



# Full wwPDB X-ray Structure Validation Report ⓘ

Jul 9, 2025 – 10:10 pm BST

PDB ID : 9FXV / pdb\_00009fxv  
Title : Influenza polymerase A C-terminal domain of PA subunit with peptide inhibitor containing two norleucines  
Authors : Radilova, K.; Brynda, J.  
Deposited on : 2024-07-02  
Resolution : 2.30 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  
Mogul : 1.8.4, CSD as541be (2020)  
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) : 2.44

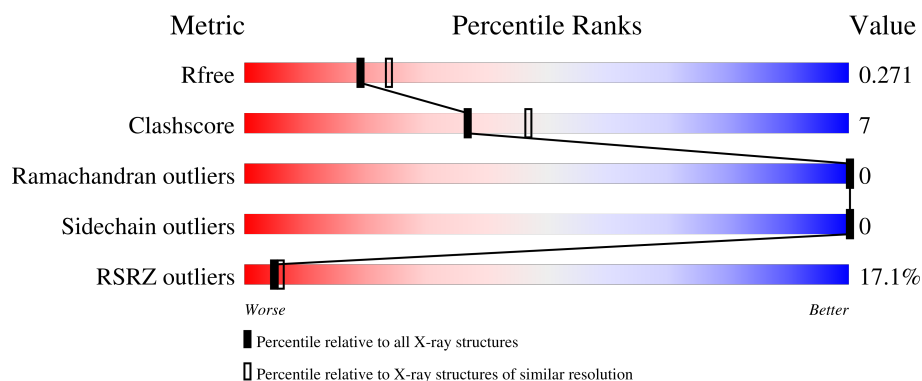
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	5963 (2.30-2.30)
Clashscore	180529	6698 (2.30-2.30)
Ramachandran outliers	177936	6640 (2.30-2.30)
Sidechain outliers	177891	6640 (2.30-2.30)
RSRZ outliers	164620	5963 (2.30-2.30)

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	461	<p>15% 78% 13% 9%</p>
2	B	10	<p>40% 50% 50%</p>

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3564 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 Polymerase acidic protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	420	3242	2075	544	598	25	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	256	SER	-	expression tag	UNP C3W5X6

- Molecule 2 is a protein called Peptide inhibitor.

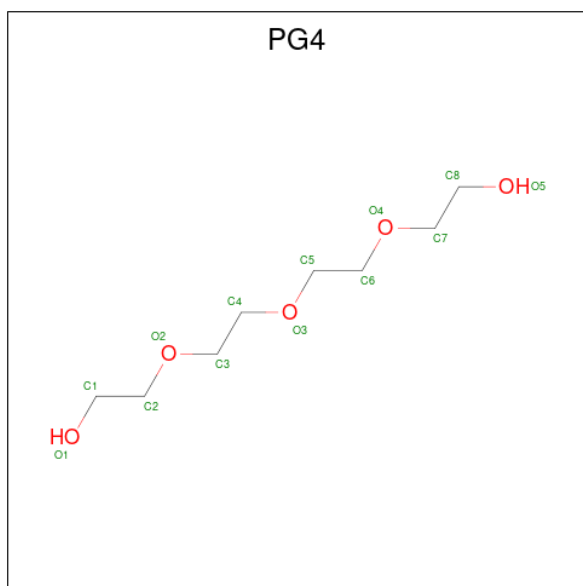
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	10	93	64	12	17	0	0	0

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

- Molecule 4 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula:  $C_8H_{18}O_5$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	8	5		

