

wwPDB X-ray Structure Validation Summary Report (i)

Nov 5, 2023 – 08:06 AM EST

:	7RNU
:	nSH2 domain of p85-beta subunit of phosphatidylinositol 3-kinase in complex
	with an actin peptide with phosphorylated tyrosine 53
:	Dai, S.; Horton, J.R.; Cheng, X.
:	2021-07-29
:	1.45 Å(reported)
	: : :

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at 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 (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:

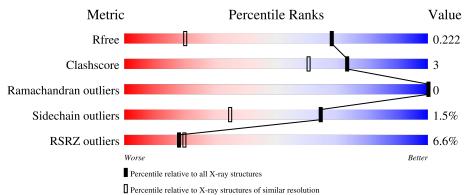
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.45 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	1156 (1.46-1.46)
Clashscore	141614	1202 (1.46-1.46)
Ramachandran outliers	138981	1178 (1.46-1.46)
Sidechain outliers	138945	1178 (1.46-1.46)
RSRZ outliers	127900	1139 (1.46-1.46)

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	А	114	6% 							
			3%							
1	С	114	88% 9% •							
1	Е	114	84% 8% · 7%							
1	G	114	89% 5% · ·							
2	В	9	22% 44% 11% 44%							



Mol	Chain	Length	Quality of chain		
2	D	9	89%		11%
2	F	9	78%	11%	11%
2	Н	9	67% 11%	22%	%



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4196 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.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	Δ	107	Total	С	Ν	0	S	0	0	0
	А	107	869	553	151	164	1	0	0	0
1	С	110	Total	С	Ν	0	S	0	3	0
	U	110	901	574	154	172	1	0	5	0
1	Е	106	Total	С	Ν	0	S	0	3	0
	Ľ	100	871	557	148	164	2	0	5	0
1	G	109	Total	С	Ν	0	S	0	3	0
	G	109	885	566	151	166	2		3	U

• Molecule 1 is a protein called Phosphatidylinositol 3-kinase regulatory subunit beta.

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	318	GLY	-	expression tag	UNP 000459
А	319	SER	-	expression tag	UNP 000459
А	320	MET	-	expression tag	UNP 000459
С	318	GLY	-	expression tag	UNP 000459
C	319	SER	-	expression tag	UNP 000459
С	320	MET	-	expression tag	UNP 000459
Ε	318	GLY	-	expression tag	UNP 000459
E	319	SER	-	expression tag	UNP 000459
E	320	MET	-	expression tag	UNP 000459
G	318	GLY	-	expression tag	UNP 000459
G	319	SER	-	expression tag	UNP 000459
G	320	MET	_	expression tag	UNP 000459

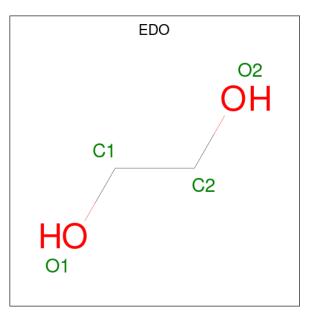
• Molecule 2 is a protein called Actin, alpha skeletal muscle.

Mol	Chain	Residues		Ate	oms			ZeroOcc	AltConf	Trace
0	р	Б	Total	С	Ν	0	Р	0	0	0
	D	5	41	23	5	12	1			0
0	р	0	Total	С	Ν	0	Р	0	1	0
	D	9	71	40	9	21	1	0		0



Conti	naca fron	i previous pu	ye							
Mol	Chain	Residues		Ate	oms			ZeroOcc	AltConf	Trace
9	Г	0	Total	С	Ν	Ο	Р	0	0	0
Z	Г	0	64	36	8	19	1	0		0
0	Н	7	Total	С	Ν	Ο	Р	0	0	0
Z	п	1	58	32	7	18	1	0		U

• Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
3	С	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
3	С	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
3	С	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
3	G	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0
3	G	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

• Molecule 4 is water.



