

Full wwPDB X-ray Structure Validation Report (i)

Aug 20, 2023 – 11:18 AM EDT

PDB ID : 2019

Title : Structure of E. coli topoisomersae III in complex with an 8-base single stranded

oligonucleotide. Frozen in glycerol at pH 5.5

Authors : Changela, A.; DiGate, R.; Mondragon, A.

Deposited on : 2006-11-28

Resolution : 2.45 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.orgA user guide is available at

https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

Mol Probity : 4.02b-467

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.35

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

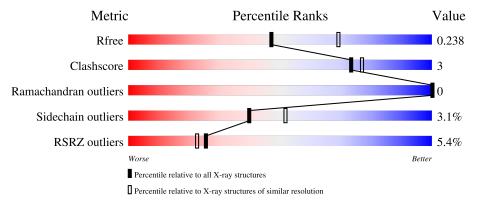
Validation Pipeline (wwPDB-VP) : 2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X- $RAY\ DIFFRACTION$

The reported resolution of this entry is 2.45 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\mathring{A})}) \end{array}$
R_{free}	130704	1544 (2.48-2.44)
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)

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 >=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 <=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	С	8	62%	25%	12%				
1	D	8	62%	25%	12%				
2	A	659	7% 85%		11% •				
2	В	659	86%		9% •				



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 10550 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 DNA chain called 5'-D(*CP*GP*CP*AP*AP*CP*TP*T)-3'.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace				
1	1 C		C	C 7	Total	С	N	О	Р	0	0	0
1		1	138	67	26	39	6	U	U			
1	D	0	Total	С	N	О	Р	0	0	0		
1		0	158	77	28	46	7	0		U		

• Molecule 2 is a protein called DNA topoisomerase 3.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	A	630	Total 5013	C 3165	N 912	O 916	S 20	0	0	0
2	В	631	Total 5016	C 3168	N 913	O 915	S 20	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

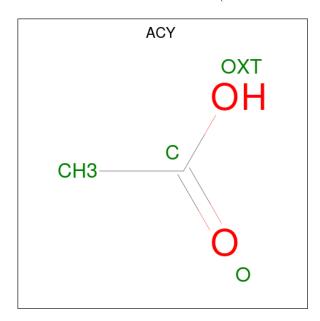
Chain	Residue	Modelled	Actual	Comment	Reference
A	654	HIS	-	expression tag	UNP P14294
A	655	HIS	-	expression tag	UNP P14294
A	656	HIS	-	expression tag	UNP P14294
A	657	HIS	-	expression tag	UNP P14294
A	658	HIS	_	expression tag	UNP P14294
A	659	HIS	-	expression tag	UNP P14294
В	654	HIS	-	expression tag	UNP P14294
В	655	HIS	-	expression tag	UNP P14294
В	656	HIS	-	expression tag	UNP P14294
В	657	HIS	_	expression tag	UNP P14294
В	658	HIS	_	expression tag	UNP P14294
В	659	HIS	-	expression tag	UNP P14294

• Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	2	Total Cl 2 2	0	0

 \bullet Molecule 4 is ACETIC ACID (three-letter code: ACY) (formula: $\mathrm{C_2H_4O_2}).$



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	В	1	Total 4	C 2	O 2	0	0

• Molecule 5 is water.

