



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 12, 2017 – 02:23 PM EST

PDB ID : 5U8J
Title : Crystal structure of a protein of unknown function ECL_02571 involved in membrane biogenesis from *Enterobacter cloacae*
Authors : Stogios, P.J.; Skarina, T.; Sandoval, J.; Grimshaw, S.; Savchenko, A.; Anderson, W.F.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on : 2016-12-14
Resolution : 2.52 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

<http://wwpdb.org/validation/2016/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
Mogul	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20028442
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20028442

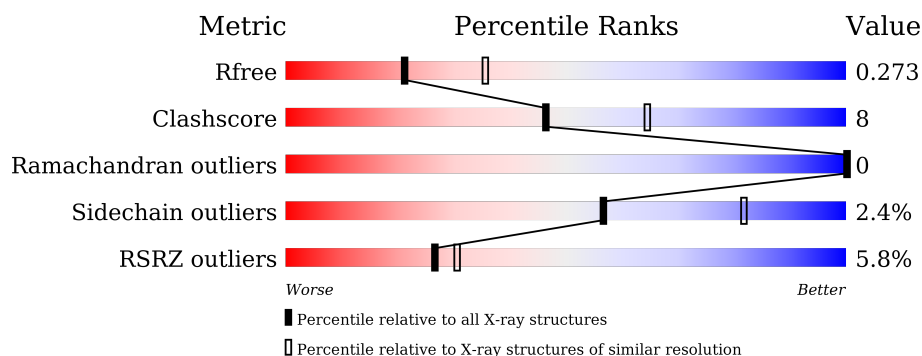
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.52 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}	91344	4241 (2.54-2.50)
Clashscore	102246	4968 (2.54-2.50)
Ramachandran outliers	100387	4873 (2.54-2.50)
Sidechain outliers	100360	4875 (2.54-2.50)
RSRZ outliers	91569	4253 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	175	<div> <div>8%</div> <div> <div></div> <div>75%</div> <div>21%</div> <div>..</div> </div> </div>
1	B	175	<div> <div>3%</div> <div> <div></div> <div>85%</div> <div>11%</div> <div>..</div> </div> </div>
1	C	175	<div> <div>3%</div> <div> <div></div> <div>79%</div> <div>18%</div> <div>..</div> </div> </div>
1	D	175	<div> <div>9%</div> <div> <div></div> <div>74%</div> <div>17%</div> <div>9%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5566 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 UPF0502 protein BFJ73_07745.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	171	Total	C	N	O	S	0	1	0
			1363	845	247	262	9			
1	B	170	Total	C	N	O	S	0	1	0
			1356	839	244	264	9			
1	C	171	Total	C	N	O	S	0	1	0
			1363	844	246	265	8			
1	D	159	Total	C	N	O	S	0	0	0
			1260	784	223	244	9			

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

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

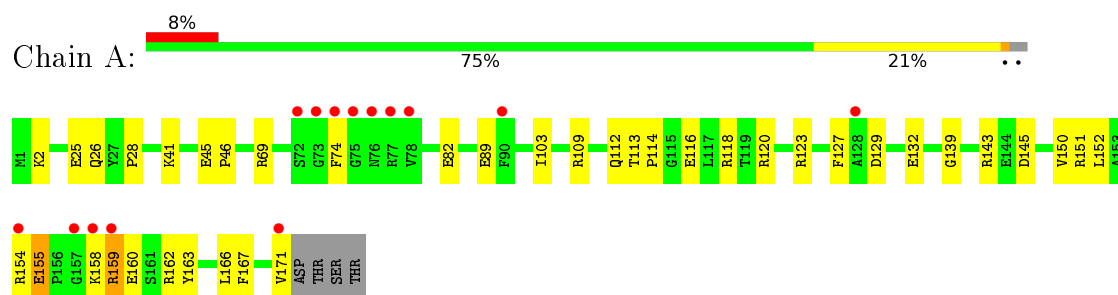
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	66	Total	O	0	0
			66	66		
3	B	56	Total	O	0	0
			56	56		
3	C	74	Total	O	0	0
			74	74		
3	D	26	Total	O	0	0
			26	26		

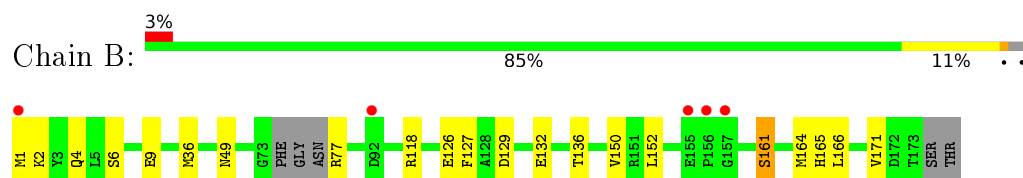
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

