

wwPDB X-ray Structure Validation Summary Report (i)

Sep 19, 2023 – 01:27 AM EDT

PDB ID : 5DBN

Title : Crystal structure of AtoDA complex

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Deposited on : 2015-08-21

Resolution : 2.55 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 : 2.35.1

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)

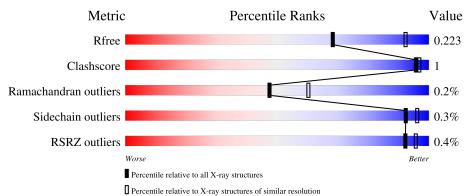
Validation Pipeline (wwPDB-VP) : 2.35.1

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 2.55 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	Similar resolution
Metric	$(\# \mathrm{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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	A	221	95%	
1	С	221	95%	•
1	Е	221	91%	5% •
1	G	221	94%	
2	В	223	92%	



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Mol	Chain	Length	Quality of chain	
2	D	223	93%	• 5%
2	F	223	94%	
2	Н	223	91%	5% •



2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 25941 atoms, of which 12811 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 Acetate CoA-transferase subunit alpha.

Mol	Chain	Residues		Atoms					ZeroOcc	AltConf	Trace
1	A	215	Total	С	Н	N	О	S	0	0	0
1	A	210	3223	1005	1630	278	302	8	0	0	
1	С	215	Total	С	Н	N	О	S	0	0	0
1		219	3235	1007	1637	279	304	8	0	U	
1	Е	213	Total	С	Н	N	О	S	0	0	0
1	12	210	3153	987	1588	273	297	8	0	0	
1	G	215	Total	С	Н	N	О	S	0	0	0
1	G		3238	1008	1638	277	307	8			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	${f Comment}$	Reference
A	0	SER	-	expression tag	UNP P76458
С	0	SER	-	expression tag	UNP P76458
E	0	SER	-	expression tag	UNP P76458
G	0	SER	-	expression tag	UNP P76458

• Molecule 2 is a protein called Acetate CoA-transferase subunit beta.

Mol	Chain	Residues		Atoms					ZeroOcc	AltConf	Trace
2	2 B	213	Total	С	Н	N	О	S	0	0	0
	Б	213	3136	979	1569	283	291	14	0		
2	D	212	Total	С	Н	N	О	S	0	0	0
	D	212	3068	965	1528	275	285	15			
2	F	214	Total	С	Н	N	О	S	0	0	0
	Г	214	3137	980	1569	284	290	14	U		0
2	П	21.4	Total	С	Н	N	О	S	0	0	0
2	2 H	214	3169	987	1594	285	288	15	0	U	

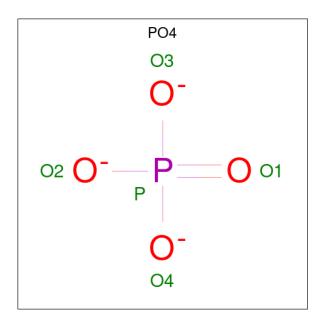
There are 28 discrepancies between the modelled and reference sequences:



Chain	Residue	Modelled	Actual	Comment	Reference
В	217	THR	-	expression tag	UNP P76459
В	218	HIS	-	expression tag	UNP P76459
В	219	HIS	-	expression tag	UNP P76459
В	220	HIS	-	expression tag	UNP P76459
В	221	HIS	-	expression tag	UNP P76459
В	222	HIS	-	expression tag	UNP P76459
В	223	HIS	-	expression tag	UNP P76459
D	217	THR	-	expression tag	UNP P76459
D	218	HIS	-	expression tag	UNP P76459
D	219	HIS	-	expression tag	UNP P76459
D	220	HIS	-	expression tag	UNP P76459
D	221	HIS	-	expression tag	UNP P76459
D	222	HIS	-	expression tag	UNP P76459
D	223	HIS	-	expression tag	UNP P76459
F	217	THR	-	expression tag	UNP P76459
F	218	HIS	-	expression tag	UNP P76459
F	219	HIS	-	expression tag	UNP P76459
F	220	HIS	-	expression tag	UNP P76459
F	221	HIS	-	expression tag	UNP P76459
F	222	HIS	-	expression tag	UNP P76459
F	223	HIS	-	expression tag	UNP P76459
Н	217	THR	-	expression tag	UNP P76459
Н	218	HIS	-	expression tag	UNP P76459
Н	219	HIS	-	expression tag	UNP P76459
Н	220	HIS	-	expression tag	UNP P76459
Н	221	HIS	-	expression tag	UNP P76459
Н	222	HIS	-	expression tag	UNP P76459
Н	223	HIS	-	expression tag	UNP P76459