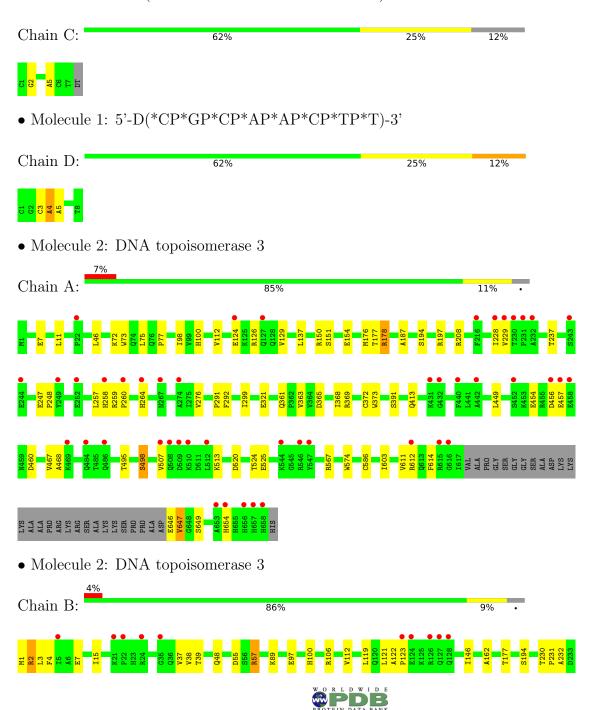
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	С	5	Total O 5 5	0	0
5	D	10	Total O 10 10	0	0
5	A	92	Total O 92 92	0	0
5	В	112	Total O 112 112	0	0

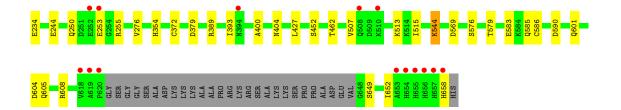


3 Residue-property plots (i)

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: 5'-D(*CP*GP*CP*AP*AP*CP*TP*T)-3'







4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants	102.16Å 102.16Å 451.72Å	Donogitor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.05 - 2.45	Depositor
Resolution (A)	29.05 - 2.45	EDS
% Data completeness	98.2 (29.05-2.45)	Depositor
(in resolution range)	98.2 (29.05-2.45)	EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) > 1$	3.13 (at 2.45Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
D D.	0.212 , 0.246	Depositor
R, R_{free}	0.205 , 0.238	DCC
R_{free} test set	4391 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	38.2	Xtriage
Anisotropy	0.237	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.36, 50.0	EDS
L-test for twinning ²	$ < L > = 0.44, < L^2> = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10550	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.04% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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: ACY, 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		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	С	1.04	0/154	1.55	0/235	
1	D	1.06	0/176	1.85	4/269~(1.5%)	
2	A	0.48	0/5123	0.60	1/6945~(0.0%)	
2	В	0.49	0/5127	0.60	0/6952	
All	All	0.51	0/10580	0.67	5/14401~(0.0%)	

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
2	A	0	1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$Ideal(^{o})$
1	D	4	DA	N1-C6-N6	6.04	122.22	118.60
1	D	5	DA	P-O3'-C3'	6.03	126.93	119.70
1	D	3	DC	O4'-C1'-N1	5.72	112.00	108.00
1	D	4	DA	C5-C6-N6	-5.38	119.40	123.70
2	A	178	ARG	NE-CZ-NH2	-5.35	117.62	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain			Group
2	A	292	PHE	Peptide



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	С	138	0	80	2	0
1	D	158	0	92	1	0
2	A	5013	0	5014	36	0
2	В	5016	0	5020	31	0
3	A	2	0	0	0	0
4	В	4	0	3	0	0
5	A	92	0	0	2	0
5	В	112	0	0	0	0
5	С	5	0	0	0	0
5	D	10	0	0	2	0
All	All	10550	0	10209	68	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 (68) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance } (\text{\AA}) \end{array}$	Clash overlap (Å)
2:B:4:PHE:HB2	2:B:38:VAL:HG12	1.43	0.97
1:D:4:DA:N3	5:D:196:HOH:O	2.07	0.87
2:B:579:THR:O	2:B:583:GLU:HG2	1.86	0.76
2:B:230:THR:HG22	2:B:232:ALA:H	1.55	0.70
1:C:5:DA:OP1	2:A:524:THR:HG23	1.91	0.69
2:A:467:VAL:HG12	2:A:468:ALA:H	1.58	0.68
2:A:467:VAL:HG12	2:A:468:ALA:N	2.10	0.66
2:B:4:PHE:CB	2:B:38:VAL:HG12	2.26	0.63
2:A:361:GLN:HG2	2:A:449:LEU:HD21	1.83	0.61
2:A:197:ARG:HD3	2:A:574:TRP:CZ3	2.35	0.61
2:B:15:ILE:HG23	2:B:146:ILE:HD11	1.81	0.61
1:C:2:DG:N7	2:A:178:ARG:HD2	2.16	0.60
2:A:197:ARG:HD3	2:A:574:TRP:CE3	2.35	0.60
2:A:73:TRP:H	2:A:646:GLU:HG2	1.66	0.59
2:A:100:HIS:CE1	2:A:112:VAL:HB	2.40	0.56
2:B:586:CYS:HB2	2:B:590:ASP:OD2	2.04	0.56
2:A:187:ALA:HB2	2:A:611:VAL:HG13	1.87	0.55



