



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 01:56 PM UTC

PDB ID : 6VCS / pdb_00006vcs
Title : SRA domain of UHRF1 in complex with DNA
Authors : Dong, C.; Tempel, W.; Bountra, C.; Edwards, A.M.; Arrowsmith, C.H.; Min, J.; Structural Genomics Consortium (SGC)
Deposited on : 2019-12-22
Resolution : 1.70 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

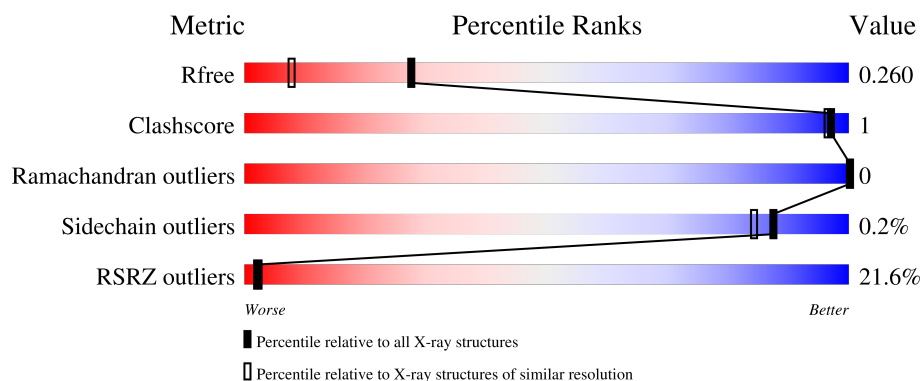
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	211	6% 88% 11%
1	B	211	9% 91% 9%
1	E	211	43% 83% 13%
2	C	12	33% 83% 17%
2	D	12	17% 83% 17%

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Mol	Chain	Length	Quality of chain
3	G	6	 100%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5084 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 E3 ubiquitin-protein ligase UHRF1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	188	Total	C	N	O	S	0	7	2
			1476	934	266	272	4			
1	B	193	Total	C	N	O	S	0	10	2
			1511	955	277	275	4			
1	E	184	Total	C	N	O	S	0	0	2
			1340	848	238	250	4			

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	413	MET	-	expression tag	UNP Q96T88
A	618	HIS	-	expression tag	UNP Q96T88
A	619	HIS	-	expression tag	UNP Q96T88
A	620	HIS	-	expression tag	UNP Q96T88
A	621	HIS	-	expression tag	UNP Q96T88
A	622	HIS	-	expression tag	UNP Q96T88
A	623	HIS	-	expression tag	UNP Q96T88
B	413	MET	-	expression tag	UNP Q96T88
B	618	HIS	-	expression tag	UNP Q96T88
B	619	HIS	-	expression tag	UNP Q96T88
B	620	HIS	-	expression tag	UNP Q96T88
B	621	HIS	-	expression tag	UNP Q96T88
B	622	HIS	-	expression tag	UNP Q96T88
B	623	HIS	-	expression tag	UNP Q96T88
E	413	MET	-	expression tag	UNP Q96T88
E	618	HIS	-	expression tag	UNP Q96T88
E	619	HIS	-	expression tag	UNP Q96T88
E	620	HIS	-	expression tag	UNP Q96T88
E	621	HIS	-	expression tag	UNP Q96T88
E	622	HIS	-	expression tag	UNP Q96T88
E	623	HIS	-	expression tag	UNP Q96T88

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

GP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	12	Total	C	N	O	P	0	0	0
			243	116	46	70	11			
2	D	12	Total	C	N	O	P	0	0	0
			235	113	43	68	11			

- Molecule 3 is a protein called UNK-UNK-UNK-UNK.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	G	6	Total	C	N	O	0	0	0
			28	16	6	6			

- Molecule 4 is UNKNOWN ATOM OR ION (CCD ID: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	29	Total	X	0	0
			29	29		
4	B	25	Total	X	0	0
			25	25		
4	E	12	Total	X	0	0
			12	12		