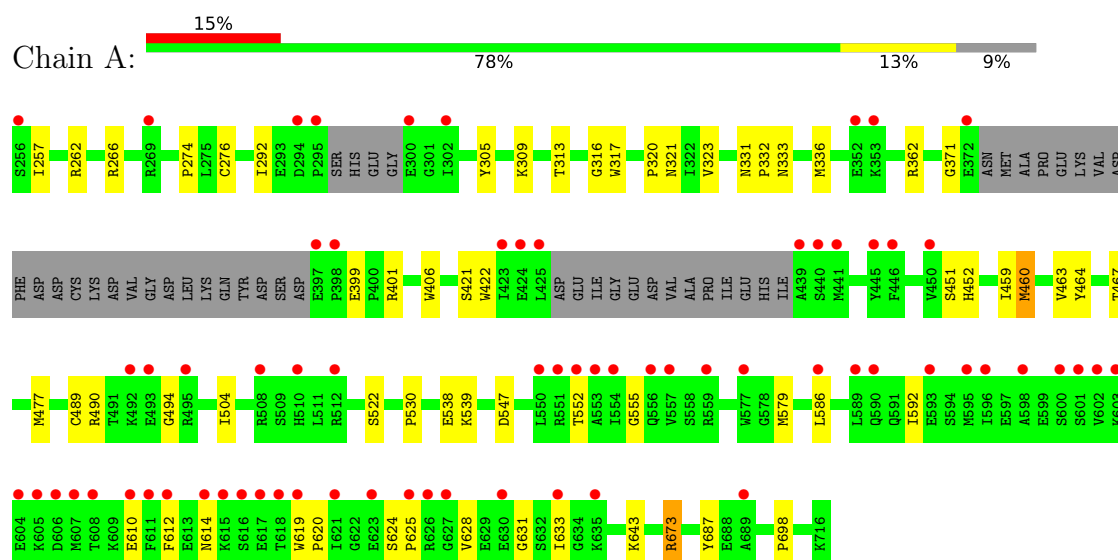
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	206	Total	O	0	0
			206	206		
5	B	6	Total	O	0	0
			6	6		

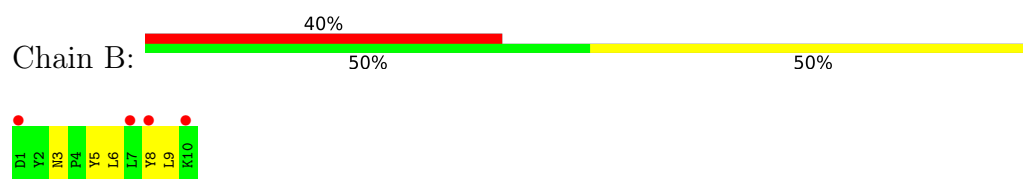
### 3 Residue-property plots [i](#)

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: Polymerase acidic protein



#### • Molecule 2: Peptide inhibitor



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	37.86Å 119.56Å 123.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	26.91 – 2.30 26.91 – 2.30	Depositor EDS
% Data completeness (in resolution range)	94.5 (26.91-2.30) 94.5 (26.91-2.30)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.27 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.8.0415	Depositor
R, $R_{free}$	0.242 , 0.279 0.229 , 0.271	Depositor DCC
$R_{free}$ test set	451 reflections (1.77%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	35.7	Xtriage
Anisotropy	0.496	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 49.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.012 for -h,l,k	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	3564	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.63% 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: PG4, EDO, NLE

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	0.64	0/3314	1.12	4/4488 (0.1%)
2	B	0.78	0/78	0.98	0/101
All	All	0.65	0/3392	1.12	4/4589 (0.1%)

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	3
2	B	0	4
All	All	0	7

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	538	GLU	CB-CA-C	-5.46	101.73	110.79
1	A	530	PRO	CB-CA-C	-5.39	103.29	111.44
1	A	460	MET	CA-C-N	5.00	127.23	120.38
1	A	460	MET	C-N-CA	5.00	127.23	120.38

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	262	ARG	Sidechain
1	A	362	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	A	673	ARG	Sidechain
2	B	5	TYR	Mainchain
2	B	6	NLE	Mainchain
2	B	8	TYR	Mainchain
2	B	9	NLE	Mainchain

## 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	3242	0	3108	42	0
2	B	93	0	90	1	0
3	A	4	0	6	0	0
4	A	13	0	18	5	0
5	A	206	0	0	13	0
5	B	6	0	0	1	0
All	All	3564	0	3222	46	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 7.