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Continued from previous		Interatomic	Clash
Atom-1	Atom-2	${\rm distance}(\mathring{\rm A})$	overlap (Å)
2:A:259:ARG:N	2:A:260:PRO:HD2	2.21	0.55
2:B:250:GLN:HA	2:B:255:ARG:O	2.09	0.53
2:A:467:VAL:CG1	2:A:468:ALA:H	2.22	0.53
2:A:520:ASP:HB3	2:A:525:GLU:OE2	2.09	0.52
2:A:176:MET:CE	2:A:603:ILE:HD13	2.39	0.52
2:A:150:ARG:HD2	5:A:875:HOH:O	2.10	0.51
2:B:177:THR:HG23	2:B:194:SER:HA	1.93	0.50
2:A:276:VAL:HG21	2:A:467:VAL:HG11	1.93	0.50
2:B:507:VAL:O	2:B:513:LYS:NZ	2.43	0.50
2:B:515:ILE:HD13	2:B:576:SER:HB2	1.94	0.49
2:A:646:GLU:HB2	2:A:649:SER:HB3	1.94	0.49
2:B:100:HIS:NE2	2:B:112:VAL:HB	2.28	0.48
2:A:177:THR:HG23	2:A:194:SER:HA	1.95	0.48
2:B:230:THR:HG21	2:B:234:GLU:OE1	2.14	0.48
2:A:507:VAL:HG23	2:A:513:LYS:HG3	1.96	0.47
2:B:230:THR:HB	2:B:234:GLU:H	1.79	0.47
2:A:467:VAL:CG1	2:A:468:ALA:N	2.77	0.47
2:B:100:HIS:CE1	2:B:112:VAL:HB	2.50	0.47
2:A:299:ILE:HD11	2:A:498:SER:HA	1.96	0.46
2:A:137:LEU:HD12	2:A:321:GLU:HA	1.98	0.46
2:A:151:SER:O	2:A:154:GLU:HG2	2.15	0.46
2:B:649:SER:HA	2:B:652:ILE:HD12	1.99	0.45
2:B:2:ARG:HG2	2:B:97:GLU:HB2	1.98	0.45
2:A:98:ILE:HB	2:A:129:VAL:HG22	1.98	0.45
2:B:585:GLN:O	2:B:586:CYS:HB3	2.17	0.45
2:A:228:ILE:CG2	2:A:229:VAL:N	2.79	0.45
2:A:75:LEU:HG	2:A:647:VAL:HG21	1.98	0.45
2:B:400:ALA:O	2:B:404:ASN:HB2	2.16	0.44
2:A:247:GLU:N	2:A:248:PRO:HD2	2.33	0.43
2:A:46:LEU:HD23	2:A:77:PRO:HA	1.99	0.43
2:B:544:LYS:O	2:B:544:LYS:HG3	2.19	0.43
2:B:3:LEU:HD11	2:B:39:THR:HG22	2.00	0.43
2:B:89:LYS:HD3	2:B:119:LEU:HD22	2.00	0.43
2:A:365:ASP:HB3	2:A:368:ILE:HD12	2.00	0.42
2:A:72:LYS:HB3	2:A:72:LYS:HE2	1.73	0.42
2:A:208:ARG:NH2	2:A:567:ARG:HE	2.17	0.42
2:A:369:ARG:HG3	2:A:373:TRP:CD1	2.54	0.42
2:A:291:PRO:HD3	2:A:413:GLN:CD	2.39	0.42
2:B:389:ARG:HH21	2:B:393:ILE:HD11	1.85	0.42
5:D:54:HOH:O	2:B:48:GLN:HG3	2.18	0.42
2:B:122:ALA:HA	2:B:123:PRO:HD3	1.88	0.42



