

Full wwPDB X-ray Structure Validation Report (i)

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PDB ID	:	3H84
Title	:	Crystal structure of GET3
Authors	:	Hu, J.; Li, J.; Qian, X.; Sha, B.
Deposited on	:	2009-04-28
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* 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
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 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575(2.30-2.30)
Sidechain outliers	138945	5575(2.30-2.30)
RSRZ outliers	127900	4938 (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 >=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	354	9%	18%	·	8%		
1	В	354	15%	18%	·	9%		



2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 5405 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 ATPase GET3.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	А	326	Total 2547	C 1600	N 428	O 502	S 17	0	0	0
1	В	323	Total 2526	C 1598	N 420	0 491	S 17	0	0	0

• Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	1	Total Zn 1 1	0	0

• Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	Total Mg 1 1	0	0
3	В	1	Total Mg 1 1	0	0

• Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	3	Total Na 3 3	0	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	В	2	Total 2	Cl 2	0	0

• Molecule 6 is water.



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	202	Total O 202 202	0	0
6	В	122	Total O 122 122	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: ATPase GET3



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants	219.40Å 113.74Å 48.37Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Bosolution (Å)	50.00 - 2.30	Depositor
Resolution (A)	49.41 - 2.30	EDS
% Data completeness	99.3 (50.00-2.30)	Depositor
(in resolution range)	99.3 (49.41-2.30)	EDS
R _{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) > 1$	3.24 (at 2.29 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R R.	0.222 , 0.247	Depositor
n, n_{free}	0.220 , 0.246	DCC
R_{free} test set	2763 reflections $(5.06%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	42.3	Xtriage
Anisotropy	0.258	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.32 , 48.2	EDS
L-test for $twinning^2$	$ < L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5405	wwPDB-VP
Average B, all atoms $(Å^2)$	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.59% 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: MG, NA, CL, ZN

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).

Mal	Chain	Bond	lengths	Bond angles		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.39	0/2588	0.58	0/3491	
1	В	0.38	0/2569	0.55	0/3466	
All	All	0.38	0/5157	0.57	0/6957	

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	2547	0	2514	46	0
1	В	2526	0	2512	47	0
2	А	1	0	0	0	0
3	А	1	0	0	0	0
3	В	1	0	0	0	0
4	А	3	0	0	0	0
5	В	2	0	0	0	0
6	А	202	0	0	0	0
6	B	122	0	0	1	0
All	All	5405	0	5026	90	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 9.

All (90) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

A + 1	A + 2	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:B:157:GLY:H	1:B:158:GLU:HA	1.26	0.97
1:A:17:THR:HG22	1:A:234:ASP:O	1.69	0.92
1:A:324:LEU:O	1:A:328:THR:HG23	1.71	0.90
1:A:189:LYS:CB	1:A:190:PHE:HA	2.02	0.88
1:B:10:HIS:HD2	1:B:335:ASN:HD21	1.22	0.88
1:A:189:LYS:HB2	1:A:190:PHE:HA	1.56	0.87
1:B:324:LEU:O	1:B:328:THR:HG23	1.84	0.77
1:A:291:ARG:O	1:A:294:MET:HG3	1.88	0.74
1:B:157:GLY:N	1:B:158:GLU:HA	1.94	0.69
1:B:196:LYS:HG2	1:B:197:LEU:H	1.65	0.62
1:A:29:VAL:HG13	1:A:241:VAL:HG12	1.82	0.62
1:B:15:SER:OG	1:B:18:HIS:HD2	1.84	0.61
1:B:7:PRO:HG2	1:B:337:GLU:HG2	1.83	0.61
1:B:10:HIS:CD2	1:B:335:ASN:HD21	2.11	0.60
1:B:146:MET:HA	1:B:146:MET:HE2	1.83	0.59
1:B:196:LYS:CG	1:B:197:LEU:H	2.16	0.58
1:B:317:CYS:SG	1:B:321:ILE:HD11	2.43	0.58
1:A:320:GLU:HG2	1:A:321:ILE:N	2.18	0.57
1:A:7:PRO:HG2	1:A:337:GLU:HG2	1.85	0.57
1:A:56:THR:CG2	1:A:168:ALA:HB2	2.34	0.57
1:B:259:LEU:HD13	1:B:266:VAL:HG11	1.89	0.55
1:A:142:PHE:HA	1:A:145:VAL:HG13	1.89	0.55
1:B:281:GLN:O	1:B:282:GLU:HB3	2.06	0.55
1:B:196:LYS:CG	1:B:197:LEU:N	2.70	0.54
1:A:189:LYS:CB	1:A:190:PHE:CA	2.83	0.54
1:B:299:LEU:HD22	1:B:313:LYS:HE2	1.89	0.54
1:A:317:CYS:SG	1:A:321:ILE:HD11	2.48	0.54
1:A:246:PHE:HE2	1:B:26:LYS:HE2	1.73	0.53
1:A:320:GLU:HG3	1:A:322:ARG:HG3	1.90	0.53
1:A:15:SER:OG	1:A:18:HIS:HD2	1.92	0.53
1:A:252:THR:O	1:A:256:ILE:HG12	2.10	0.52
1:A:29:VAL:HA	1:A:243:ILE:HD13	1.90	0.52
1:B:281:GLN:NE2	1:B:281:GLN:HA	2.25	0.52
1:A:20:TRP:HB2	1:A:236:THR:HG23	1.91	0.52
1:B:145:VAL:O	1:B:149:ILE:HG12	2.10	0.52
1:A:324:LEU:O	1:A:328:THR:CG2	2.54	0.51
1:A:146:MET:HA	1:A:146:MET:HE2	1.92	0.51
1:A:281:GLN:O	1:A:282:GLU:HB2	2.10	0.51