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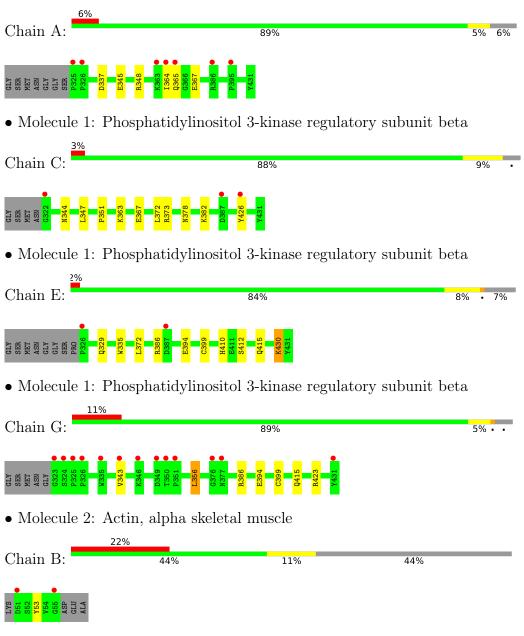
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	96	Total O 96 96	0	0
4	В	4	Total O 4 4	0	0
4	С	107	Total O 107 107	0	0
4	D	10	Total O 10 10	0	0
4	Е	96	Total O 96 96	0	0
4	F	11	Total O 11 11	0	0
4	G	74	Total O 74 74	0	0
4	Н	6	Total O 6 6	0	0



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: Phosphatidylinositol 3-kinase regulatory subunit beta



• Molecule 2: Actin, alpha skeletal muscle



Chain D:	11%		110/
Unann D.	89%		11%
K50 Y53 A58			
• Molecul	e 2: Actin, alpha skeletal muscle		
Chain F:	78%	11%	11%
K50 Y53 E57 ALA			
• Molecul	e 2: Actin, alpha skeletal muscle		
	22%		
Chain H:	67% 11%	22	2%
LYS D51 X53 Y53 V54 G55 D56	PIR		



4 Data and refinement statistics (i)

Property	Value	Source	
Space group	C 1 2 1	Depositor	
Cell constants	188.08Å 41.43Å 65.88Å	Depositor	
a, b, c, α , β , γ	90.00° 100.29° 90.00°	Depositor	
Resolution (Å)	34.92 - 1.45	Depositor	
Resolution (A)	34.92 - 1.45	EDS	
% Data completeness	89.5 (34.92-1.45)	Depositor	
(in resolution range)	89.5(34.92 - 1.45)	EDS	
R _{merge}	(Not available)	Depositor	
R _{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	$1.64 (at 1.45 \text{\AA})$	Xtriage	
Refinement program	PHENIX 1.18.2_3874	Depositor	
B B.	0.191 , 0.222	Depositor	
R, R_{free}	0.191 , 0.222	DCC	
R_{free} test set	2000 reflections $(2.51%)$	wwPDB-VP	
Wilson B-factor $(Å^2)$	15.1	Xtriage	
Anisotropy	0.547	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.35 , 45.0	EDS	
L-test for twinning ²	$ \langle L \rangle = 0.49, \langle L^2 \rangle = 0.32$	Xtriage	
Estimated twinning fraction	No twinning to report.	Xtriage	
F_o, F_c correlation	0.96	EDS	
Total number of atoms	4196	wwPDB-VP	
Average B, all atoms $(Å^2)$	23.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.13% of the height of the origin peak. No significant pseudotranslation is detected.

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.



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: PTR, EDO

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	Bond lengths		angles
IVIOI	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.29	0/892	0.54	0/1208
1	С	0.37	0/931	0.55	0/1262
1	Ε	0.36	0/902	0.57	0/1220
1	G	0.30	0/914	0.51	0/1240
2	В	0.25	0/23	0.31	0/28
2	D	0.28	0/55	0.54	0/70
2	F	0.32	0/46	0.60	0/59
2	Н	0.25	0/40	0.40	0/51
All	All	0.33	0/3803	0.54	0/5138

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	А	869	0	831	3	0
1	С	901	0	861	8	0
1	Е	871	0	844	7	0
1	G	885	0	848	8	0
2	В	41	0	27	0	0



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	71	0	49	0	0
2	F	64	0	41	0	0
2	Н	58	0	37	0	0
3	А	12	0	18	2	0
3	С	12	0	18	0	0
3	G	8	0	12	0	0
4	А	96	0	0	0	0
4	В	4	0	0	0	0
4	С	107	0	0	3	1
4	D	10	0	0	0	0
4	Ε	96	0	0	2	0
4	F	11	0	0	0	0
4	G	74	0	0	1	1
4	Н	6	0	0	0	0
All	All	4196	0	3586	24	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 3.