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Atom-1	Atom-2	$egin{aligned} & ext{Interatomic} \ & ext{distance} \ & ext{(Å)} \end{aligned}$	Clash overlap (Å)
2:B:230:THR:HG23	2:B:231:PRO:HD2	2.02	0.42
2:B:605:GLN:HG3	2:B:608:ARG:HH22	1.85	0.42
2:B:276:VAL:HA	2:B:427:LEU:HD23	2.02	0.41
2:A:495:THR:HB	5:A:886:HOH:O	2.19	0.41
2:B:106:ARG:HG3	2:B:162:ALA:HB2	2.03	0.41
2:B:1:MET:HE1	2:B:37:VAL:HB	2.02	0.41
2:B:55:ASP:OD1	2:B:57:ARG:HB2	2.21	0.41
2:B:354:HIS:HE1	2:B:389:ARG:O	2.04	0.41
2:A:7:GLU:H	2:A:11:LEU:HD23	1.86	0.40
2:A:187:ALA:HB3	2:A:614:PHE:HB2	2.04	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	Perce	ntiles
2	A	626/659~(95%)	611 (98%)	15 (2%)	0	100	100
2	В	627/659~(95%)	609 (97%)	18 (3%)	0	100	100
All	All	1253/1318 (95%)	1220 (97%)	33 (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
2	A	535/555 (96%)	517 (97%)	18 (3%)	37 48
2	В	535/555~(96%)	520 (97%)	15 (3%)	43 56
All	All	1070/1110 (96%)	1037 (97%)	33 (3%)	40 52

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	124	GLU
2	A	126	ARG
2	A	237	THR
2	A	257	LEU
2	A A A A A A A A A A A A	258	HIS
2	A	264	HIS
2	A	363	VAL
2	A	372	CYS SER
2	A	391	SER
2	A	454	GLU
2	A	456	ASP GLU
2	A A A A	457	GLU
2 2	A	460	ASP
	A	498	SER
2	A	586	CYS
2	A	612	ARG
2	A A A B	647	VAL
2	A	654	HIS
2	В	2	ARG
2	В	7	GLU
2	В	57	ARG
2	В	121	LEU
2	В	244	GLU
2	В	253	GLU
2	В	372	CYS
2	В	379	ASP
2	В	452	SER
2	В	462	THR
2	В	544	LYS
2	В	569	ASP
2	В	601	GLN
2	В	604	ASP
2	В	658	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:



Mol	Chain	Res	Type
2	A	250	GLN
2	В	241	GLN
2	В	354	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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| > 2 is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

1/1	[a]	Type	Chain	Res	Link	\mathbf{B}	ond leng	${ m gths}$	В	ond ang	gles
Mol Ty	туре	Chain	rtes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
4	4	ACY	В	803	-	3,3,3	0.83	0	3,3,3	1.00	0

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 (i)