	io de page	Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:B:49:LYS:O	1:B:82:ASN:OD1	2.29	0.51	
1:B:284:ASN:HD22	1:B:284:ASN:N	2.09	0.51	
1:A:152:GLN:C	1:A:154:GLN:H	2.14	0.51	
1:B:122:GLN:HE21	1:B:215:LYS:HB2	1.75	0.51	
1:B:281:GLN:HA	1:B:281:GLN:HE21	1.76	0.50	
1:B:179:LEU:N	1:B:180:PRO:HD2	2.26	0.50	
1:A:246:PHE:CD2	1:B:27:GLY:HA2	2.47	0.50	
1:B:157:GLY:N	1:B:158:GLU:CA	2.72	0.50	
1:A:69:LYS:H	1:A:69:LYS:CD	2.24	0.49	
1:B:238:PHE:HB3	1:B:266:VAL:HG12	1.95	0.48	
1:B:29:VAL:HG13	1:B:241:VAL:HG12	1.94	0.48	
1:A:292:TRP:NE1	1:A:296:LYS:HD2	2.29	0.48	
1:B:281:GLN:O	1:B:282:GLU:CB	2.61	0.48	
1:A:27:GLY:HA2	1:B:246:PHE:CD2	2.49	0.48	
1:A:69:LYS:H	1:A:69:LYS:HD3	1.80	0.47	
1:B:20:TRP:HB2	1:B:236:THR:HG23	1.95	0.47	
1:A:254:ARG:NH2	1:A:258:GLU:OE1	2.48	0.47	
1:B:77:VAL:HG22	1:B:80:MET:HG3	1.96	0.47	
1:A:176:PHE:O	1:A:179:LEU:HB2	2.15	0.47	
1:A:64:ASP:OD1	1:A:322:ARG:NH1	2.48	0.47	
1:B:324:LEU:O	1:B:328:THR:CG2	2.58	0.46	
1:B:345:LYS:O	1:B:349:GLU:HB3	2.16	0.45	
1:A:222:ASN:O	1:A:226:ILE:HG12	2.16	0.45	
1:A:56:THR:HG22	1:A:168:ALA:HB2	1.98	0.45	
1:B:10:HIS:HD2	1:B:335:ASN:ND2	2.03	0.45	
1:B:278:GLU:OE1	1:B:292:TRP:HZ3	2.00	0.44	
1:A:146:MET:CE	1:A:149:ILE:HD12	2.48	0.44	
1:B:201:LEU:O	1:B:205:MET:HG2	2.18	0.44	
1:B:6:GLU:O	1:B:310:HIS:HD2	2.01	0.44	
1:A:72:LYS:HA	1:A:88:ILE:HG22	2.01	0.43	
1:B:238:PHE:HB3	1:B:266:VAL:CG1	2.48	0.43	
1:A:178:GLN:O	1:A:182:THR:HG23	2.19	0.43	
1:B:43:ALA:O	1:B:82:ASN:ND2	2.51	0.42	
1:B:347:ILE:C	1:B:349:GLU:H	2.23	0.42	
1:A:189:LYS:HB3	1:A:190:PHE:HA	1.96	0.42	
1:A:339:ASN:HA	1:A:340:PRO:HD2	1.93	0.42	
1:A:54:ILE:HD11	1:A:88:ILE:CD1	2.50	0.42	
1:B:196:LYS:HE2	1:B:201:LEU:HD23	2.02	0.42	
1:B:50:GLN:NE2	6:B:379:HOH:O	2.53	0.41	
1:B:275:LEU:HD11	1:B:291:ARG:HD3	2.01	0.41	
1:A:73:ASP:O	1:A:75:ARG:HD3	2.21	0.41	