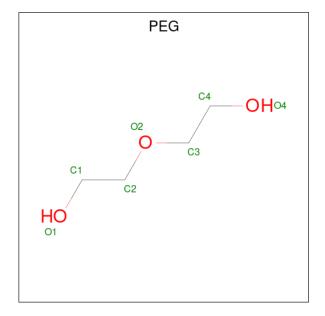
 \bullet Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: $\mathrm{O_4P}).$





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O P	0	0
	71		5 4 1		
3	В	1	Total O P	0	0
3	Б	1	5 4 1		U
3	E	1	Total O P	0	0
3	<u> 1</u> 2	1	5 4 1		
3	G	1	Total O P	0	0
3	G	1	5 4 1	U	U
3	Н	1	Total O P	0	0
3	П	1	5 4 1		

 $\bullet \ \ Molecule\ 4\ is\ DI(HYDROXYETHYL)ETHER\ (three-letter\ code:\ PEG)\ (formula:\ C_4H_{10}O_3).$



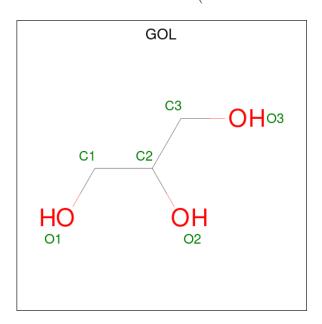


Mol	Chain	Residues	Ato	ms		ZeroOcc	AltConf	
1	4 B	1	Total C	Η	О	0	0	
4			17 4	10	3	O	U	
4	4 B	1	Total C	Η	О	0	0	
-	D	1	17 4	10	3	O		
4	\mathbf{C}	\mathbf{C}	1	Total C	Η	O	0	0
	C	1	17 4	10	3	O	U	
4	F	1	Total C	Η	O	0	0	
	1	1	17 4	10	3	O	U	
4	Н	1	Total C	Η	O	0	0	
1	11		17 4	10	3			

• Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	E	1	Total Cl 1 1	0	0

 \bullet Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $\mathrm{C_3H_8O_3}).$



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	E	1	Total	С	Н	О	0	0
U	Г	1	14	3	8	3	U	U

• Molecule 7 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	59	Total O 59 59	0	0
7	В	71	Total O 71 71	0	0
7	С	66	Total O 66 66	0	0
7	D	41	Total O 41 41	0	0
7	E	35	Total O 35 35	0	0
7	F	60	Total O 60 60	0	0
7	G	67	Total O 67 67	0	0
7	Н	58	Total O 58 58	0	0



3 Residue-property plots (i)

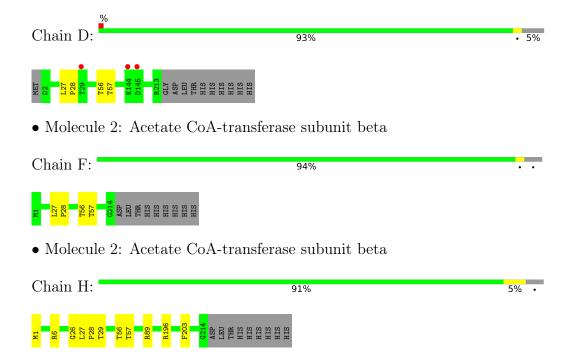
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Acetate CoA-transferase subunit alpha



• Molecule 2: Acetate CoA-transferase subunit beta







4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	73.68Å 175.68Å 76.16Å	Donositor
a, b, c, α , β , γ	90.00° 113.01° 90.00°	Depositor
Resolution (Å)	44.32 - 2.55	Depositor
resolution (A)	87.84 - 2.55	EDS
% Data completeness	98.9 (44.32-2.55)	Depositor
(in resolution range)	98.9 (87.84-2.55)	EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	2.31 (at 2.55Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.188 , 0.221	Depositor
it, it free	0.192 , 0.223	DCC
R_{free} test set	2869 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	30.4	Xtriage
Anisotropy	0.023	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.38, 51.0	EDS
L-test for twinning ²	$< L > = 0.46, < L^2> = 0.29$	Xtriage
Estimated twinning fraction	0.045 for l,-k,h	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	25941	wwPDB-VP
Average B, all atoms (\mathring{A}^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.81% 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: PEG, PO4, CL, GOL