6.1 Protein, DNA and RNA chains (i)

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^{th} 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>	$\#\mathrm{RSRZ}{>}2$	$\mathbf{OWAB}(\mathbf{\mathring{A}}^2)$	Q<0.9
1	С	7/8 (87%)	-0.38	0 100 100	21, 23, 46, 75	0
1	D	8/8 (100%)	-0.76	0 100 100	20, 26, 44, 56	0
2	A	$630/659 \ (95\%)$	0.15	45 (7%) 16 12	19, 42, 115, 173	0
2	В	631/659 (95%)	-0.06	24 (3%) 40 37	16, 39, 80, 114	0
All	All	1276/1334 (95%)	0.04	69 (5%) 25 23	16, 40, 89, 173	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ	
2	A	654	HIS	7.6	
2	A	658	HIS	6.1	
2	A	656	HIS	5.9	
2	A	657	HIS	5.4	
2	В	658	HIS	5.3	
2	A	249	TYR	5.1	
2	A	252	GLU	4.8	
2	В	657	HIS	4.8	
2	A	243	SER	4.7	
2	В	654	HIS	4.1	
2	A	456	ASP	3.8	
2	A	486	GLN	3.8	
2	В	656	HIS	3.8	
2	A	544	LYS	3.5	
2	В	124	GLU	3.5	
2	В	619	ALA	3.4	
2	A	264	HIS	3.3	
2	A	547	TYR	3.2	
2	В	24	ARG	3.2	
2	A	232	ALA	3.1	
2	A	512	LEU	3.0	



