



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 07:36 PM GMT

PDB ID : 1GA5
Title : CRYSTAL STRUCTURE OF THE ORPHAN NUCLEAR RECEPTOR REV-
ERB(ALPHA) DNA-BINDING DOMAIN BOUND TO ITS COGNATE RE-
SPONSE ELEMENT
Authors : Sierk, M.L.; Zhao, Q.; Rastinejad, F.
Deposited on : 2000-11-29
Resolution : 2.40 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

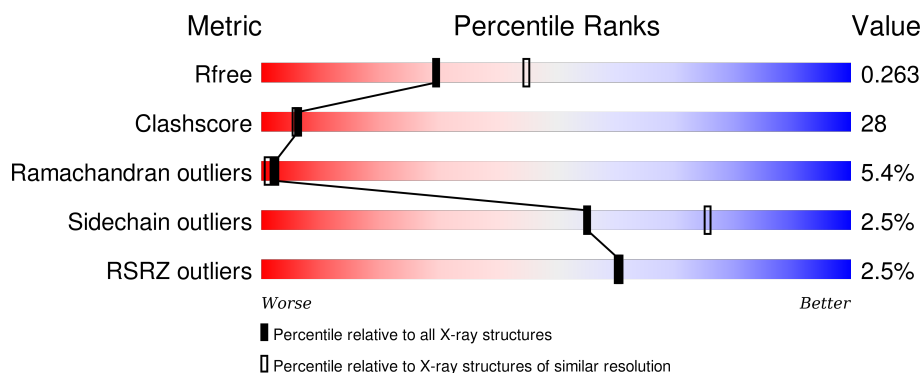
1 Overall quality at a glance ⓘ

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}	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	20	<div> <div>25%</div> <div>70%</div> <div>5%</div> </div>
1	G	20	<div> <div>20%</div> <div>75%</div> <div>5%</div> </div>
2	D	20	<div> <div>30%</div> <div>70%</div> </div>
2	H	20	<div> <div>25%</div> <div>70%</div> <div>5%</div> </div>
3	A	94	<div> <div>4%</div> <div>49%</div> <div>34%</div> <div>• •</div> <div>13%</div> </div>

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Mol	Chain	Length	Quality of chain
3	B	94	<div><div><div></div><div></div><div></div><div></div></div><div>3%49%31%•16%</div></div>
3	E	94	<div><div><div></div><div></div><div></div><div></div></div><div>2%52%32%•14%</div></div>
3	F	94	<div><div><div></div><div></div><div></div><div></div></div><div>%64%16%•17%</div></div>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4278 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 5'-D(*CP*AP*AP*CP*TP*AP*GP*GP*TP*CP*AP*C P*TP*AP*GP*GP*TP*CP*AP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	20	Total	C	N	O	P	0	0	0
			408	195	78	116	19			
1	G	20	Total	C	N	O	P	0	0	0
			408	195	78	116	19			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	20	Total	C	I	N	O	P	0	0
			406	194	1	72	120	19		
2	H	20	Total	C	I	N	O	P	0	0
			406	194	1	72	120	19		

- Molecule 3 is a protein called ORPHAN NUCLEAR RECEPTOR NR1D1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	82	Total	C	N	O	S	0	0	0
			603	377	117	99	10			
3	B	79	Total	C	N	O	S	0	0	0
			585	365	113	97	10			
3	E	81	Total	C	N	O	S	0	0	0
			606	379	117	100	10			
3	F	78	Total	C	N	O	S	0	0	0
			569	353	108	98	10			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	16	LEU	HIS	CLONING ARTIFACT	UNP P20393
B	16	LEU	HIS	CLONING ARTIFACT	UNP P20393

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Chain	Residue	Modelled	Actual	Comment	Reference
E	16	LEU	HIS	CLONING ARTIFACT	UNP P20393
F	16	LEU	HIS	CLONING ARTIFACT	UNP P20393

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 5 is water.

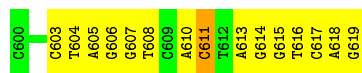
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	31	Total O 31 31	0	0
5	B	39	Total O 39 39	0	0
5	C	37	Total O 37 37	0	0
5	D	32	Total O 32 32	0	0
5	E	38	Total O 38 38	0	0
5	F	29	Total O 29 29	0	0
5	G	42	Total O 42 42	0	0
5	H	31	Total O 31 31	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

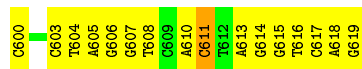
- Molecule 1: 5'-D(*CP*AP*AP*CP*TP*AP*GP*GP*TP*CP*AP*CP*TP*AP*GP*GP*TP*CP*AP*G)-3'

Chain C: 



- Molecule 1: 5'-D(*CP*AP*AP*CP*TP*AP*GP*GP*TP*CP*AP*CP*TP*AP*GP*GP*TP*CP*AP*G)-3'