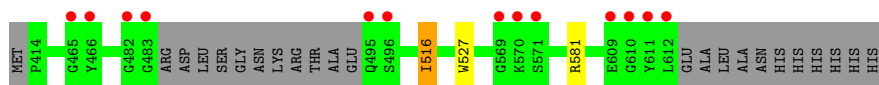
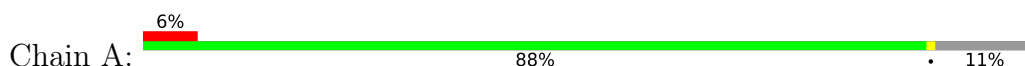
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	86	Total	O	0	0
			86	86		
5	B	82	Total	O	0	0
			82	82		
5	C	3	Total	O	0	0
			3	3		
5	D	4	Total	O	0	0
			4	4		
5	E	10	Total	O	0	0
			10	10		

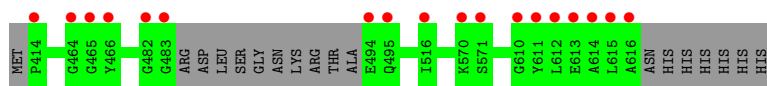
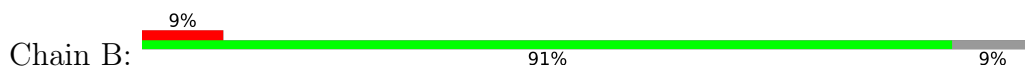
3 Residue-property plots [i](#)

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.

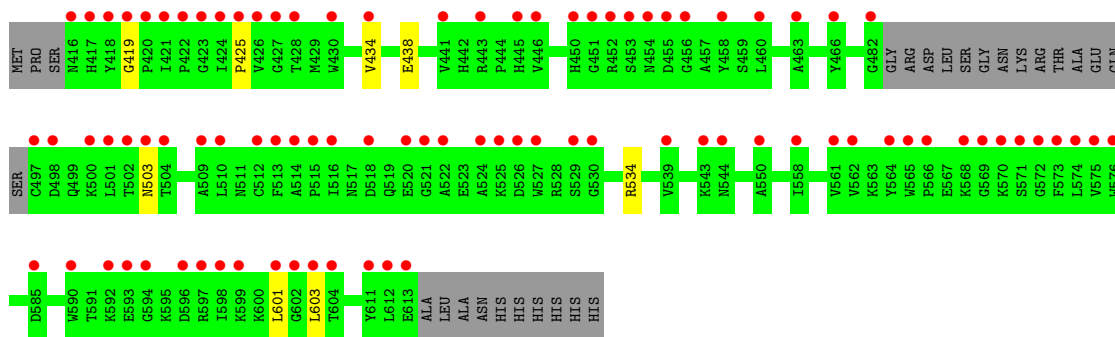
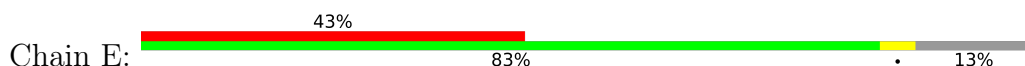
- Molecule 1: E3 ubiquitin-protein ligase UHRF1



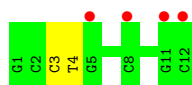
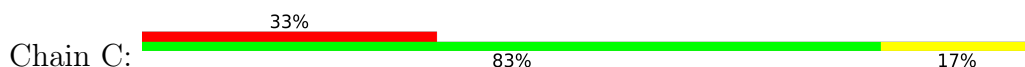
- Molecule 1: E3 ubiquitin-protein ligase UHRF1



- Molecule 1: E3 ubiquitin-protein ligase UHRF1

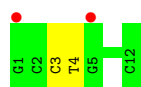


- Molecule 2: DNA (5'-D(*GP*CP*CP*TP*GP*TP*AP*CP*AP*GP*GP*C)-3')



- Molecule 2: DNA (5'-D(*GP*CP*CP*TP*GP*TP*AP*CP*AP*GP*GP*C)-3')

Chain D:  17% 83% 17%



- Molecule 3: UNK-UNK-UNK-UNK

Chain G:  100%

There are no outlier residues recorded for this chain.