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	A	0.22	0/1615	0.44	0/2197	
1	С	0.22	0/1620	0.42	0/2203	
1	Е	0.21	0/1587	0.41	0/2160	
1	G	0.24	0/1622	0.48	0/2206	
2	В	0.22	0/1592	0.43	0/2158	
2	D	0.21	0/1565	0.42	0/2124	
2	F	0.22	0/1593	0.42	0/2160	
2	Н	0.22	0/1600	0.43	0/2167	
All	All	0.22	0/12794	0.43	0/17375	

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	1593	1630	1630	1	0
1	С	1598	1637	1639	2	0
1	Е	1565	1588	1588	7	0
1	G	1600	1638	1638	4	0
2	В	1567	1569	1568	4	0



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Mol	Chain	Non-H		H(added)	Clashes	Symm-Clashes
2	D	1540	1528	1529	2	0
2	F	1568	1569	1569	2	0
2	Н	1575	1594	1594	6	0
3	A	5	0	0	0	0
3	В	5	0	0	0	0
3	Е	5	0	0	0	0
3	G	5	0	0	0	0
3	Н	5	0	0	0	0
4	В	14	20	20	0	0
4	С	7	10	10	0	0
4	F	7	10	10	0	0
4	Н	7	10	10	0	0
5	Е	1	0	0	0	0
6	F	6	8	8	0	0
7	A	59	0	0	0	0
7	В	71	0	0	0	0
7	С	66	0	0	0	0
7	D	41	0	0	0	0
7	Е	35	0	0	0	0
7	F	60	0	0	0	0
7	G	67	0	0	1	0
7	Н	58	0	0	0	0
All	All	13130	12811	12813	27	0

The all-atom clash score is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clash score for this structure is 1.

The worst 5 of 27 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{aligned} & ext{Interatomic} \ & ext{distance} \ & ext{(Å)} \end{aligned}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:E:137:ASP:OD2	1:G:145:ARG:NH2	2.32	0.63
2:H:1:MET:O	2:H:6:ARG:NH1	2.38	0.56
1:E:158:ARG:NH2	1:E:193:VAL:HG11	2.23	0.53
1:A:67:ASN:HB3	1:A:69:ARG:HE	1.74	0.52
1:E:83:GLU:HG3	1:E:87:ARG:HE	1.75	0.51

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	\mathbf{ntiles}
1	A	213/221 (96%)	206 (97%)	6 (3%)	1 (0%)	29	40
1	С	213/221 (96%)	205 (96%)	7 (3%)	1 (0%)	29	40
1	E	211/221 (96%)	204 (97%)	6 (3%)	1 (0%)	29	40
1	G	213/221 (96%)	205 (96%)	7 (3%)	1 (0%)	29	40
2	В	211/223 (95%)	205 (97%)	6 (3%)	0	100	100
2	D	210/223 (94%)	204 (97%)	6 (3%)	0	100	100
2	F	212/223 (95%)	206 (97%)	6 (3%)	0	100	100
2	Н	212/223 (95%)	206 (97%)	6 (3%)	0	100	100
All	All	1695/1776~(95%)	1641 (97%)	50 (3%)	4 (0%)	47	60

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	С	173	ASN
1	Е	173	ASN
1	G	173	ASN
1	A	173	ASN

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	171/181 (94%)	170 (99%)	1 (1%)	86 92		



Continued	trom	mmoninonic	maaa
COHABABACA		DIEUIUU	DUIUE
0 0 1000100000			

Mol	Chain	Analysed	Rotameric Outliers		Perce	ntiles
1	C	173/181~(96%)	173 (100%)	0	100	100
1	E	166/181~(92%)	166 (100%)	0	100	100
1	G	$174/181\ (96\%)$	173 (99%)	1 (1%)	86	92
2	В	160/173~(92%)	158 (99%)	2 (1%)	69	80
2	D	155/173~(90%)	155 (100%)	0	100	100
2	F	$159/173\ (92\%)$	159 (100%)	0	100	100
2	Н	161/173~(93%)	161 (100%)	0	100	100
All	All	$1319/1416 \ (93\%)$	1315 (100%)	4 (0%)	92	96

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	ASP
2	В	130	THR
2	В	213	ARG
1	G	136	LEU

Sometimes 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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 1 is monoatomic - leaving 11 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).