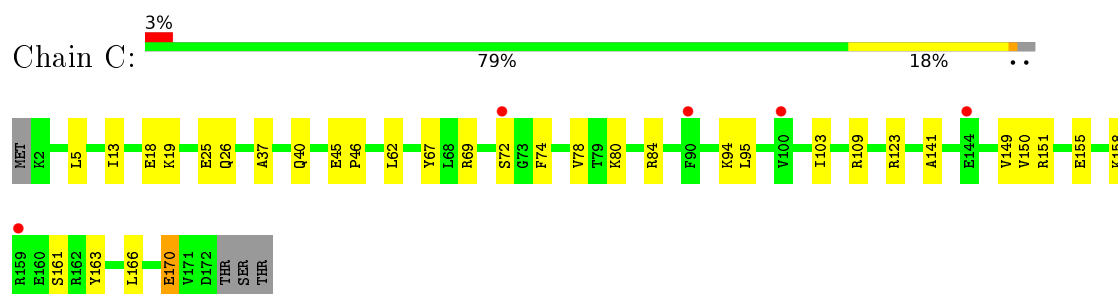
• Molecule 1: UPF0502 protein BFJ73_07745



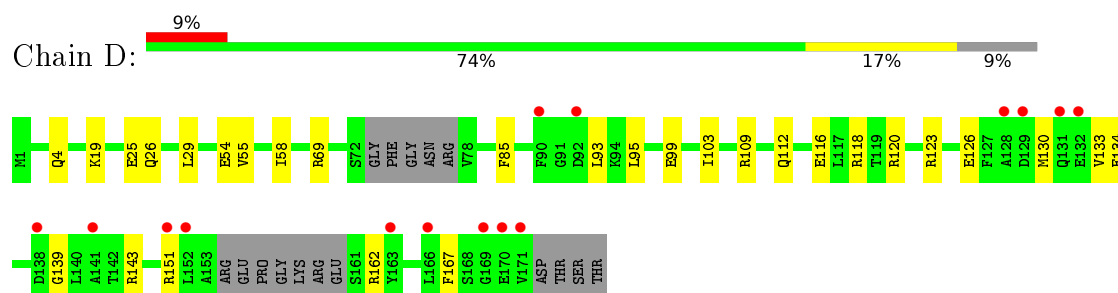
• Molecule 1: UPF0502 protein BFJ73_07745



• Molecule 1: UPF0502 protein BFJ73_07745



• Molecule 1: UPF0502 protein BFJ73_07745



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	87.17Å 53.89Å 90.00Å 90.00° 100.04° 90.00°	Depositor
Resolution (Å)	29.56 – 2.52 29.56 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.3 (29.56-2.52) 97.6 (29.56-2.50)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 2.51Å)	Xtriage
Refinement program	PHENIX (dev_2481: ???)	Depositor
R, R_{free}	0.213 , 0.274 0.212 , 0.273	Depositor DCC
R_{free} test set	1362 reflections (4.92%)	DCC
Wilson B-factor (Å ²)	47.5	Xtriage
Anisotropy	0.096	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 40.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.018 for l,-k,h	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5566	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.90% 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 [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	0.32	0/1386	0.52	0/1869
1	B	0.26	0/1377	0.45	0/1856
1	C	0.24	0/1386	0.41	0/1870
1	D	0.26	0/1276	0.43	0/1721
All	All	0.27	0/5425	0.45	0/7316

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 [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	1363	0	1362	30	0
1	B	1356	0	1354	12	0
1	C	1363	0	1352	24	0
1	D	1260	0	1259	18	0
2	A	1	0	0	0	0
2	C	1	0	0	0	0
3	A	66	0	0	1	0
3	B	56	0	0	1	0
3	C	74	0	0	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	26	0	0	2	0
All	All	5566	0	5327	81	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 8.

