



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:47 AM UTC

PDB ID : 5T00 / pdb_00005t00
Title : Human CTCF ZnF3-7 and methylated DNA complex
Authors : Hashimoto, H.; Wang, D.; Cheng, X.
Deposited on : 2016-08-15
Resolution : 2.19 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

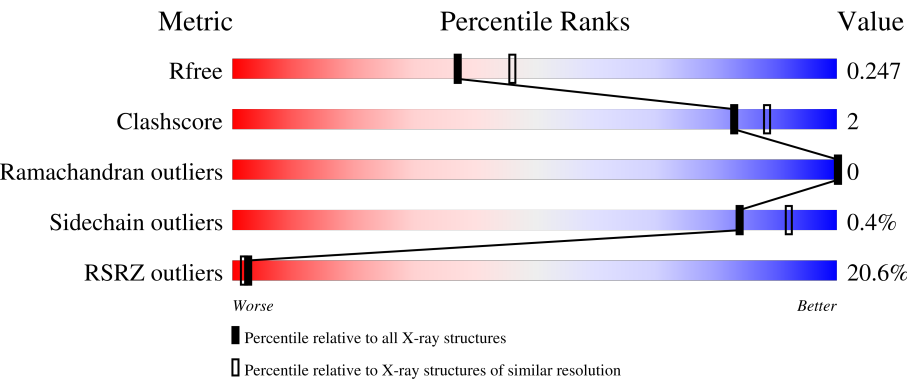
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.19 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}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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 $\leq 5\%$. 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	150	14% 89%6%5%
1	D	150	34% 90%5%5%
2	B	17	94%6%
2	E	17	88%12%
3	C	17	88%12%

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Mol	Chain	Length	Quality of chain
3	F	17	76% 18% 6%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6860 atoms, of which 3028 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 Transcriptional repressor CTCF.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	143	Total	C	H	N	O	S	0	0	0
			2306	726	1135	228	202	15			
1	D	143	Total	C	H	N	O	S	0	0	0
			2289	723	1121	226	204	15			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	316	GLY	-	expression tag	UNP P49711
A	317	PRO	-	expression tag	UNP P49711
A	318	LEU	-	expression tag	UNP P49711
A	319	GLY	-	expression tag	UNP P49711
A	320	SER	-	expression tag	UNP P49711
D	316	GLY	-	expression tag	UNP P49711
D	317	PRO	-	expression tag	UNP P49711
D	318	LEU	-	expression tag	UNP P49711
D	319	GLY	-	expression tag	UNP P49711
D	320	SER	-	expression tag	UNP P49711

- Molecule 2 is a DNA chain called DNA (5'-TAG(5CM)GCCCCCTGCTGGC-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	17	Total	C	H	N	O	P	0	0	0
			535	163	194	60	102	16			
2	E	17	Total	C	H	N	O	P	0	0	0
			535	163	194	60	102	16			

- Molecule 3 is a DNA chain called DNA (5'-GCCAGCAGGGGG(5CM)GCTA-3').

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	17	Total	C	H	N	O	P	0	0	0
			544	166	192	72	98	16			

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	F	17	Total	C	H	N	O	P	0	0	0
			544	166	192	72	98	16			

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	5	Total	Zn	0	0
			5	5		
4	D	5	Total	Zn	0	0
			5	5		

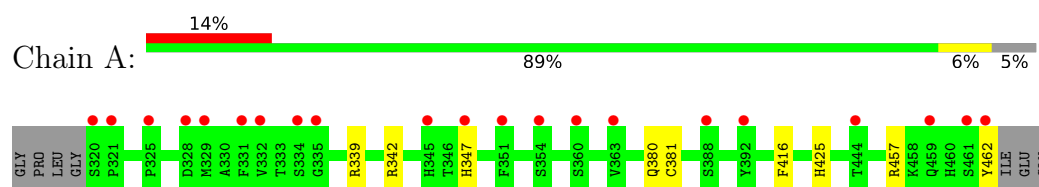
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	28	Total	O	0	0
			28	28		
5	B	22	Total	O	0	0
			22	22		
5	C	13	Total	O	0	0
			13	13		
5	D	15	Total	O	0	0
			15	15		
5	E	10	Total	O	0	0
			10	10		
5	F	9	Total	O	0	0
			9	9		