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	51.99Å 113.81Å 133.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.60 – 1.70 44.60 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.1 (44.60-1.70) 99.2 (44.60-1.70)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.56 (at 1.70Å)	Xtriage
Refinement program	PHENIX 1.17.1 _3660	Depositor
R, R_{free}	0.237 , 0.258 0.240 , 0.260	Depositor DCC
R_{free} test set	4348 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	22.1	Xtriage
Anisotropy	0.493	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 37.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5084	wwPDB-VP
Average B, all atoms (Å ²)	37.0	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 50.15 % 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 6.7427e-05. 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, 0.333 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: UNX

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	0.32	0/1543	0.52	0/2096
1	B	0.32	0/1598	0.49	0/2169
1	E	0.17	0/1377	0.36	1/1879 (0.1%)
2	C	0.28	0/272	0.49	0/418
2	D	0.30	0/263	0.49	0/403
All	All	0.28	0/5053	0.47	1/6965 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	503	ASN	CB-CA-C	-5.22	110.53	116.54

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	1476	0	1376	2	0
1	B	1511	0	1409	0	0
1	E	1340	0	1179	4	0
2	C	243	0	136	1	0
2	D	235	0	129	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	28	0	6	0	0
4	A	29	0	0	0	0
4	B	25	0	0	0	0
4	E	12	0	0	0	0
5	A	86	0	0	0	0
5	B	82	0	0	0	0
5	C	3	0	0	0	0
5	D	4	0	0	0	0
5	E	10	0	0	0	0
All	All	5084	0	4235	8	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 1.

All (8) 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)
1:E:434:VAL:O	1:E:438:GLU:HG3	2.09	0.52
2:C:3:DC:H2'	2:C:4:DT:C6	2.49	0.48
1:E:425:PRO:HG2	1:E:603:LEU:HD11	1.96	0.47
2:D:3:DC:H2'	2:D:4:DT:C6	2.52	0.45
1:A:527:TRP:CZ2	1:A:581:ARG:HD2	2.52	0.44
1:E:601:LEU:HB2	1:E:603:LEU:HG	2.00	0.43
1:A:516:ILE:HD13	1:A:516:ILE:HA	1.94	0.42
1:E:419:GLY:O	1:E:534:ARG:HD3	2.21	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	A	191/211 (90%)	184 (96%)	7 (4%)	0	100	100
1	B	199/211 (94%)	193 (97%)	6 (3%)	0	100	100
1	E	180/211 (85%)	173 (96%)	7 (4%)	0	100	100
All	All	570/633 (90%)	550 (96%)	20 (4%)	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	149/172 (87%)	148 (99%)	1 (1%)	76	69
1	B	152/172 (88%)	152 (100%)	0	100	100
1	E	119/172 (69%)	119 (100%)	0	100	100
All	All	420/516 (81%)	419 (100%)	1 (0%)	87	84

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

Mol	Chain	Res	Type
1	A	516	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 66 ligands modelled in this entry, 66 are unknown - 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, 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	188/211 (89%)	0.37	13 (6%) 23 25	16, 24, 47, 65	7 (3%)
1	B	193/211 (91%)	0.46	18 (9%) 14 15	12, 25, 54, 97	10 (5%)
1	E	184/211 (87%)	2.20	90 (48%) 0 0	31, 57, 85, 105	0
2	C	12/12 (100%)	1.63	4 (33%) 1 1	39, 53, 59, 62	0
2	D	12/12 (100%)	1.60	2 (16%) 4 4	44, 50, 59, 68	0
3	G	0/6	-	-	-	-
All	All	589/663 (88%)	1.02	127 (21%) 2 2	12, 31, 73, 105	17 (2%)

All (127) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	615	LEU	8.9
1	B	483	GLY	8.7
1	E	416	ASN	8.3
1	B	616	ALA	6.7
1	E	573	PHE	5.7
1	A	612	LEU	5.1
1	E	453	SER	4.7
1	E	572	GLY	4.7
1	E	571	SER	4.6
1	B	494	GLU	4.5
1	E	497	CYS	4.5
1	B	612	LEU	4.5
1	E	516	ILE	4.4
1	A	466[A]	TYR	4.4
1	B	614	ALA	4.4
1	E	544	ASN	4.3
1	E	454	ASN	4.3
1	E	570	LYS	4.2
1	E	529	SER	4.2