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2 A 260 PRO 3.0 2 A 432 GLY 3.0 2 B 655 HIS 3.0 2 B 22 PRO 3.0 2 A 440 PHE 3.0 2 A 230 THR 2.9 2 B 618 VAL 2.8 2 A 230 THR 2.9 2 B 618 VAL 2.8 2 A 258 HIS 2.8 2 A 508 GLN 2.7 2 A 510 LYS 2.7 2 B 128 GLN 2.7 2 A 653 ALA 2.6 2 A 442 ALA 2.6 2 A 459 ASP 2.6 2 B 653 ALA 2.5 <	Continued from previous page								
2 A 432 GLY 3.0 2 B 655 HIS 3.0 2 B 22 PRO 3.0 2 A 440 PHE 3.0 2 A 230 THR 2.9 2 B 618 VAL 2.8 2 A 258 HIS 2.8 2 A 258 HIS 2.8 2 A 508 GLN 2.7 2 A 508 GLN 2.7 2 A 510 LYS 2.7 2 B 128 GLN 2.7 2 A 653 ALA 2.6 2 A 442 ALA 2.6 2 B 653 ALA 2.5 2 B 653 ALA 2.5 2 A 267 ASN 2.5 <	Mol	Chain	Res	Type	RSRZ				
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2 B 253 GLU 2.6 2 A 509 ASP 2.6 2 B 653 ALA 2.5 2 A 267 ASN 2.5 2 A 458 GLU 2.5 2 A 124 GLU 2.5 2 B 35 GLY 2.4 2 B 123 PRO 2.4 2 A 274 ALA 2.4 2 A 546 ARG 2.4 2 A 244 GLU 2.4 2 A 246 PHE 2.4 2 A 231 PRO 2.4 2 A 228 ILE 2.4 2 A 228 ILE 2.4 2 B 21 LYS 2.3 2 A 616 GLY 2.3 2 B 510 LYS 2.3 2 B 126									
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2 B 123 PRO 2.4 2 A 274 ALA 2.4 2 A 546 ARG 2.4 2 A 244 GLU 2.4 2 A 216 PHE 2.4 2 A 231 PRO 2.4 2 A 22 PRO 2.4 2 A 228 ILE 2.4 2 B 21 LYS 2.3 2 B 21 LYS 2.3 2 A 457 GLU 2.3 2 B 510 LYS 2.3 2 B 510 LYS 2.3 2 B 126 ARG 2.3 2 B 252 GLU 2.3 2 A 615 ARG 2.2 2 A 452 SER 2.2 2 A 469 LYS 2.2 2 A 612<		A	124	GLU					
2 A 274 ALA 2.4 2 A 546 ARG 2.4 2 A 244 GLU 2.4 2 A 216 PHE 2.4 2 A 231 PRO 2.4 2 A 22 PRO 2.4 2 A 228 ILE 2.4 2 B 21 LYS 2.3 2 A 457 GLU 2.3 2 A 616 GLY 2.3 2 B 510 LYS 2.3 2 B 126 ARG 2.3 2 B 252 GLU 2.3 2 A 615 ARG 2.2 2 A 452 SER 2.2 2 A 469 LYS 2.2 2 A 507 VAL 2.2 2 A 612 ARG 2.2	1	В	35	GLY	2.4				
2 A 546 ARG 2.4 2 A 244 GLU 2.4 2 A 216 PHE 2.4 2 A 231 PRO 2.4 2 A 22 PRO 2.4 2 A 228 ILE 2.4 2 B 21 LYS 2.3 2 A 457 GLU 2.3 2 A 616 GLY 2.3 2 B 510 LYS 2.3 2 B 126 ARG 2.3 2 B 252 GLU 2.3 2 A 615 ARG 2.2 2 A 229 VAL 2.2 2 A 452 SER 2.2 2 A 469 LYS 2.2 2 A 507 VAL 2.2 2 A 612 ARG 2.2	1	В	123	PRO	2.4				
2 A 244 GLU 2.4 2 A 216 PHE 2.4 2 A 231 PRO 2.4 2 A 22 PRO 2.4 2 A 228 ILE 2.4 2 B 21 LYS 2.3 2 A 457 GLU 2.3 2 A 616 GLY 2.3 2 B 510 LYS 2.3 2 B 126 ARG 2.3 2 B 252 GLU 2.3 2 A 615 ARG 2.2 2 A 229 VAL 2.2 2 A 452 SER 2.2 2 A 469 LYS 2.2 2 A 507 VAL 2.2 2 A 612 ARG 2.2	2	A	274	ALA	2.4				
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2 A 231 PRO 2.4 2 A 22 PRO 2.4 2 A 228 ILE 2.4 2 B 21 LYS 2.3 2 A 457 GLU 2.3 2 A 616 GLY 2.3 2 B 510 LYS 2.3 2 B 126 ARG 2.3 2 B 252 GLU 2.3 2 A 615 ARG 2.2 2 A 229 VAL 2.2 2 A 452 SER 2.2 2 A 469 LYS 2.2 2 A 507 VAL 2.2 2 B 5 ILE 2.2 2 A 612 ARG 2.2	1	A	244	GLU	2.4				