All (81) 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:158:LYS:HD2	1:A:160:GLU:O	1.82	0.80
1:C:150:VAL:HG23	1:C:166:LEU:HD11	1.65	0.78
1:A:155:GLU:HG3	1:A:162:ARG:HH12	1.51	0.74
1:A:154:ARG:HG2	1:A:154:ARG:HH11	1.56	0.70
1:A:159:ARG:O	1:A:159:ARG:HG3	1.94	0.67
1:A:113:THR:HG21	1:A:158:LYS:HE3	1.77	0.66
1:C:84:ARG:NH1	3:C:302:HOH:O	2.29	0.66
1:A:69:ARG:NH1	1:A:82:GLU:OE1	2.29	0.66
1:A:155:GLU:HB3	1:A:158:LYS:HB2	1.78	0.64
1:A:143:ARG:HE	1:A:145:ASP:HB3	1.64	0.63
1:D:25:GLU:HG2	1:D:26:GLN:HG3	1.84	0.60
1:C:94:LYS:NZ	3:C:303:HOH:O	2.35	0.59
1:A:127:PHE:HD1	1:A:132:GLU:HB3	1.67	0.59
1:D:55:VAL:HA	1:D:58:ILE:HD12	1.85	0.58
1:A:152:LEU:HD21	1:A:171:VAL:HG21	1.86	0.58
1:D:118:ARG:HB2	1:D:133:VAL:HG21	1.87	0.55
1:A:116:GLU:O	1:A:120:ARG:HG3	2.06	0.55
1:C:155:GLU:HG3	1:C:158:LYS:HG3	1.89	0.54
1:D:19:LYS:HG3	1:D:29:LEU:HD21	1.89	0.54
1:D:123:ARG:NH2	3:D:203:HOH:O	2.42	0.52
1:D:143:ARG:NH2	3:D:202:HOH:O	2.40	0.52
1:A:155:GLU:CB	1:A:158:LYS:HB2	2.39	0.52
1:B:1:MET:HG2	1:B:2:LYS:HD3	1.91	0.52
1:A:155:GLU:HB2	1:A:158:LYS:HG3	1.90	0.52
1:A:150:VAL:HB	1:A:166:LEU:HD21	1.90	0.52
1:C:141:ALA:HB2	1:C:149:VAL:HG23	1.92	0.52
1:C:45:GLU:HB2	1:C:109:ARG:HA	1.92	0.52
1:D:116:GLU:OE2	1:D:162:ARG:NH2	2.43	0.51
1:D:4:GLN:N	1:D:4:GLN:OE1	2.44	0.51
1:D:95:LEU:HG	1:D:99:GLU:HB3	1.93	0.51
1:D:116:GLU:O	1:D:120:ARG:HG3	2.11	0.51
1:A:113:THR:CG2	1:A:158:LYS:HE3	2.41	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:103:ILE:HD12	1:A:167:PHE:HE2	1.77	0.49
1:C:69:ARG:HB3	1:C:84:ARG:HD2	1.93	0.49
1:D:139:GLY:O	1:D:143:ARG:HG3	2.12	0.49
1:C:151:ARG:HG3	1:C:163:TYR:CZ	2.48	0.49
1:C:25:GLU:HG2	1:C:26:GLN:HG3	1.94	0.49
1:B:152:LEU:O	1:B:161:SER:OG	2.31	0.48
1:A:2:LYS:O	1:B:4:GLN:NE2	2.47	0.48
1:C:18:GLU:OE1	1:C:19:LYS:HE2	2.14	0.48
1:A:139:GLY:O	1:A:143:ARG:HG3	2.13	0.48
1:A:154:ARG:HG2	1:A:154:ARG:NH1	2.22	0.48
1:B:164:MET:SD	1:B:165:HIS:N	2.87	0.47
1:C:74:PHE:CE2	1:C:80:LYS:HD2	2.49	0.47
1:A:28:PRO:HB3	1:A:82:GLU:HG2	1.97	0.47
1:A:151:ARG:HB2	1:A:163:TYR:CE1	2.51	0.46
1:C:95:LEU:HD13	1:C:103:ILE:HD12	1.98	0.46
1:C:74:PHE:HB2	1:C:78:VAL:O	2.16	0.46
1:C:13:ILE:HG13	1:C:62:LEU:HD13	1.98	0.46
1:C:74:PHE:CZ	1:C:80:LYS:HD2	2.50	0.46
1:D:103:ILE:HD12	1:D:167:PHE:HE2	1.81	0.46
1:A:25:GLU:HG2	1:A:26:GLN:HG3	1.98	0.45
1:B:49:ASN:ND2	3:B:207:HOH:O	2.43	0.45
1:B:132:GLU:O	1:B:136:THR:HG23	2.16	0.45
1:B:152:LEU:HD21	1:B:171:VAL:HG21	1.98	0.45
1:C:151:ARG:NH2	1:C:161:SER:OG	2.50	0.45
1:A:89:GLU:HG2	1:C:74:PHE:CZ	2.51	0.45
1:D:109:ARG:HB2	1:D:112:GLN:NE2	2.32	0.45
1:B:1:MET:HG2	1:B:2:LYS:CD	2.47	0.45
1:D:54:GLU:O	1:D:58:ILE:HD12	2.16	0.45
1:C:166:LEU:HD22	1:C:170:GLU:HG2	1.99	0.44
1:A:151:ARG:HD3	1:A:163:TYR:CZ	2.53	0.44
1:B:6:SER:H	1:B:9:GLU:HB2	1.83	0.44
1:A:114:PRO:HD2	1:A:160:GLU:OE1	2.17	0.43
1:C:37:ALA:O	1:C:40:GLN:HG3	2.19	0.43
1:C:72:SER:O	1:C:74:PHE:N	2.51	0.42
1:A:41:LYS:NZ	3:A:307:HOH:O	2.52	0.42
1:D:109:ARG:HB2	1:D:112:GLN:HE21	1.84	0.42
1:B:126:GLU:OE1	1:D:126:GLU:HG3	2.20	0.42
1:A:103:ILE:HA	1:A:103:ILE:HD13	1.94	0.42
1:C:18:GLU:OE2	1:C:123:ARG:NH2	2.52	0.41
1:C:5:LEU:HD21	1:C:67:TYR:CE2	2.54	0.41
1:B:127:PHE:HD1	1:B:132:GLU:HB3	1.85	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:150:VAL:HB	1:B:166:LEU:HD21	2.01	0.41
1:A:143:ARG:NH2	1:A:145:ASP:OD1	2.54	0.41
1:A:45:GLU:HA	1:A:46:PRO:HA	1.90	0.41
1:C:69:ARG:HB3	1:C:84:ARG:CD	2.51	0.41
1:D:130:MET:O	1:D:134:GLU:HG2	2.20	0.41
1:A:109:ARG:HB2	1:A:112:GLN:OE1	2.21	0.40
1:C:45:GLU:HA	1:C:46:PRO:HA	1.82	0.40
1:D:85:PHE:O	1:D:93:LEU:HD23	2.20	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	170/175 (97%)	163 (96%)	7 (4%)	0	100	100
1	B	167/175 (95%)	162 (97%)	5 (3%)	0	100	100
1	C	170/175 (97%)	165 (97%)	5 (3%)	0	100	100
1	D	153/175 (87%)	149 (97%)	4 (3%)	0	100	100
All	All	660/700 (94%)	639 (97%)	21 (3%)	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	149/152 (98%)	143 (96%)	6 (4%)	38	63
1	B	149/152 (98%)	144 (97%)	5 (3%)	44	70
1	C	149/152 (98%)	148 (99%)	1 (1%)	88	97
1	D	139/152 (91%)	137 (99%)	2 (1%)	74	91
All	All	586/608 (96%)	572 (98%)	14 (2%)	57	82