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Mol	Chain	Res	Type	RSRZ
1	E	513	PHE	4.2
1	E	510	LEU	4.2
1	E	574	LEU	4.2
1	E	603	LEU	4.2
1	E	458	TYR	4.1
1	E	527	TRP	4.1
1	E	421	ILE	4.1
1	A	482	GLY	4.1
1	B	611	TYR	4.0
1	E	426	VAL	4.0
1	E	613	GLU	3.9
2	D	1	DG	3.9
1	E	417	HIS	3.8
1	E	593	GLU	3.8
1	A	570	LYS	3.8
1	E	598	ILE	3.7
1	E	597	ARG	3.7
1	A	610	GLY	3.7
1	A	465	GLY	3.6
1	A	483	GLY	3.6
1	E	561	VAL	3.6
1	A	611	TYR	3.6
1	E	514	ALA	3.6
1	E	418	TYR	3.6
1	E	611	TYR	3.6
1	E	443	ARG	3.5
1	E	569	GLY	3.5
1	E	558	ILE	3.5
1	E	576	TRP	3.5
1	E	425	PRO	3.5
1	E	424	ILE	3.4
1	E	612	LEU	3.4
1	B	466[A]	TYR	3.4
1	E	463	ALA	3.4
1	E	503	ASN	3.4
1	E	568	LYS	3.3
1	E	482	GLY	3.2
1	E	515	PRO	3.2
1	E	501	LEU	3.2
1	E	446	VAL	3.2
1	E	450	HIS	3.2
1	E	590	TRP	3.1