All (46) 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:463:VAL:O	1:A:467:THR:HG23	1.77	0.84
1:A:673:ARG:HH21	1:A:673:ARG:HG3	1.46	0.80
1:A:371:GLY:HA2	5:A:1030:HOH:O	1.91	0.70
1:A:547:ASP:OD2	5:A:902:HOH:O	2.12	0.67
1:A:266:ARG:HE	4:A:802:PG4:H62	1.57	0.67
1:A:490:ARG:NH1	1:A:494:GLY:O	2.29	0.66
1:A:460:MET:HA	1:A:460:MET:HE2	1.78	0.65
1:A:586:LEU:HG	5:A:984:HOH:O	1.96	0.65
1:A:539:LYS:N	5:A:901:HOH:O	2.21	0.64
1:A:331:ASN:N	1:A:332:PRO:CD	2.66	0.58
1:A:467:THR:HG22	1:A:579:MET:HE3	1.85	0.58
1:A:624:SER:HB2	1:A:625:PRO:HD2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:459:ILE:HG22	1:A:460:MET:HE3	1.88	0.55
1:A:422:TRP:CZ3	1:A:489:CYS:HB3	2.44	0.53
1:A:421:SER:HB2	1:A:452:HIS:CE1	2.44	0.53
1:A:620:PRO:HB3	1:A:628:VAL:CG1	2.39	0.52
1:A:464:TYR:C	1:A:464:TYR:CD1	2.88	0.52
1:A:257:ILE:HG12	5:A:945:HOH:O	2.10	0.52
1:A:399:GLU:CB	5:A:1090:HOH:O	2.58	0.51
1:A:592:ILE:O	1:A:592:ILE:CG2	2.60	0.49
1:A:320:PRO:O	1:A:321:ASN:CG	2.56	0.49
1:A:406:TRP:HA	5:A:962:HOH:O	2.13	0.49
1:A:422:TRP:CE3	1:A:489:CYS:HB3	2.48	0.49
1:A:467:THR:HG22	1:A:579:MET:HG2	1.95	0.48
1:A:612:PHE:HA	1:A:633:ILE:HG21	1.94	0.48
1:A:451:SER:OG	1:A:452:HIS:ND1	2.41	0.47
4:A:802:PG4:H12	5:A:1041:HOH:O	2.14	0.47
1:A:619:TRP:O	1:A:631:GLY:N	2.42	0.46
1:A:305:TYR:CE1	1:A:309:LYS:CD	2.99	0.45
1:A:274:PRO:O	1:A:401:ARG:HD2	2.17	0.45
4:A:802:PG4:C1	5:A:1041:HOH:O	2.65	0.44
2:B:3:ASN:OD1	2:B:3:ASN:C	2.60	0.44
4:A:802:PG4:H11	5:A:1044:HOH:O	2.18	0.44
1:A:292:ILE:HG22	1:A:313:THR:HG21	2.00	0.43
1:A:610:GLU:O	1:A:614:ASN:N	2.46	0.43
1:A:673:ARG:NE	5:B:102:HOH:O	2.52	0.43
1:A:316:GLY:O	1:A:317:TRP:C	2.62	0.43
1:A:643:LYS:NZ	5:A:922:HOH:O	2.50	0.43
1:A:620:PRO:HB3	1:A:628:VAL:HG11	2.00	0.43
1:A:333:ASN:HA	1:A:336:MET:HE3	2.01	0.42
1:A:477:MET:HG3	5:A:972:HOH:O	2.19	0.41
1:A:323:VAL:HB	5:A:966:HOH:O	2.19	0.41
1:A:276:CYS:SG	1:A:698:PRO:HB3	2.60	0.40
1:A:504:ILE:HD13	1:A:522:SER:HA	2.03	0.40
1:A:552:THR:N	1:A:555:GLY:O	2.50	0.40
1:A:687:TYR:CD1	4:A:802:PG4:H42	2.57	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	412/461 (89%)	399 (97%)	13 (3%)	0	100	100
2	B	6/10 (60%)	6 (100%)	0	0	100	100
All	All	418/471 (89%)	405 (97%)	13 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	332/412 (81%)	332 (100%)	0	100	100
2	B	8/8 (100%)	8 (100%)	0	100	100
All	All	340/420 (81%)	340 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	NLE	B	6	2	6,7,8	0.66	0	2,7,9	0.12	0
2	NLE	B	9	2	6,7,8	0.61	0	2,7,9	0.27	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NLE	B	6	2	-	0/5/6/8	-
2	NLE	B	9	2	-	3/5/6/8	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	9	NLE	O-C-CA-CB
2	B	9	NLE	C-CA-CB-CG
2	B	9	NLE	N-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry

2 ligands are modelled in this entry.

