



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:21 AM UTC

PDB ID : 5E6D / pdb_00005e6d
Title : Glucocorticoid receptor DNA binding domain - ICAM1 NF-kB response element complex
Authors : Hudson, W.H.; Rye, E.A.; Herbst, A.G.; Ortlund, E.A.
Deposited on : 2015-10-09
Resolution : 2.40 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
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

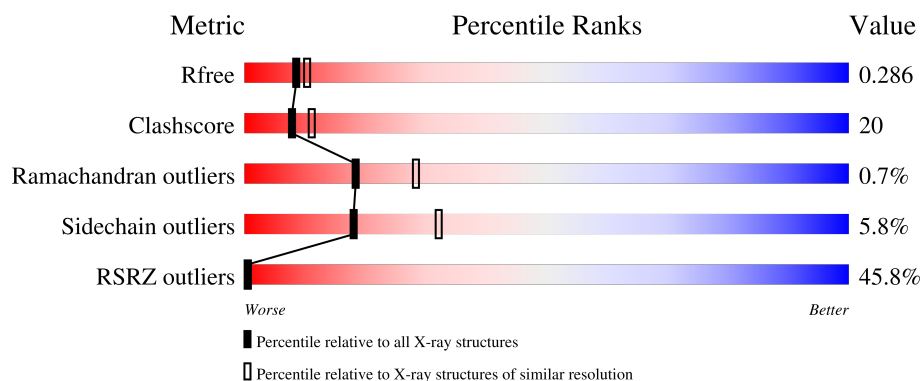
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	C	16	44% 75% 25%
2	D	16	56% 44% 56%
3	A	114	29% 41% 21% 36%
3	B	114	28% 42% 14% 6% 37%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 1786 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 DNA chain called DNA (5'-D(*GP*CP*TP*CP*CP*GP*GP*AP*AP*TP*TP*TP*CP*CP*AP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	16	Total	C	N	O	P	0	0	0
			322	155	58	94	15			

- Molecule 2 is a DNA chain called DNA (5'-D(*TP*TP*GP*GP*AP*AP*AP*TP*TP*CP*CP*GP*GP*AP*GP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	16	Total	C	N	O	P	0	0	0
			328	157	62	94	15			

- Molecule 3 is a protein called Glucocorticoid receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	73	Total	C	N	O	S	0	0	0
			560	344	107	98	11			
3	B	72	Total	C	N	O	S	0	0	0
			553	339	106	97	11			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	393	MET	-	initiating methionine	UNP P04150
A	394	HIS	-	expression tag	UNP P04150
A	395	HIS	-	expression tag	UNP P04150
A	396	HIS	-	expression tag	UNP P04150
A	397	HIS	-	expression tag	UNP P04150
A	398	HIS	-	expression tag	UNP P04150
A	399	HIS	-	expression tag	UNP P04150
A	400	SER	-	expression tag	UNP P04150
A	401	SER	-	expression tag	UNP P04150
A	402	GLY	-	expression tag	UNP P04150

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Chain	Residue	Modelled	Actual	Comment	Reference
A	403	VAL	-	expression tag	UNP P04150
A	404	ASP	-	expression tag	UNP P04150
A	405	LEU	-	expression tag	UNP P04150
A	406	GLY	-	expression tag	UNP P04150
A	407	THR	-	expression tag	UNP P04150
A	408	GLU	-	expression tag	UNP P04150
A	409	ASN	-	expression tag	UNP P04150
A	410	LEU	-	expression tag	UNP P04150
A	411	TYR	-	expression tag	UNP P04150
A	412	PHE	-	expression tag	UNP P04150
A	413	GLN	-	expression tag	UNP P04150
A	414	SER	-	expression tag	UNP P04150
A	415	ASN	-	expression tag	UNP P04150
A	416	ALA	-	expression tag	UNP P04150
B	393	MET	-	initiating methionine	UNP P04150
B	394	HIS	-	expression tag	UNP P04150
B	395	HIS	-	expression tag	UNP P04150
B	396	HIS	-	expression tag	UNP P04150
B	397	HIS	-	expression tag	UNP P04150
B	398	HIS	-	expression tag	UNP P04150
B	399	HIS	-	expression tag	UNP P04150
B	400	SER	-	expression tag	UNP P04150
B	401	SER	-	expression tag	UNP P04150
B	402	GLY	-	expression tag	UNP P04150
B	403	VAL	-	expression tag	UNP P04150
B	404	ASP	-	expression tag	UNP P04150
B	405	LEU	-	expression tag	UNP P04150
B	406	GLY	-	expression tag	UNP P04150
B	407	THR	-	expression tag	UNP P04150
B	408	GLU	-	expression tag	UNP P04150
B	409	ASN	-	expression tag	UNP P04150
B	410	LEU	-	expression tag	UNP P04150
B	411	TYR	-	expression tag	UNP P04150
B	412	PHE	-	expression tag	UNP P04150
B	413	GLN	-	expression tag	UNP P04150
B	414	SER	-	expression tag	UNP P04150
B	415	ASN	-	expression tag	UNP P04150
B	416	ALA	-	expression tag	UNP P04150