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Mol	Chain	Res	Type	RSRZ
1	E	601	LEU	3.1
1	A	495	GLN	3.0
2	D	5	DG	2.9
1	E	419	GLY	2.9
1	E	420	PRO	2.9
1	E	423	GLY	2.8
1	E	428	THR	2.8
1	E	585	ASP	2.8
1	E	592	LYS	2.8
1	B	610	GLY	2.8
1	E	596	ASP	2.8
1	B	414	PRO	2.8
1	E	466	TYR	2.7
1	B	465	GLY	2.7
1	E	452	ARG	2.7
1	E	575	VAL	2.7
1	B	613	GLU	2.7
1	E	520	GLU	2.7
1	B	570	LYS	2.7
1	E	564	TYR	2.7
1	E	602	GLY	2.6
1	E	550	ALA	2.6
1	E	604	THR	2.6
1	E	543	LYS	2.6
1	E	562	VAL	2.6
1	E	500	LYS	2.5
1	B	482	GLY	2.5
1	E	530	GLY	2.5
1	E	504	THR	2.5
1	A	569	GLY	2.4
1	E	522	ALA	2.4
1	B	516	ILE	2.4
1	B	495	GLN	2.4
1	A	609	GLU	2.4
2	C	12	DC	2.4
1	E	434	VAL	2.4
1	E	455	ASP	2.4
1	E	594	GLY	2.4
1	E	502	THR	2.4
1	A	571	SER	2.3
1	B	464	GLY	2.3
1	E	451	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	E	445	HIS	2.2
1	B	571	SER	2.2
2	C	8	DC	2.2
1	E	599	LYS	2.2
1	E	498	ASP	2.2
1	E	456	GLY	2.2
2	C	11	DG	2.2
1	E	525	LYS	2.2
1	E	512	CYS	2.2
1	E	460	LEU	2.2
1	E	509	ALA	2.1
1	E	524	ALA	2.1
1	A	496	SER	2.1
1	E	526	ASP	2.1
1	E	422	PRO	2.1
1	E	521	GLY	2.1
1	E	518	ASP	2.1
2	C	5	DG	2.1
1	E	427	GLY	2.1
1	E	566	PRO	2.1
1	E	441	VAL	2.0
1	E	539	VAL	2.0
1	E	430	TRP	2.0
1	E	565	TRP	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($\text{\AA}^2$)	Q<0.9
4	UNX	A	710	1/1	0.75	0.21	39,39,39,39	0
4	UNX	A	707	1/1	0.81	0.24	35,35,35,35	0
4	UNX	E	709	1/1	0.81	0.51	31,31,31,31	1
4	UNX	B	701	1/1	0.82	0.17	34,34,34,34	0
4	UNX	A	723	1/1	0.83	0.12	35,35,35,35	0
4	UNX	A	726	1/1	0.83	0.18	36,36,36,36	0
4	UNX	E	712	1/1	0.83	0.17	39,39,39,39	0
4	UNX	B	723	1/1	0.84	0.18	31,31,31,31	0
4	UNX	A	714	1/1	0.86	0.27	27,27,27,27	0
4	UNX	A	724	1/1	0.87	0.15	26,26,26,26	0
4	UNX	E	703	1/1	0.87	0.21	34,34,34,34	0
4	UNX	A	718	1/1	0.87	0.19	27,27,27,27	0
4	UNX	A	708	1/1	0.87	0.12	29,29,29,29	0
4	UNX	A	729	1/1	0.88	0.15	33,33,33,33	0
4	UNX	B	715	1/1	0.88	0.14	33,33,33,33	0
4	UNX	E	704	1/1	0.88	0.21	41,41,41,41	0
4	UNX	B	716	1/1	0.88	0.12	27,27,27,27	0
4	UNX	B	720	1/1	0.88	0.31	22,22,22,22	1
4	UNX	E	705	1/1	0.89	0.15	40,40,40,40	0
4	UNX	A	719	1/1	0.89	0.12	28,28,28,28	0
4	UNX	E	710	1/1	0.89	0.18	31,31,31,31	0
4	UNX	B	714	1/1	0.89	0.12	26,26,26,26	0
4	UNX	A	727	1/1	0.90	0.14	33,33,33,33	0
4	UNX	A	722	1/1	0.90	0.14	37,37,37,37	0
4	UNX	A	711	1/1	0.90	0.13	29,29,29,29	0
4	UNX	B	717	1/1	0.90	0.23	11,11,11,11	1
4	UNX	B	710	1/1	0.91	0.13	24,24,24,24	0
4	UNX	B	725	1/1	0.91	0.15	25,25,25,25	0
4	UNX	A	702	1/1	0.91	0.20	38,38,38,38	0
4	UNX	A	728	1/1	0.91	0.11	33,33,33,33	0
4	UNX	A	704	1/1	0.92	0.10	26,26,26,26	0
4	UNX	B	724	1/1	0.92	0.16	36,36,36,36	0
4	UNX	E	707	1/1	0.92	0.13	34,34,34,34	0
4	UNX	A	705	1/1	0.93	0.18	33,33,33,33	0
4	UNX	B	722	1/1	0.93	0.11	26,26,26,26	0
4	UNX	A	706	1/1	0.93	0.13	26,26,26,26	0
4	UNX	E	702	1/1	0.94	0.17	35,35,35,35	0
4	UNX	B	707	1/1	0.94	0.10	18,18,18,18	0
4	UNX	B	719	1/1	0.94	0.08	22,22,22,22	0
4	UNX	A	725	1/1	0.94	0.13	28,28,28,28	0
4	UNX	B	713	1/1	0.94	0.12	32,32,32,32	0
4	UNX	E	708	1/1	0.94	0.33	22,22,22,22	1
4	UNX	A	716	1/1	0.94	0.11	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	UNX	B	702	1/1	0.94	0.18	28,28,28,28	0
4	UNX	E	711	1/1	0.94	0.12	36,36,36,36	0
4	UNX	B	705	1/1	0.94	0.08	29,29,29,29	0
4	UNX	B	721	1/1	0.95	0.19	10,10,10,10	1
4	UNX	A	715	1/1	0.95	0.15	23,23,23,23	0
4	UNX	B	718	1/1	0.95	0.21	25,25,25,25	0
4	UNX	B	708	1/1	0.96	0.11	27,27,27,27	0
4	UNX	A	703	1/1	0.96	0.09	29,29,29,29	0
4	UNX	A	720	1/1	0.96	0.15	20,20,20,20	0
4	UNX	A	721	1/1	0.96	0.13	23,23,23,23	0
4	UNX	B	703	1/1	0.96	0.22	38,38,38,38	0
4	UNX	B	704	1/1	0.96	0.12	28,28,28,28	0
4	UNX	A	717	1/1	0.96	0.09	28,28,28,28	0
4	UNX	E	701	1/1	0.96	0.08	40,40,40,40	0
4	UNX	A	701	1/1	0.96	0.16	18,18,18,18	0
4	UNX	B	712	1/1	0.97	0.07	26,26,26,26	0
4	UNX	E	706	1/1	0.97	0.07	33,33,33,33	0
4	UNX	B	709	1/1	0.97	0.10	21,21,21,21	0
4	UNX	A	712	1/1	0.97	0.16	27,27,27,27	0
4	UNX	A	713	1/1	0.98	0.06	21,21,21,21	0
4	UNX	B	711	1/1	0.98	0.05	21,21,21,21	0
4	UNX	A	709	1/1	0.98	0.04	20,20,20,20	0
4	UNX	B	706	1/1	0.98	0.16	26,26,26,26	0

6.5 Other polymers [i](#)

There are no such residues in this entry.