2 A 22 PRO 2.4 2 A 228 ILE 2.4 2 B 21 LYS 2.3 2 A 457 GLU 2.3 2 A 616 GLY 2.3 2 B 510 LYS 2.3 2 B 126 ARG 2.3 2 B 252 GLU 2.3 2 A 615 ARG 2.2 2 A 229 VAL 2.2 2 A 452 SER 2.2 2 A 469 LYS 2.2 2 A 507 VAL 2.2 2 B 5 ILE 2.2 2 A 612 ARG 2.2	2	A	216	PHE	2.4				
2 A 228 ILE 2.4 2 B 21 LYS 2.3 2 A 457 GLU 2.3 2 A 616 GLY 2.3 2 B 510 LYS 2.3 2 B 126 ARG 2.3 2 B 252 GLU 2.3 2 A 615 ARG 2.2 2 A 229 VAL 2.2 2 A 452 SER 2.2 2 A 469 LYS 2.2 2 A 507 VAL 2.2 2 B 5 ILE 2.2 2 A 612 ARG 2.2	2	A	231	PRO	2.4				
2 B 21 LYS 2.3 2 A 457 GLU 2.3 2 A 616 GLY 2.3 2 B 510 LYS 2.3 2 B 126 ARG 2.3 2 B 252 GLU 2.3 2 A 615 ARG 2.2 2 A 229 VAL 2.2 2 A 452 SER 2.2 2 A 469 LYS 2.2 2 A 507 VAL 2.2 2 B 5 ILE 2.2 2 A 612 ARG 2.2	2	A	22	PRO	2.4				
2 A 457 GLU 2.3 2 A 616 GLY 2.3 2 B 510 LYS 2.3 2 B 126 ARG 2.3 2 B 252 GLU 2.3 2 A 615 ARG 2.2 2 A 229 VAL 2.2 2 A 452 SER 2.2 2 A 469 LYS 2.2 2 A 507 VAL 2.2 2 B 5 ILE 2.2 2 A 612 ARG 2.2	2	A	228	ILE	2.4				
2 A 616 GLY 2.3 2 B 510 LYS 2.3 2 B 126 ARG 2.3 2 B 252 GLU 2.3 2 A 615 ARG 2.2 2 A 229 VAL 2.2 2 A 452 SER 2.2 2 A 469 LYS 2.2 2 A 507 VAL 2.2 2 B 5 ILE 2.2 2 A 612 ARG 2.2	2	В	21	LYS	2.3				
2 B 510 LYS 2.3 2 B 126 ARG 2.3 2 B 252 GLU 2.3 2 A 615 ARG 2.2 2 A 229 VAL 2.2 2 A 452 SER 2.2 2 A 469 LYS 2.2 2 A 507 VAL 2.2 2 B 5 ILE 2.2 2 A 612 ARG 2.2	2	A	457	GLU	2.3				
2 B 126 ARG 2.3 2 B 252 GLU 2.3 2 A 615 ARG 2.2 2 A 229 VAL 2.2 2 A 452 SER 2.2 2 A 469 LYS 2.2 2 A 507 VAL 2.2 2 B 5 ILE 2.2 2 A 612 ARG 2.2	2	A	616	GLY	2.3				
2 B 252 GLU 2.3 2 A 615 ARG 2.2 2 A 229 VAL 2.2 2 A 452 SER 2.2 2 A 469 LYS 2.2 2 A 507 VAL 2.2 2 B 5 ILE 2.2 2 A 612 ARG 2.2	2	В	510	LYS	2.3				
2 B 252 GLU 2.3 2 A 615 ARG 2.2 2 A 229 VAL 2.2 2 A 452 SER 2.2 2 A 469 LYS 2.2 2 A 507 VAL 2.2 2 B 5 ILE 2.2 2 A 612 ARG 2.2	2	В	126						
2 A 615 ARG 2.2 2 A 229 VAL 2.2 2 A 452 SER 2.2 2 A 469 LYS 2.2 2 A 507 VAL 2.2 2 B 5 ILE 2.2 2 A 612 ARG 2.2		В		GLU					
2 A 452 SER 2.2 2 A 469 LYS 2.2 2 A 507 VAL 2.2 2 B 5 ILE 2.2 2 A 612 ARG 2.2	2	A	615						
2 A 452 SER 2.2 2 A 469 LYS 2.2 2 A 507 VAL 2.2 2 B 5 ILE 2.2 2 A 612 ARG 2.2	2	A	229		l				
2 A 469 LYS 2.2 2 A 507 VAL 2.2 2 B 5 ILE 2.2 2 A 612 ARG 2.2	2		452						
2 A 507 VAL 2.2 2 B 5 ILE 2.2 2 A 612 ARG 2.2	2		469	LYS					
2 B 5 ILE 2.2 2 A 612 ARG 2.2	2		507		2.2				
2 A 612 ARG 2.2	2	В	5	ILE					
		A							
2 A 404 GLIN 2.1	2	A	484	GLN	2.1				



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Mol	Chain	Res Type		RSRZ	
2	В	127	GLN	2.1	
2	В	508	GLN	2.1	
2	A	431	LYS	2.1	
2	В	394	ASN	2.1	
2	A	127	GLN	2.0	
2	В	620	PRO	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 monosaccharides 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^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
4	ACY	В	803	4/4	0.89	0.23	36,37,38,38	0
3	CL	A	801	1/1	0.99	0.10	21,21,21,21	0
3	CL	A	800	1/1	1.00	0.09	20,20,20,20	0

6.5 Other polymers (i)

There are no such residues in this entry.