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total 2	Zn 2	0	0
4	B	2	Total 2	Zn 2	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	1	Total 1	O 1	0	0
5	A	9	Total 9	O 9	0	0
5	B	9	Total 9	O 9	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	39.06Å 97.14Å 104.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.66 – 2.40 32.66 – 2.40	Depositor EDS
% Data completeness (in resolution range)	97.7 (32.66-2.40) 97.7 (32.66-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.49 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.257 , 0.283 0.259 , 0.286	Depositor DCC
R_{free} test set	789 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	62.0	Xtriage
Anisotropy	0.279	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 73.0	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	0.92	EDS
Total number of atoms	1786	wwPDB-VP
Average B, all atoms (Å ²)	96.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.00% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	C	0.22	0/360	0.43	0/553
2	D	0.23	0/368	0.47	0/567
3	A	0.41	0/568	0.93	0/758
3	B	0.67	1/560 (0.2%)	1.12	4/747 (0.5%)
All	All	0.46	1/1856 (0.1%)	0.83	4/2625 (0.2%)

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
3	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	443	VAL	CA-C	5.16	1.60	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	444	PHE	N-CA-C	7.43	122.78	112.45
3	B	446	LYS	CB-CG-CD	-7.05	95.09	111.30
3	B	442	LYS	N-CA-C	6.70	121.16	112.92
3	B	443	VAL	N-CA-C	-5.62	107.26	112.83

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	B	445	PHE	Peptide

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	C	322	0	182	3	0
2	D	328	0	182	8	0
3	A	560	0	555	22	0
3	B	553	0	547	33	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
5	A	9	0	0	2	0
5	B	9	0	0	1	0
5	D	1	0	0	0	0
All	All	1786	0	1466	61	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 20.