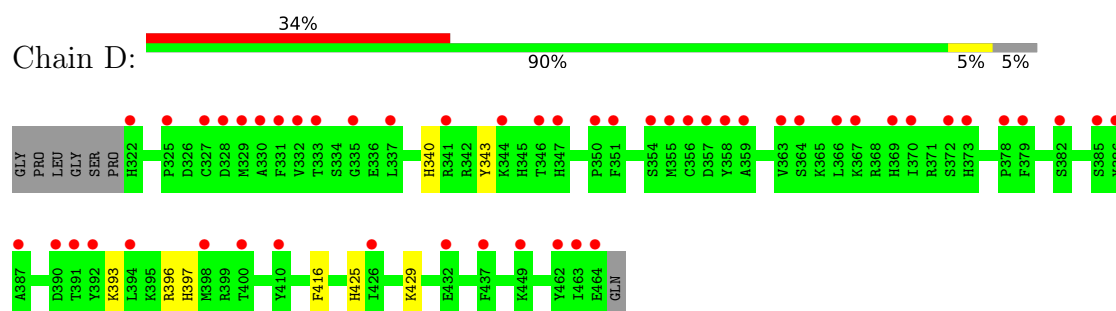
3 Residue-property plots [i](#)

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.

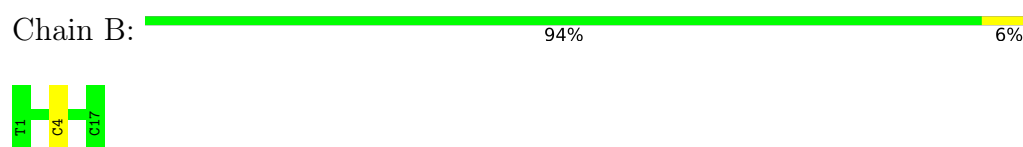
- Molecule 1: Transcriptional repressor CTCF



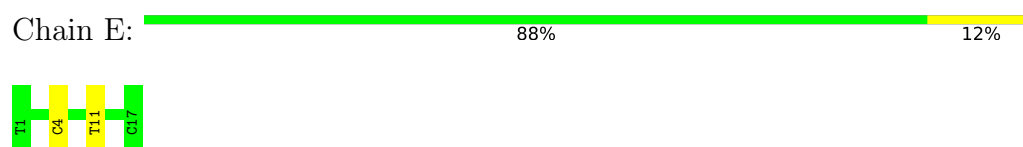
- Molecule 1: Transcriptional repressor CTCF



- Molecule 2: DNA (5'-TAG(5CM)GCCCCCTGCTGGC-3')

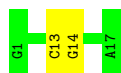


- Molecule 2: DNA (5'-TAG(5CM)GCCCCCTGCTGGC-3')



- Molecule 3: DNA (5'-GCCAGCAGGGGG(5CM)GCTA-3')





- Molecule 3: DNA (5'-GCCAGCAGGGGG(5CM)GCTA-3')

Chain F:  76% 18% 6%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	40.99Å 44.91Å 86.80Å 98.33° 92.40° 94.80°	Depositor
Resolution (Å)	41.96 – 2.19 41.96 – 2.19	Depositor EDS
% Data completeness (in resolution range)	98.7 (41.96-2.19) 97.2 (41.96-2.19)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 2.18Å)	Xtriage
Refinement program	PHENIX (dev_2257: ???)	Depositor
R, R_{free}	0.218 , 0.243 0.225 , 0.247	Depositor DCC
R_{free} test set	1566 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	42.0	Xtriage
Anisotropy	0.025	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 41.9	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	0.95	EDS
Total number of atoms	6860	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.96% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

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: ZN, 5CM

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	0.13	0/1203	0.32	0/1612
1	D	0.11	0/1199	0.27	0/1608
2	B	0.21	0/357	0.47	0/546
2	E	0.19	0/357	0.46	0/546
3	C	0.23	0/373	0.44	0/573
3	F	0.21	0/373	0.40	0/573
All	All	0.16	0/3862	0.36	0/5458