Atom_1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:115:ASP:HA	1:A:116:ASP:HA	1.80	0.41
1:B:259:LEU:CD1	1:B:266:VAL:HG11	2.50	0.41
1:B:306:TYR:HB3	1:B:309:PHE:HB2	2.02	0.41
1:A:292:TRP:CE2	1:A:296:LYS:HD2	2.56	0.41
1:B:292:TRP:CH2	1:B:296:LYS:HD3	2.56	0.41
1:A:181:ASN:O	1:A:185:LYS:HG2	2.20	0.41
1:A:146:MET:HE1	1:A:149:ILE:HD12	2.02	0.40
1:A:133:ILE:HA	1:A:134:PRO:HD2	1.95	0.40
1:A:211:ASP:O	1:A:215:LYS:HG2	2.21	0.40
1:A:320:GLU:CG	1:A:322:ARG:HG3	2.51	0.40
1:B:344:GLY:O	1:B:348:TYR:HD2	2.03	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	А	322/354~(91%)	297~(92%)	19~(6%)	6(2%)	8 7
1	В	319/354~(90%)	303~(95%)	12~(4%)	4 (1%)	12 12
All	All	641/708~(90%)	600 (94%)	31 (5%)	10 (2%)	99

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	281	GLN
1	А	282	GLU
1	В	283	HIS
1	А	113	GLN
1	А	280	ASP
1	В	282	GLU
1	В	285	CYS



Continued from previous page...

Mol	Chain	Res	Type
1	В	212	ILE
1	А	285	CYS
1	А	321	ILE

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	Perce	ntiles
1	А	286/309~(93%)	265~(93%)	21 (7%)	14	18
1	В	284/309~(92%)	265~(93%)	19 (7%)	16	21
All	All	570/618~(92%)	530~(93%)	40 (7%)	15	19

All (40) residues with a non-rotameric side chain are listed below:

Mol	Chain	Res	Type
1	А	12	LEU
1	А	29	VAL
1	А	52	LEU
1	А	56	THR
1	А	69	LYS
1	А	77	VAL
1	А	88	ILE
1	А	115	ASP
1	А	145	VAL
1	А	159	THR
1	А	177	LEU
1	А	216	LEU
1	А	243	ILE
1	А	247	LEU
1	А	249	LEU
1	А	254	ARG
1	А	255	LEU
1	А	264	MET
1	А	312	VAL
1	А	328	THR



Mol	Chain	Res	Type
1	А	342	THR
1	В	12	LEU
1	В	29	VAL
1	В	32	THR
1	В	77	VAL
1	В	129	LEU
1	В	158	GLU
1	В	162	THR
1	В	183	LEU
1	В	218	GLU
1	В	255	LEU
1	В	264	MET
1	В	281	GLN
1	В	284	ASN
1	В	287	ARG
1	В	305	LEU
1	В	312	VAL
1	В	320	GLU
1	В	324	LEU
1	В	328	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	18	HIS
1	А	46	GLN
1	А	60	HIS
1	А	148	HIS
1	А	257	GLN
1	А	332	GLN
1	В	10	HIS
1	В	18	HIS
1	В	46	GLN
1	В	50	GLN
1	В	122	GLN
1	В	154	GLN
1	В	202	ASN
1	В	281	GLN
1	В	284	ASN
1	В	301	GLN
1	В	310	HIS
1	В	332	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)