All (61) 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)
3:B:442:LYS:C	3:B:446:LYS:HD3	2.02	0.84
3:A:473:CYS:SG	5:A:706:HOH:O	2.44	0.75
3:A:419:LYS:O	3:A:428:ALA:N	2.16	0.74
3:B:432:HIS:HB2	3:B:442:LYS:CD	2.18	0.73
3:A:426:ASP:OD1	3:A:427:GLU:N	2.23	0.71
3:B:438:CYS:O	3:B:442:LYS:HG3	1.91	0.70
3:B:433:TYR:CE2	3:B:446:LYS:NZ	2.60	0.69
3:A:424:CYS:HB3	3:A:441:CYS:SG	2.32	0.68
3:B:445:PHE:N	3:B:446:LYS:HD2	2.12	0.64
3:B:445:PHE:N	3:B:446:LYS:HB2	2.13	0.63
3:B:446:LYS:O	3:B:447:ARG:HB3	1.98	0.63
3:A:452:GLN:N	3:A:452:GLN:OE1	2.33	0.62
3:A:438:CYS:SG	3:A:440:SER:OG	2.55	0.61
3:B:432:HIS:HB2	3:B:442:LYS:HD2	1.81	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:453:HIS:HB2	5:A:704:HOH:O	2.02	0.60
2:D:14:DA:H2''	2:D:15:DG:H5''	1.84	0.59
3:B:421:CYS:SG	3:B:437:THR:HB	2.42	0.58
3:B:445:PHE:H	3:B:446:LYS:HD2	1.67	0.58
3:A:453:HIS:O	3:A:455:TYR:N	2.38	0.57
3:B:445:PHE:HB3	3:B:446:LYS:HE2	1.87	0.57
3:B:421:CYS:HA	3:B:437:THR:HA	1.87	0.57
3:A:462:ASP:OD2	3:B:460:ARG:NH2	2.37	0.56
3:B:432:HIS:HB2	3:B:442:LYS:HD3	1.89	0.55
3:B:445:PHE:HB3	3:B:446:LYS:CE	2.37	0.55
2:D:15:DG:H2''	2:D:16:DC:H5'	1.89	0.54
3:B:488:LEU:O	3:B:489:GLU:HG3	2.07	0.54
3:B:440:SER:HA	3:B:443:VAL:HG12	1.90	0.54
3:B:480:LYS:O	5:B:701:HOH:O	2.18	0.53
3:B:437:THR:HG23	3:B:442:LYS:HE3	1.90	0.53
3:B:444:PHE:C	3:B:446:LYS:HB2	2.34	0.53
1:C:7:DG:H2''	1:C:8:DA:C8	2.44	0.52
3:A:453:HIS:N	3:A:453:HIS:CD2	2.79	0.51
3:A:430:GLY:O	3:A:432:HIS:ND1	2.44	0.51
3:B:445:PHE:O	3:B:448:ALA:HB3	2.11	0.50
3:A:422:LEU:HD13	3:A:436:LEU:HB3	1.95	0.49
3:B:426:ASP:CG	3:B:467:LYS:HD3	2.37	0.49
3:B:460:ARG:O	3:B:461:ASN:HB2	2.11	0.49
3:A:420:LEU:HD22	3:A:427:GLU:HA	1.94	0.48
3:A:453:HIS:C	3:A:455:TYR:H	2.22	0.46
3:B:437:THR:OG1	3:B:438:CYS:N	2.46	0.46
2:D:7:DA:OP1	3:A:470:ARG:NE	2.37	0.46
3:B:454:ASN:OD1	3:B:454:ASN:N	2.46	0.46
2:D:5:DA:H2''	2:D:6:DA:H8	1.81	0.45
3:A:424:CYS:O	3:A:466:ASP:HA	2.16	0.44
3:A:456:LEU:HD12	3:B:468:ILE:HD11	2.00	0.44
2:D:2:DT:H2''	2:D:3:DG:OP2	2.18	0.44
3:B:442:LYS:HG3	3:B:442:LYS:HZ2	1.71	0.44
3:A:466:ASP:O	3:A:470:ARG:N	2.50	0.43
3:B:432:HIS:CG	3:B:442:LYS:HD2	2.54	0.43
3:A:462:ASP:CG	3:B:460:ARG:HH12	2.27	0.43
3:A:429:SER:HB3	3:A:432:HIS:HE1	1.84	0.42
3:A:488:LEU:HD23	3:A:488:LEU:HA	1.84	0.42
1:C:14:DC:H42	2:D:3:DG:H1	1.68	0.42
3:B:443:VAL:HG22	3:B:447:ARG:NH2	2.35	0.42
3:B:423:VAL:HA	3:B:480:LYS:HE2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:5:DA:H2''	2:D:6:DA:C8	2.55	0.41
3:B:437:THR:O	3:B:442:LYS:NZ	2.53	0.41
2:D:4:DG:H2''	2:D:5:DA:C8	2.56	0.40
3:A:463:CYS:HB2	3:A:476:CYS:SG	2.61	0.40
3:B:487:ASN:OD1	3:B:488:LEU:N	2.54	0.40
1:C:14:DC:H2''	1:C:15:DA:C8	2.56	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	
3	A	71/114 (62%)	69 (97%)	2 (3%)	0	100	100
3	B	70/114 (61%)	61 (87%)	8 (11%)	1 (1%)	9	13
All	All	141/228 (62%)	130 (92%)	10 (7%)	1 (1%)	18	28

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	B	446	LYS

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	
3	A	61/96 (64%)	58 (95%)	3 (5%)	22	39
3	B	60/96 (62%)	56 (93%)	4 (7%)	15	26
All	All	121/192 (63%)	114 (94%)	7 (6%)	18	32

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	420	LEU
3	A	471	LYS
3	A	488	LEU
3	B	437	THR
3	B	446	LYS
3	B	447	ARG
3	B	467	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	453	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 4 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

There are no such residues in this entry.