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	74	PHE
1	A	118	ARG
1	A	123	ARG
1	A	129	ASP
1	A	155	GLU
1	A	159	ARG
1	B	36	MET
1	B	77	ARG
1	B	118	ARG
1	B	129	ASP
1	B	161	SER
1	C	170	GLU
1	D	69	ARG
1	D	151	ARG

Some 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 carbohydrates in this entry.

5.6 Ligand geometry

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

There are no such residues in this entry.

5.8 Polymer linkage issues

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	171/175 (97%)	0.31	14 (8%) 14 16	37, 58, 116, 184	0
1	B	170/175 (97%)	0.18	5 (2%) 55 60	40, 60, 103, 138	0
1	C	171/175 (97%)	-0.01	5 (2%) 55 60	39, 59, 107, 136	0
1	D	159/175 (90%)	0.56	15 (9%) 11 11	50, 74, 116, 153	0
All	All	671/700 (95%)	0.25	39 (5%) 26 30	37, 62, 112, 184	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	73	GLY	7.3
1	A	74	PHE	5.5
1	B	156	PRO	4.8
1	D	171	VAL	4.5
1	D	92	ASP	4.0
1	D	90	PHE	3.8
1	D	170	GLU	3.8
1	C	159	ARG	3.7
1	B	92	ASP	3.7
1	A	158	LYS	3.7
1	A	76	ASN	3.7
1	A	90	PHE	3.6
1	D	128	ALA	3.6
1	C	90	PHE	3.3
1	D	131	GLN	3.3
1	D	129	ASP	2.9
1	A	171	VAL	2.9
1	D	151	ARG	2.9
1	A	159	ARG	2.9
1	A	128	ALA	2.9
1	D	141	ALA	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	138	ASP	2.6
1	B	1	MET	2.6
1	C	72	SER	2.5
1	D	163	TYR	2.5
1	B	155	GLU	2.4
1	A	157	GLY	2.4
1	A	75	GLY	2.4
1	A	154	ARG	2.4
1	A	72	SER	2.4
1	D	152	LEU	2.4
1	D	132	GLU	2.2
1	A	77	ARG	2.2
1	B	157	GLY	2.2
1	A	78	VAL	2.2
1	D	169	GLY	2.1
1	D	166	LEU	2.1
1	C	144	GLU	2.1
1	C	100	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 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	CL	A	201	1/1	0.95	0.05	-2.50	73,73,73,73	0
2	CL	C	201	1/1	0.88	0.09	-	87,87,87,87	0

6.5 Other polymers

There are no such residues in this entry.