The worst 5 of 24 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:C:367:GLU:OE1	4:C:601:HOH:O	2.08	0.72
1:G:343:VAL:HG13	1:G:356[A]:LEU:HD11	1.73	0.70
1:G:386:ARG:NH2	1:G:394:GLU:OE2	2.25	0.66
1:E:415:GLN:O	4:E:501:HOH:O	2.15	0.64
1:C:382:LYS:NZ	4:C:601:HOH:O	2.30	0.62

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)
4:C:691:HOH:O	4:G:667:HOH:O[1_565]	2.19	0.01



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	Percer	ntiles
1	А	105/114~(92%)	104 (99%)	1 (1%)	0	100	100
1	\mathbf{C}	111/114~(97%)	110 (99%)	1 (1%)	0	100	100
1	Ε	107/114~(94%)	106 (99%)	1 (1%)	0	100	100
1	G	110/114~(96%)	109 (99%)	1 (1%)	0	100	100
2	В	2/9~(22%)	2 (100%)	0	0	100	100
2	D	7/9~(78%)	7 (100%)	0	0	100	100
2	F	5/9~(56%)	5 (100%)	0	0	100	100
2	Н	4/9~(44%)	4 (100%)	0	0	100	100
All	All	451/492 (92%)	447 (99%)	4 (1%)	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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	93/100~(93%)	92~(99%)	1 (1%)	73 48
1	С	97/100~(97%)	96~(99%)	1 (1%)	76 52
1	Ε	95/100~(95%)	92~(97%)	3~(3%)	39 8
1	G	95/100~(95%)	93~(98%)	2(2%)	53 19
2	В	3/6~(50%)	3 (100%)	0	100 100
2	D	6/6~(100%)	6 (100%)	0	100 100



Conti	Continueu from previous page					
Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	F	5/6~(83%)	5~(100%)	0	100 100	
2	Н	5/6~(83%)	5 (100%)	0	100 100	
All	All	399/424~(94%)	392~(98%)	7 (2%)	65 26	

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5 of 7 residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
1	Ε	410	HIS
1	Ε	430	LYS
1	G	356[B]	LEU
1	G	356[A]	LEU
1	Е	372	LEU

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

Mol	Chain	Res	Type
1	А	365	GLN
1	G	415	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

4 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	Mal Tuna Chain Dag L		Link	Link Bond lengths		\mathbf{ths}	Bond angles			
IVIOI	Type	Chain	Res	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
2	PTR	Н	53	2	15, 16, 17	1.29	1 (6%)	19,22,24	0.75	0
2	PTR	В	53	2	15, 16, 17	1.23	1 (6%)	19,22,24	0.81	0



Mal	Turne	Type Chain Res Link		Bo	Bond lengths			Bond angles		
IVIOI	Type	Chain	res	Link	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
2	PTR	D	53	2	$15,\!16,\!17$	1.29	1 (6%)	19,22,24	1.00	0
2	PTR	F	53	2	15, 16, 17	1.14	1 (6%)	19,22,24	0.92	1 (5%)

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	PTR	Н	53	2	-	2/10/11/13	0/1/1/1
2	PTR	В	53	2	-	4/10/11/13	0/1/1/1
2	PTR	D	53	2	-	2/10/11/13	0/1/1/1
2	PTR	F	53	2	-	2/10/11/13	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	53	PTR	OH-CZ	-4.42	1.30	1.40
2	В	53	PTR	OH-CZ	-4.40	1.30	1.40
2	F	53	PTR	OH-CZ	-4.03	1.31	1.40
2	Н	53	PTR	OH-CZ	-3.96	1.31	1.40

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	F	53	PTR	O3P-P-OH	2.18	112.05	105.24

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	53	PTR	C-CA-CB-CG
2	F	53	PTR	C-CA-CB-CG
2	Н	53	PTR	C-CA-CB-CG
2	D	53	PTR	N-CA-CB-CG
2	Н	53	PTR	N-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.