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	1171	1135	1135	5	0
1	D	1168	1121	1121	6	0
2	B	341	194	194	0	0
2	E	341	194	194	1	0
3	C	352	192	192	1	0
3	F	352	192	192	6	0
4	A	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	5	0	0	0	0
5	A	28	0	0	0	0
5	B	22	0	0	0	0
5	C	13	0	0	0	0
5	D	15	0	0	1	0
5	E	10	0	0	1	0
5	F	9	0	0	2	0
All	All	3832	3028	3028	14	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 2.

All (14) 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)
2:E:11:DT:OP2	5:E:101:HOH:O	2.06	0.74
1:D:393:LYS:NZ	3:F:10:DG:O6	2.23	0.71
1:A:339:ARG:NH1	3:C:14:DG:N7	2.45	0.61
3:F:2:DC:OP1	5:F:101:HOH:O	2.16	0.58
3:F:10:DG:OP2	5:F:102:HOH:O	2.17	0.57
1:D:396:ARG:NH1	3:F:7:DA:N7	2.52	0.55
1:D:340:HIS:ND1	3:F:13:5CM:OP1	2.41	0.51
1:A:457:ARG:HA	1:A:462:TYR:HB2	1.98	0.46
1:D:416:PHE:CZ	1:D:425:HIS:CG	3.04	0.45
1:A:342:ARG:O	1:A:347:HIS:HA	2.18	0.43
1:D:429:LYS:NZ	5:D:603:HOH:O	2.50	0.43
1:D:397:HIS:ND1	3:F:7:DA:OP1	2.47	0.43
1:A:380:GLN:NE2	1:A:381:CYS:O	2.45	0.42
1:A:416:PHE:CZ	1:A:425:HIS:CG	3.08	0.41

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	A	141/150 (94%)	137 (97%)	4 (3%)	0	100	100
1	D	141/150 (94%)	138 (98%)	3 (2%)	0	100	100
All	All	282/300 (94%)	275 (98%)	7 (2%)	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	131/137 (96%)	131 (100%)	0	100	100
1	D	130/137 (95%)	129 (99%)	1 (1%)	73	85
All	All	261/274 (95%)	260 (100%)	1 (0%)	84	92

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	343	TYR

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

Mol	Chain	Res	Type
1	A	347	HIS
1	D	441	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	5CM	E	4	3,2	18,21,22	0.59	0	24,30,33	0.84	2 (8%)
2	5CM	B	4	3,2	18,21,22	0.61	0	24,30,33	0.90	2 (8%)
3	5CM	F	13	3,2	18,21,22	0.61	0	24,30,33	0.90	1 (4%)
3	5CM	C	13	3,2	18,21,22	0.62	0	24,30,33	0.96	1 (4%)

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	5CM	E	4	3,2	-	2/7/21/22	0/2/2/2
2	5CM	B	4	3,2	-	0/7/21/22	0/2/2/2
3	5CM	F	13	3,2	-	0/7/21/22	0/2/2/2
3	5CM	C	13	3,2	-	0/7/21/22	0/2/2/2

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	13	5CM	C5A-C5-C4	2.19	124.11	120.51
2	B	4	5CM	C5A-C5-C4	2.14	124.03	120.51
2	E	4	5CM	C5A-C5-C4	2.14	124.03	120.51
2	B	4	5CM	C5A-C5-C6	-2.04	120.09	122.85
2	E	4	5CM	C5A-C5-C6	-2.01	120.13	122.85
3	F	13	5CM	C5A-C5-C4	2.00	123.80	120.51

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	4	5CM	C3'-C4'-C5'-O5'
2	E	4	5CM	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	13	5CM	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 10 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 ⓘ