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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
4	PG4	A	802	-	12,12,12	0.25	0	11,11,11	0.24	0
3	EDO	A	801	-	3,3,3	0.19	0	2,2,2	0.29	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PG4	A	802	-	-	4/10/10/10	-
3	EDO	A	801	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	802	PG4	C8-C7-O4-C6
4	A	802	PG4	C1-C2-O2-C3
4	A	802	PG4	C4-C3-O2-C2
4	A	802	PG4	O3-C5-C6-O4

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	802	PG4	5	0

## 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	420/461 (91%)	0.97	69 (16%) <b>5</b> <b>6</b>	39, 58, 111, 153	1 (0%)
2	B	8/10 (80%)	1.94	4 (50%) <b>0</b> <b>0</b>	52, 66, 96, 111	0
All	All	428/471 (90%)	0.99	73 (17%) <b>5</b> <b>6</b>	39, 58, 111, 153	1 (0%)

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	439	ALA	5.8
1	A	611	PHE	5.7
1	A	621	ILE	5.6
1	A	425	LEU	5.0
1	A	557	VAL	4.9
1	A	606	ASP	4.9
1	A	596	ILE	4.6
1	A	617	GLU	4.6
1	A	602	VAL	4.0
1	A	612	PHE	3.9
1	A	552	THR	3.9
1	A	550	LEU	3.8
1	A	295	PRO	3.8
1	A	577	TRP	3.8
1	A	300	GLU	3.7
1	A	551	ARG	3.7
1	A	605	LYS	3.7
1	A	397	GLU	3.7
1	A	618	THR	3.6
2	B	7	LEU	3.5
1	A	614	ASN	3.5
1	A	446	PHE	3.5
1	A	610	GLU	3.4
2	B	10	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	554	ILE	3.3
1	A	608	THR	3.3
1	A	625	PRO	3.3
1	A	553	ALA	3.3
1	A	633	ILE	3.2
1	A	352	GLU	3.2
1	A	512	ARG	3.1
1	A	616	SER	3.1
1	A	302	ILE	3.0
1	A	615	LYS	3.0
1	A	603	LYS	2.9
1	A	600	SER	2.9
1	A	440	SER	2.9
2	B	8	TYR	2.9
1	A	372	GLU	2.8
1	A	556	GLN	2.8
1	A	256	SER	2.8
1	A	423	ILE	2.7
1	A	445	TYR	2.7
1	A	441	MET	2.6
1	A	607	MET	2.6
1	A	495	ARG	2.6
1	A	593	GLU	2.5
1	A	598	ALA	2.5
1	A	294	ASP	2.5
1	A	424	GLU	2.5
1	A	601	SER	2.5
1	A	492	LYS	2.4
1	A	619	TRP	2.4
1	A	586	LEU	2.4
1	A	589	LEU	2.4
1	A	635	LYS	2.4
1	A	604	GLU	2.3
1	A	353	LYS	2.3
1	A	493	GLU	2.3
1	A	595	MET	2.3
1	A	623	GLU	2.3
1	A	627	GLY	2.3
1	A	630	GLU	2.2
1	A	626	ARG	2.2
1	A	689	ALA	2.2
1	A	590	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	450	VAL	2.1
1	A	269	ARG	2.1
1	A	559	ARG	2.1
2	B	1	ASP	2.1
1	A	398	PRO	2.1
1	A	508	ARG	2.0
1	A	510	HIS	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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	NLE	B	9	8/9	0.84	0.18	67,73,97,100	0
2	NLE	B	6	8/9	0.90	0.15	62,74,83,83	0

## 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
3	EDO	A	801	4/4	0.78	0.20	74,83,84,85	0
4	PG4	A	802	13/13	0.87	0.15	66,78,82,85	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.