5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

8 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	Turne	Chain	Res	Link	B	ond leng	gths	B	Bond ang	gles
	Type	Unam	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
3	EDO	А	503	-	3,3,3	0.47	0	$2,\!2,\!2$	0.36	0
3	EDO	С	503	-	3,3,3	0.43	0	2,2,2	0.44	0
3	EDO	G	501	-	3,3,3	0.51	0	2,2,2	0.42	0
3	EDO	G	502	-	3,3,3	0.48	0	2,2,2	0.42	0
3	EDO	С	501	-	3,3,3	0.57	0	2,2,2	0.16	0
3	EDO	А	502	-	3,3,3	0.45	0	2,2,2	0.36	0
3	EDO	А	501	-	3,3,3	0.47	0	2,2,2	0.21	0
3	EDO	С	502	-	3,3,3	0.39	0	2,2,2	0.53	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
3	EDO	А	503	-	-	0/1/1/1	-
3	EDO	С	503	-	-	0/1/1/1	-
3	EDO	G	501	-	-	0/1/1/1	-
3	EDO	G	502	-	-	1/1/1/1	-
3	EDO	С	501	-	-	1/1/1/1	-
3	EDO	А	502	-	-	0/1/1/1	-
3	EDO	А	501	-	-	1/1/1/1	-
3	EDO	C	502	-	-	0/1/1/1	-

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
3	А	501	EDO	O1-C1-C2-O2
3	С	501	EDO	O1-C1-C2-O2
3	G	502	EDO	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	А	502	EDO	1	0
3	А	501	EDO	2	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 (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>2	$OWAB(A^2)$	Q<0.9
1	А	107/114~(93%)	0.52	7 (6%) 18 21	11, 20, 44, 61	0
1	С	110/114~(96%)	0.38	3 (2%) 54 56	10, 16, 37, 46	0
1	Ε	106/114~(92%)	0.26	2 (1%) 66 68	10, 16, 34, 52	0
1	G	109/114~(95%)	0.80	13 (11%) 4 5	11, 25, 44, 49	0
2	В	4/9~(44%)	2.47	2 (50%) 0 0	28, 40, 40, 55	0
2	D	8/9~(88%)	0.56	1 (12%) 3 4	13, 16, 33, 33	0
2	F	7/9~(77%)	-0.18	0 100 100	16, 19, 35, 37	0
2	Н	6/9~(66%)	1.85	2 (33%) 0 0	31, 47, 54, 59	0
All	All	457/492~(92%)	0.52	30 (6%) 18 20	10, 19, 44, 61	0

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	365	GLN	5.7
1	Е	326	PRO	5.6
1	G	431	TYR	5.6
1	А	325	PRO	5.4
2	В	55	GLY	5.1

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^{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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q < 0.9
2	PTR	D	53	16/17	0.95	0.10	$8,\!10,\!22,\!29$	0



Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
2	PTR	В	53	16/17	0.96	0.09	$19,\!21,\!30,\!33$	0
2	PTR	F	53	16/17	0.96	0.09	10,13,24,30	0
2	PTR	Н	53	16/17	0.96	0.08	$14,\!17,\!28,\!30$	0

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	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
3	EDO	С	503	4/4	0.85	0.19	40,40,41,47	0
3	EDO	А	503	4/4	0.87	0.20	31,41,43,49	0
3	EDO	G	502	4/4	0.87	0.14	24,30,33,51	0
3	EDO	А	501	4/4	0.91	0.40	28,42,50,51	0
3	EDO	G	501	4/4	0.91	0.12	23,24,30,33	0
3	EDO	С	501	4/4	0.91	0.11	18,18,18,22	0
3	EDO	А	502	4/4	0.92	0.28	36,39,53,72	0
3	EDO	С	502	4/4	0.98	0.07	18,21,22,23	0

6.5 Other polymers (i)

There are no such residues in this entry.

