	79
2	C	112/117 (96%)	111 (99%)	1 (1%)	75	89
All	All	874/891 (98%)	864 (99%)	10 (1%)	70	86

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

Mol	Chain	Res	Type
1	A	184	GLN
1	A	365	GLN
1	A	367	GLU
1	B	6	ARG
1	B	140	ARG
1	B	217	HIS
1	B	260	ARG
1	B	325	THR
1	B	386	MET
2	C	303	VAL

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	147	ASN
1	A	217	HIS
1	A	239	HIS
2	C	247	HIS
2	C	280	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 oligosaccharides 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	453/458 (98%)	0.52	30 (6%) 26 25	60, 78, 129, 166	0
1	B	455/458 (99%)	1.13	82 (18%) 4 5	62, 98, 161, 199	0
2	C	128/133 (96%)	0.70	9 (7%) 24 23	68, 92, 125, 155	0
All	All	1036/1049 (98%)	0.81	121 (11%) 10 10	60, 88, 151, 199	0

All (121) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	234	ALA	6.2
1	B	79	VAL	5.5
2	C	361	GLY	5.5
1	A	1	ALA	5.0
1	B	122	ILE	4.9
1	A	0	ASN	4.8
1	A	170	LEU	4.8
1	B	109	MET	4.3
1	B	29	ALA	4.1
2	C	235	THR	3.9
1	B	453	LEU	3.8
1	A	93	HIS	3.7
1	B	104	ALA	3.6
1	A	165	LYS	3.6
1	B	2	SER	3.6
1	B	97	PHE	3.5
1	A	172	PRO	3.4
1	B	188	ALA	3.4
1	B	93	HIS	3.4
1	B	144	PHE	3.3
1	B	99	VAL	3.3
1	B	148	VAL	3.2
1	A	321	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	456	LYS	3.1
1	B	69	PRO	3.0
1	B	33	LEU	3.0
1	B	32	ILE	3.0
1	B	95	GLY	3.0
1	B	168	GLN	3.0
1	B	60	SER	3.0
1	B	176	THR	3.0
1	B	30	ALA	2.9
1	B	111	THR	2.9
1	A	144	PHE	2.9
1	B	108	ASP	2.9
1	B	357	LEU	2.9
1	A	92	SER	2.9
1	A	356	ASN	2.9
1	B	103	THR	2.9
2	C	326	SER	2.9
1	B	92	SER	2.8
1	B	26	GLY	2.8
1	B	138	LEU	2.7
1	B	440	ALA	2.7
1	B	4	GLY	2.7
1	A	232	THR	2.7
1	B	74	GLU	2.6
1	A	415	PHE	2.6
1	B	98	LEU	2.6
1	A	380	SER	2.6
1	B	236	ALA	2.6
1	A	171	LYS	2.6
1	B	110	GLN	2.6
1	B	61	ARG	2.6
1	B	63	SER	2.5
1	B	101	SER	2.5
1	B	352	ILE	2.5
1	B	140	ARG	2.5
1	A	52	LEU	2.5
1	B	68	TRP	2.5
1	B	94	PRO	2.5
1	A	173	ILE	2.5
2	C	281	HIS	2.5
1	B	371	ILE	2.5
1	B	170	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	119	VAL	2.4
1	A	2	SER	2.4
1	B	127	ILE	2.4
1	A	358	ASN	2.4
2	C	327	VAL	2.4
1	B	130	HIS	2.4
1	B	58	CYS	2.4
1	B	31	ALA	2.4
1	B	255	GLY	2.4
1	B	9	LEU	2.3
1	B	64	ASP	2.3
1	B	142	GLY	2.3
1	B	318	PRO	2.3
1	B	248	GLU	2.3
1	B	441	VAL	2.3
1	A	175	PHE	2.3
1	B	358	ASN	2.3
1	A	368	ARG	2.3
2	C	254	TYR	2.3
1	B	53	VAL	2.3
1	B	121	ALA	2.3
1	B	131	SER	2.2
1	B	456	LYS	2.2
1	B	16	MET	2.2
2	C	360	VAL	2.2
1	B	359	ALA	2.2
1	B	418	LEU	2.2
1	B	437	THR	2.2
1	B	137	ARG	2.2
1	A	365	GLN	2.2
1	A	145	ALA	2.2
1	B	76	ALA	2.2
1	A	197	GLY	2.2
1	B	107	SER	2.2
1	A	219	HIS	2.2
1	B	419	ALA	2.2
1	B	443	GLY	2.2
1	B	54	PRO	2.2
1	B	59	LYS	2.1
1	B	72	TYR	2.1
1	A	372	THR	2.1
1	B	125	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	91	HIS	2.1
1	A	292	MET	2.1
1	B	112	MET	2.1
1	A	255	GLY	2.1
1	A	418	LEU	2.1
1	B	43	LEU	2.1
1	B	351	LEU	2.1
1	B	366	LEU	2.1
1	B	435	LEU	2.1
1	A	435	LEU	2.0
2	C	301	PHE	2.0
1	B	85	MET	2.0
1	B	86	SER	2.0
1	B	106	SER	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( $\text{\AA}^2$ )	Q<0.9
3	NA	B	601	1/1	0.60	0.43	91,91,91,91	0
3	NA	A	601	1/1	0.67	0.24	76,76,76,76	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.