5.8 Polymer linkage issues

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	C	16/16 (100%)	1.96	7 (43%) 0 0	93, 108, 125, 125	0
2	D	16/16 (100%)	2.05	9 (56%) 0 0	98, 112, 133, 139	0
3	A	73/114 (64%)	1.97	33 (45%) 0 0	52, 81, 111, 122	0
3	B	72/114 (63%)	2.14	32 (44%) 0 0	58, 98, 122, 133	0
All	All	177/260 (68%)	2.04	81 (45%) 0 0	52, 94, 123, 139	0

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	B	442	LYS	7.0
3	A	418	PRO	6.0
3	B	437	THR	5.5
3	B	445	PHE	5.1
3	A	426	ASP	4.9
3	A	425	SER	4.8
3	A	490	ALA	4.6
3	B	433	TYR	4.3
3	B	443	VAL	4.1
3	A	453	HIS	4.1
3	B	431	CYS	4.0
3	B	451	GLY	3.9
3	B	436	LEU	3.8
3	A	427	GLU	3.8
3	B	432	HIS	3.7
3	B	490	ALA	3.7
3	B	446	LYS	3.6
3	A	420	LEU	3.6
3	A	424	CYS	3.6
3	B	449	VAL	3.6
3	B	419	LYS	3.5

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Mol	Chain	Res	Type	RSRZ
3	A	429	SER	3.5
3	B	435	VAL	3.5
3	A	455	TYR	3.5
3	B	478	TYR	3.5
3	A	440	SER	3.4
3	A	437	THR	3.2
3	B	430	GLY	3.0
3	B	444	PHE	3.0
2	D	1	DT	3.0
3	A	436	LEU	3.0
3	A	466	ASP	3.0
1	C	1	DG	2.9
3	B	482	LEU	2.9
3	A	428	ALA	2.9
3	B	434	GLY	2.9
1	C	11	DT	2.8
3	B	447	ARG	2.7
1	C	2	DC	2.7
2	D	16	DC	2.7
3	B	439	GLY	2.7
2	D	10	DC	2.7
3	B	454	ASN	2.6
3	A	456	LEU	2.6
3	B	452	GLN	2.6
3	B	455	TYR	2.6
1	C	8	DA	2.5
3	B	488	LEU	2.5
3	B	448	ALA	2.5
2	D	3	DG	2.5
3	A	442	LYS	2.5
3	A	468	ILE	2.4
3	B	483	GLN	2.4
2	D	13	DG	2.4
3	A	488	LEU	2.4
3	B	453	HIS	2.4
3	B	479	ARG	2.4
3	B	441	CYS	2.3
2	D	6	DA	2.3
3	A	432	HIS	2.3
1	C	14	DC	2.3
3	A	452	GLN	2.2
3	A	419	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
3	A	421	CYS	2.2
3	A	430	GLY	2.2
3	B	468	ILE	2.2
3	A	449	VAL	2.1
3	A	464	ILE	2.1
3	A	481	CYS	2.1
3	B	470	ARG	2.1
2	D	5	DA	2.1
2	D	11	DC	2.1
3	A	431	CYS	2.1
3	A	467	LYS	2.1
1	C	10	DT	2.1
3	A	454	ASN	2.1
3	A	441	CYS	2.1
2	D	9	DT	2.1
3	A	461	ASN	2.0
3	A	439	GLY	2.0
1	C	13	DC	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 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	A	601	1/1	0.96	0.08	95,95,95,95	0
4	ZN	B	601	1/1	0.99	0.04	54,54,54,54	0
4	ZN	B	602	1/1	0.99	0.03	89,89,89,89	0
4	ZN	A	602	1/1	1.00	0.02	51,51,51,51	0

6.5 Other polymers [i](#)

There are no such residues in this entry.