Mal	Trino	Chain	Res	Link	В	ond leng	$_{ m gths}$	В	ond ang	gles
Mol	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	PO4	A	301	-	4,4,4	0.92	0	6,6,6	0.43	0
4	PEG	F	301	-	6,6,6	0.28	0	5,5,5	0.24	0
6	GOL	F	302	-	5,5,5	0.38	0	5,5,5	0.18	0
4	PEG	Н	301	-	6,6,6	0.29	0	5,5,5	0.27	0
3	PO4	Е	302	-	4,4,4	0.91	0	6,6,6	0.43	0
3	PO4	Н	302	-	4,4,4	0.90	0	6,6,6	0.42	0
4	PEG	В	301	-	6,6,6	0.26	0	5,5,5	0.29	0
4	PEG	С	301	-	6,6,6	0.27	0	5,5,5	0.27	0
3	PO4	G	301	-	4,4,4	0.91	0	6,6,6	0.43	0
3	PO4	В	303	-	4,4,4	0.90	0	6,6,6	0.42	0
4	PEG	В	302	-	6,6,6	0.28	0	5,5,5	0.28	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	PEG	F	301	-	-	0/4/4/4	-
4	PEG	Н	301	-	-	0/4/4/4	-
4	PEG	В	301	_	-	1/4/4/4	-
4	PEG	С	301	_	-	0/4/4/4	-
6	GOL	F	302	-	-	2/4/4/4	_
4	PEG	В	302	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

\mathbf{M}	ol	Chain	Res	Type	Atoms
6	;	F	302	GOL	O1-C1-C2-C3
6	j	F	302	GOL	O1-C1-C2-O2



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M	ol	Chain	Res	Type	Atoms
4	1	В	301	PEG	O1-C1-C2-O2

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>	# RSRZ > 2	$OWAB(A^2)$	Q < 0.9
1	A	$215/221 \ (97\%)$	0.08	1 (0%) 91 94	21, 38, 62, 72	0
1	С	215/221 (97%)	-0.09	1 (0%) 91 94	15, 30, 47, 59	0
1	E	213/221 (96%)	0.18	1 (0%) 91 94	21, 46, 80, 91	0
1	G	215/221 (97%)	0.00	0 100 100	14, 31, 53, 66	0
2	В	213/223 (95%)	0.01	1 (0%) 91 94	19, 35, 58, 72	0
2	D	212/223~(95%)	0.23	3 (1%) 75 81	19, 45, 72, 86	0
2	F	214/223 (95%)	-0.10	0 100 100	19, 33, 55, 64	0
2	Н	214/223 (95%)	-0.05	0 100 100	16, 32, 56, 64	0
All	All	1711/1776 (96%)	0.03	7 (0%) 92 96	14, 36, 64, 91	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Ε	66	VAL	2.6
2	D	145	ASP	2.5
1	A	23	VAL	2.2
2	D	29	THR	2.2
1	С	86	ARG	2.1

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	PEG	F	301	7/7	0.79	0.19	50,61,63,63	0
4	PEG	В	302	7/7	0.80	0.20	57,68,70,70	0
5	CL	Ε	301	1/1	0.80	0.15	62,62,62,62	0
4	PEG	Н	301	7/7	0.82	0.26	47,57,61,61	0
3	PO4	Н	302	5/5	0.83	0.19	83,83,83,83	0
4	PEG	С	301	7/7	0.84	0.22	51,62,63,64	0
4	PEG	В	301	7/7	0.87	0.17	46,56,58,58	0
6	GOL	F	302	6/6	0.89	0.18	46,55,57,59	0
3	PO4	G	301	5/5	0.95	0.15	67,67,68,68	0
3	PO4	A	301	5/5	0.95	0.14	63,63,64,64	0
3	PO4	Е	302	5/5	0.95	0.14	77,77,77,77	0
3	PO4	В	303	5/5	0.96	0.16	63,63,63,63	0

6.5 Other polymers (i)

There are no such residues in this entry.