Chain G: 



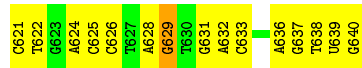
- Molecule 2: 5'-D(*CP*TP*GP*AP*CP*CP*TP*AP*GP*TP*GP*AP*CP*CP*TP*AP*GP*TP*(5IT)P*G)-3'

Chain D: 



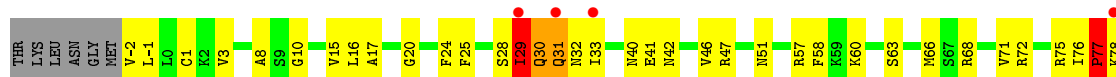
- Molecule 2: 5'-D(*CP*TP*GP*AP*CP*CP*TP*AP*GP*TP*GP*AP*CP*CP*TP*AP*GP*TP*(5IT)P*G)-3'

Chain H: 



- Molecule 3: ORPHAN NUCLEAR RECEPTOR NR1D1

Chain A: 



ARG
GLU
LYS
GLN
ARG
MET

• Molecule 3: ORPHAN NUCLEAR RECEPTOR NR1D1



THR LYS LYS LEU LEU ASN GLY GLY MET V-2 L-1 L-1 L-1 C1 C1 C2 V7 A8 S9 G10 G10 F11 F11 H12 H12 V13 G14 V15 C18 E19 R27 S28 S28 I29 I33 I33 I33A Y34 Y34 R35 R36 C37 I40 E41 E41 N42 C43 S44 I45 R52 F58 F59 K59 L62 R68 V71 G74 G75 ILE PRO LYS ARG

GLU
LYS
GLN
ARG
MET

• Molecule 3: ORPHAN NUCLEAR RECEPTOR NR1D1



THR LYS LYS LEU LEU ASN GLY GLY MET V-2 L-1 L-1 L-1 C1 C1 C2 V3 G10 L16 L16 E19 K22 G23 F24 F25 R26 R27 S28 I29 Q30 Q30 Q31 N32 N32 I33 R36 R36 C37 L38 K39 V46 R47 I48 I48 N49 R50 N51 Q55 C56 C56 R57 K60 S63 R72 R75 I76 I76 F77 LYS LYS ARG GLU

LYS
GLN
ARG
MET

• Molecule 3: ORPHAN NUCLEAR RECEPTOR NR1D1



THR LYS LYS LEU LEU ASN GLY GLY MET V-2 L-1 L-1 L-1 C2 V3 A8 F11 G14 G14 V15 E19 R27 R32 R32 I33 R36 R36 C37 L38 R39 R40 E41 E41 R52 K60 V71 G74 ARG ILE PRO LYS LYS ARG GLU LYS ARG MET

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	44.92Å 52.02Å 78.88Å 85.84° 76.61° 74.48°	Depositor
Resolution (Å)	19.60 – 2.40 19.60 – 2.35	Depositor EDS
% Data completeness (in resolution range)	75.0 (19.60-2.40) 73.8 (19.60-2.35)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.54 (at 2.35Å)	Xtriage
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.253 , 0.299 0.239 , 0.263	Depositor DCC
R_{free} test set	1940 reflections (10.97%)	DCC
Wilson B-factor (Å ²)	39.1	Xtriage
Anisotropy	0.297	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 54.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 25370 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4278	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 73.78 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.7254e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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, 5IU

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	0.41	0/458	0.68	0/705
1	G	0.42	0/458	0.71	0/705
2	D	0.44	0/431	0.72	0/661
2	H	0.44	0/431	0.74	0/661
3	A	0.42	0/611	0.76	1/817 (0.1%)
3	B	0.44	0/592	0.72	0/789
3	E	0.41	0/614	0.64	0/821
3	F	0.45	0/576	0.72	0/769
All	All	0.43	0/4171	0.71	1/5928 (0.0%)

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
1	C	0	1
1	G	0	1
2	H	0	1
All	All	0	3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	77	PRO	N-CA-C	5.03	125.17	112.10

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	611	DC	Sidechain
1	G	611	DC	Sidechain
2	H	629	DG	Sidechain

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	408	0	226	26	0
1	G	408	0	226	24	0
2	D	406	0	226	26	0
2	H	406	0	226	30	0
3	A	603	0	582	36	0
3	B	585	0	564	30	0
3	E	606	0	592	30	0
3	F	569	0	531	17	0
4	A	2	0	0	0	0
4	B	2	0	0	1	0
4	E	2	0	0	0	0
4	F	2	0	0	0	0
5	A	31	0	0	1	0
5	B	39	0	0	10	0
5	C	37	0	0	6	0
5	D	32	0	0	2	0
5	E	38	0	0	3	0
5	F	29	0	0	2	0
5	G	42	0	0	4	0
5	H	31	0	0	2	0
All	All	4278	0	3173	201	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 28.