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, 95th 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 ²)	Q<0.9
1	A	143/150 (95%)	1.06	21 (14%)	6 4	31, 57, 113, 139	0
1	D	143/150 (95%)	1.70	51 (35%)	1 0	35, 93, 142, 154	0
2	B	16/17 (94%)	0.22	0	100 100	42, 53, 88, 96	0
2	E	16/17 (94%)	0.24	0	100 100	44, 67, 101, 104	0
3	C	16/17 (94%)	0.02	0	100 100	34, 41, 93, 97	0
3	F	16/17 (94%)	0.08	0	100 100	35, 71, 101, 112	0
All	All	350/368 (95%)	1.15	72 (20%)	2 2	31, 68, 127, 154	0

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	463	ILE	5.2
1	A	332	VAL	5.0
1	A	461	SER	4.9
1	D	330	ALA	4.5
1	A	462	TYR	4.4
1	D	332	VAL	4.1
1	A	320	SER	4.1
1	D	366	LEU	4.0
1	D	370	ILE	3.7
1	D	329	MET	3.7
1	D	325	PRO	3.6
1	D	387	ALA	3.6
1	D	322	HIS	3.6
1	D	378	PRO	3.5
1	D	355	MET	3.5
1	D	346	THR	3.4
1	D	385	SER	3.4
1	D	328	ASP	3.4
1	D	426	ILE	3.4

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Mol	Chain	Res	Type	RSRZ
1	D	367	LYS	3.4
1	D	331	PHE	3.2
1	D	347	HIS	3.2
1	D	373	HIS	3.2
1	D	394	LEU	3.1
1	D	400	THR	3.1
1	A	321	PRO	3.0
1	D	372	SER	3.0
1	A	351	PHE	2.9
1	D	379	PHE	2.9
1	D	382	SER	2.9
1	A	335	GLY	2.9
1	A	328	ASP	2.8
1	D	359	ALA	2.8
1	D	391	THR	2.8
1	D	341	ARG	2.7
1	A	360	SER	2.7
1	D	386	TYR	2.7
1	D	350	PRO	2.6
1	D	390	ASP	2.6
1	A	459	GLN	2.5
1	D	392	TYR	2.5
1	A	345	HIS	2.5
1	D	432	GLU	2.5
1	A	331	PHE	2.5
1	D	462	TYR	2.5
1	D	357	ASP	2.4
1	A	363	VAL	2.4
1	D	327	CYS	2.3
1	A	392	TYR	2.3
1	A	325	PRO	2.3
1	A	444	THR	2.3
1	D	356	CYS	2.3
1	D	364	SER	2.3
1	D	363	VAL	2.3
1	D	344	LYS	2.3
1	D	369	HIS	2.2
1	A	354	SER	2.2
1	D	354	SER	2.2
1	D	437	PHE	2.2
1	D	333	THR	2.2
1	D	398	MET	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	335	GLY	2.2
1	A	347	HIS	2.2
1	D	358	TYR	2.2
1	D	449	LYS	2.2
1	A	334	SER	2.1
1	A	329	MET	2.1
1	A	388	SER	2.1
1	D	337	LEU	2.1
1	D	464	GLU	2.1
1	D	410	TYR	2.1
1	D	351	PHE	2.1

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, 95th 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 ²)	Q<0.9
2	5CM	B	4	20/21	0.86	0.12	67,72,87,87	0
2	5CM	E	4	20/21	0.87	0.12	88,104,122,125	0
3	5CM	F	13	20/21	0.91	0.11	62,74,92,93	0
3	5CM	C	13	20/21	0.92	0.12	60,73,96,97	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, 95th 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 ²)	Q<0.9
4	ZN	D	502	1/1	0.96	0.07	93,93,93,93	0
4	ZN	D	503	1/1	0.97	0.08	74,74,74,74	0
4	ZN	D	501	1/1	0.98	0.04	89,89,89,89	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	ZN	A	501	1/1	0.98	0.04	72,72,72,72	0
4	ZN	A	502	1/1	0.98	0.03	46,46,46,46	0
4	ZN	D	505	1/1	0.98	0.04	39,39,39,39	0
4	ZN	A	503	1/1	0.99	0.03	45,45,45,45	0
4	ZN	D	504	1/1	0.99	0.03	54,54,54,54	0
4	ZN	A	504	1/1	0.99	0.03	38,38,38,38	0
4	ZN	A	505	1/1	1.00	0.03	47,47,47,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.