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 8 ligands modelled in this entry, 8 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 (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	2	$\mathbf{OWAB}(\mathbf{A}^2)$	Q<0.9
1	А	326/354~(92%)	0.79	31 (9%) 8	11	39, 47, 68, 76	0
1	В	323/354~(91%)	0.99	54 (16%) 1	2	40, 49, 66, 70	0
All	All	649/708~(91%)	0.89	85 (13%) 3	4	39, 48, 67, 76	0

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	281	GLN	10.8
1	А	113	GLN	9.0
1	В	120	LEU	8.5
1	В	280	ASP	7.6
1	А	283	HIS	7.4
1	А	190	PHE	7.4
1	В	283	HIS	7.4
1	А	280	ASP	7.2
1	А	115	ASP	7.2
1	В	284	ASN	6.9
1	В	197	LEU	5.5
1	А	282	GLU	5.4
1	В	282	GLU	5.4
1	А	114	GLY	5.4
1	В	205	MET	5.3
1	А	156	GLU	5.1
1	В	204	PHE	5.1
1	А	284	ASN	5.0
1	В	195	ASN	5.0
1	А	157	GLY	4.7
1	В	126	LEU	4.7
1	В	190	PHE	4.5
1	В	192	GLU	4.4
1	В	121	LEU	4.3



Mol	Chain	Res Type		RSRZ	
1	А	155 GLY		4.2	
1	В	200	MET	4.0	
1	А	108	ASN	4.0	
1	В	214	GLY	3.9	
1	В	158	GLU	3.9	
1	В	318	ALA	3.9	
1	В	207	ALA	3.9	
1	А	279	ASN	3.9	
1	В	286	LYS	3.8	
1	А	318	ALA	3.7	
1	В	196	LYS	3.6	
1	А	112	GLY	3.6	
1	В	154	GLN	3.6	
1	В	91	SER	3.5	
1	В	187	LEU	3.5	
1	А	116	ASP	3.5	
1	В	228	GLN	3.2	
1	В	279	ASN	3.2	
1	В	157	GLY	3.2	
1	В	208	GLY	3.2	
1	А	117	LEU	3.1	
1	А	320	GLU	3.1	
1	В	156	GLU	3.1	
1	В	119	SER	3.1	
1	В	191	GLY	3.0	
1	В	155	GLY	2.8	
1	В	117	LEU	2.7	
1	В	183	LEU	2.7	
1	В	186	LEU	2.7	
1	A	111	ASP	2.7	
1	A	277	ALA	2.7	
1	В	159	THR	2.7	
1	В	218	GLU	2.7	
1	A	286	LYS	2.7	
1	В	150	LYS	2.7	
1	В	125	ALA	2.5	
1	A	278	GLU	2.5	
1	A	349	GLU	2.4	
1	В	122	GLN	2.4	
1	В	291	ARG	2.4	
1	В	320	GLU	2.4	
1	A	281	GLN	2.3	



Mol	Chain	Res	Type	RSRZ
1	В	226	ILE	2.2
1	В	133	ILE	2.2
1	В	201	LEU	2.2
1	В	194	THR	2.2
1	В	199	PRO	2.2
1	В	209	ASN	2.2
1	В	193	ILE	2.2
1	В	216	LEU	2.2
1	А	218	GLU	2.2
1	А	350	LEU	2.1
1	А	348	TYR	2.1
1	В	225	THR	2.1
1	А	23	VAL	2.1
1	А	77	VAL	2.1
1	В	293	LYS	2.1
1	В	212	ILE	2.1
1	А	36	CYS	2.1
1	В	348	TYR	2.0
1	А	285	CYS	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	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	Q<0.9
4	NA	А	358	1/1	0.87	0.17	46,46,46,46	0
5	CL	В	357	1/1	0.89	0.16	$67,\!67,\!67,\!67$	0
4	NA	А	357	1/1	0.90	0.21	58, 58, 58, 58	0
5	CL	В	356	1/1	0.93	0.08	73,73,73,73	0



Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-factors}(\mathrm{\AA}^2)$	Q<0.9
3	MG	В	355	1/1	0.93	0.39	40,40,40,40	0
4	NA	А	359	1/1	0.95	0.22	$53,\!53,\!53,\!53$	0
2	ZN	А	355	1/1	0.98	0.03	$54,\!54,\!54,\!54$	0
3	MG	А	356	1/1	0.98	0.41	30,30,30,30	0

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6.5 Other polymers (i)

There are no such residues in this entry.