The worst 5 of 201 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:D:639:5IU:H3'	2:D:640:DG:P	1.91	1.10

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:628:DA:H2"	2:D:629:DG:H5"	1.39	1.04
3:E:75:ARG:HD3	5:E:1034:HOH:O	1.57	1.02
3:A:-2:VAL:HG12	3:A:-1:LEU:H	1.29	0.95
3:B:43:CYS:HG	4:B:551:ZN:ZN	0.64	0.94

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	80/94 (85%)	64 (80%)	9 (11%)	7 (9%)	1	0
3	B	77/94 (82%)	64 (83%)	10 (13%)	3 (4%)	4	3
3	E	79/94 (84%)	68 (86%)	7 (9%)	4 (5%)	2	1
3	F	76/94 (81%)	63 (83%)	10 (13%)	3 (4%)	4	3
All	All	312/376 (83%)	259 (83%)	36 (12%)	17 (5%)	2	1

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	30	GLN
3	A	32	ASN
3	A	41	GLU
3	B	33	ILE
3	B	41	GLU

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	60/83 (72%)	59 (98%)	1 (2%)	68	85
3	B	58/83 (70%)	56 (97%)	2 (3%)	44	65
3	E	62/83 (75%)	61 (98%)	1 (2%)	70	86
3	F	56/83 (68%)	54 (96%)	2 (4%)	42	63
All	All	236/332 (71%)	230 (98%)	6 (2%)	55	76

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	75	ARG
3	F	52	ARG
3	E	38	LEU
3	B	52	ARG
3	F	38	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	51	ASN
3	B	51	ASN
3	E	51	ASN
3	E	55	GLN
3	F	51	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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	5IU	D	639	1,2	12,21,22	6.22	3 (25%)	14,30,33	3.74	1 (7%)
2	5IU	H	639	1,2	12,21,22	6.00	3 (25%)	14,30,33	3.77	1 (7%)

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	5IU	D	639	1,2	-	0/3/21/22	0/2/2/2
2	5IU	H	639	1,2	-	0/3/21/22	0/2/2/2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	639	5IU	C5-I5	-21.09	1.63	2.10
2	H	639	5IU	C5-I5	-20.32	1.65	2.10
2	D	639	5IU	C6-N1	2.48	1.38	1.35
2	H	639	5IU	C6-N1	2.62	1.38	1.35
2	H	639	5IU	C4-N3	3.08	1.38	1.33

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	639	5IU	C4-N3-C2	13.89	127.26	115.25
2	H	639	5IU	C4-N3-C2	14.05	127.39	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	639	5IU	5	0
2	H	639	5IU	4	0

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

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

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	20/20 (100%)	-0.50	0 100 100	33, 49, 78, 80	0
1	G	20/20 (100%)	-0.56	0 100 100	35, 47, 78, 79	0
2	D	19/20 (95%)	-0.47	0 100 100	27, 50, 78, 80	0
2	H	19/20 (95%)	-0.61	0 100 100	29, 47, 73, 77	0
3	A	82/94 (87%)	0.08	4 (4%) 33 34	23, 46, 78, 80	0
3	B	79/94 (84%)	-0.11	3 (3%) 44 45	24, 43, 73, 80	0
3	E	81/94 (86%)	-0.03	2 (2%) 61 60	25, 43, 73, 80	0
3	F	78/94 (82%)	-0.14	1 (1%) 79 79	22, 42, 77, 80	0
All	All	398/456 (87%)	-0.14	10 (2%) 61 60	22, 45, 78, 80	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	B	75	ARG	4.6
3	B	74	GLY	3.8
3	A	31	GLN	3.4
3	E	32	ASN	2.9
3	A	33	ILE	2.7

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

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	5IU	H	639	20/21	0.95	0.12	-	51,62,71,77	1
2	5IU	D	639	20/21	0.94	0.12	-	57,62,68,77	1

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
4	ZN	A	450	1/1	0.99	0.11	-0.56	42,42,42,42	0
4	ZN	B	550	1/1	0.99	0.12	-0.56	33,33,33,33	0
4	ZN	F	550	1/1	0.99	0.09	-0.84	31,31,31,31	0
4	ZN	F	551	1/1	0.98	0.04	-1.46	51,51,51,51	0
4	ZN	E	450	1/1	1.00	0.08	-2.02	32,32,32,32	0
4	ZN	B	551	1/1	0.99	0.07	-2.27	41,41,41,41	0
4	ZN	A	451	1/1	0.99	0.03	-2.48	49,49,49,49	0
4	ZN	E	451	1/1	0.99	0.02	-3.57	50,50,50,50	0

6.5 Other polymers [i](#)

There are no such residues in this entry.