



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 5, 2023 – 02:37 PM EDT

PDB ID : 6VCS
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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

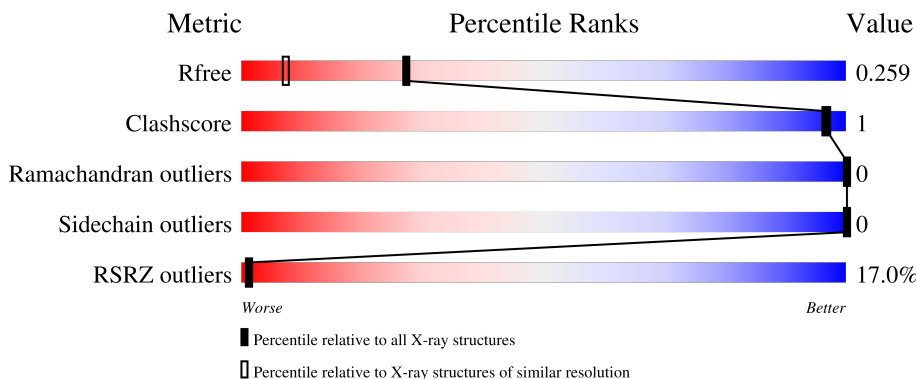
1 Overall quality at a glance

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}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (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	 4% 88% 11%
1	B	211	 5% 91% 9%
1	E	211	 38% 84% 13%
2	C	12	 8% 83% 17%
2	D	12	 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
			Total	C	N	O	S			
1	A	188	1476	934	266	272	4	0	7	2
1	B	193	1511	955	277	275	4	0	10	2
1	E	184	1340	848	238	250	4	0	0	2

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 (three-letter code: 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		

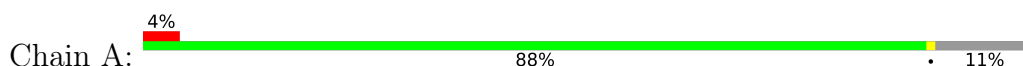
- Molecule 5 is water.

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		

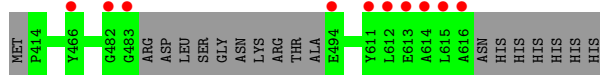
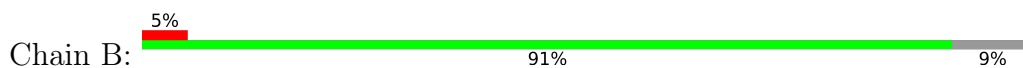
3 Residue-property plots [i](#)

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.

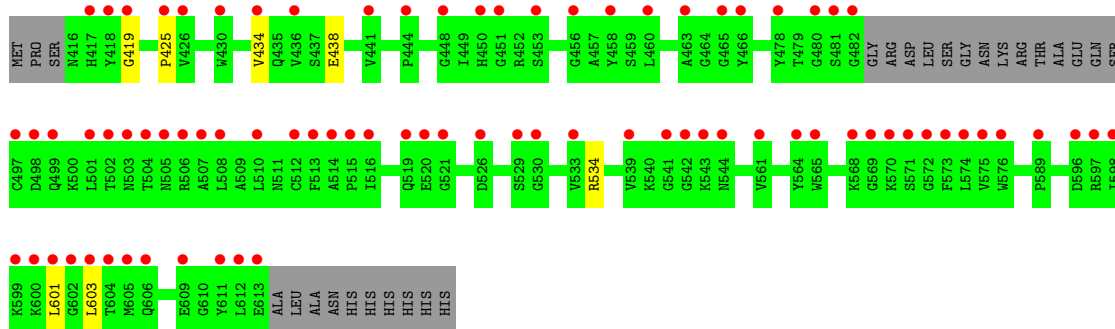
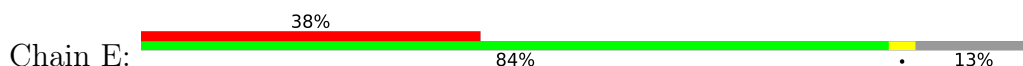
- Molecule 1: E3 ubiquitin-protein ligase UHRF1



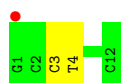
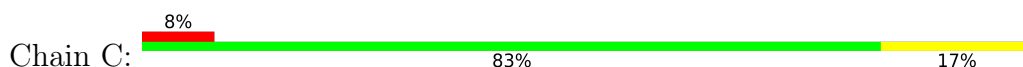
- Molecule 1: E3 ubiquitin-protein ligase UHRF1




- 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:  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) 99.1 (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)	Xtrriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.237 , 0.258 0.239 , 0.259	Depositor DCC
R_{free} test set	4338 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	22.1	Xtrriage
Anisotropy	0.493	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 45.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5084	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtrriage'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	0.39	0/1543	0.59	0/2096
1	B	0.41	0/1598	0.58	0/2169
1	E	0.27	0/1377	0.44	0/1879
2	C	0.67	0/272	0.89	0/418
2	D	0.64	0/263	0.91	0/403
All	All	0.40	0/5053	0.60	0/6965

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	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
3	G	28	0	6	0	0
4	A	29	0	0	0	0
4	B	25	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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 [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	
1	A	149/172 (87%)	149 (100%)	0	100	100
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%)	420 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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

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

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

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 [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	8 (4%) 35 39	16, 24, 47, 65	0
1	B	193/211 (91%)	0.51	10 (5%) 27 30	17, 26, 54, 97	0
1	E	184/211 (87%)	2.25	81 (44%) 0 0	31, 57, 85, 105	0
2	C	12/12 (100%)	0.61	1 (8%) 11 13	39, 53, 59, 62	0
2	D	12/12 (100%)	0.24	0 100 100	44, 50, 59, 68	0
3	G	0/6	-	-	-	-
All	All	589/663 (88%)	1.01	100 (16%) 1 1	16, 32, 73, 105	0

All (100) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	616	ALA	21.1
1	B	483	GLY	15.2
1	B	615	LEU	12.1
1	E	497	CYS	11.0
1	B	614	ALA	9.2
1	E	571	SER	8.2
1	E	529	SER	7.8
1	B	612	LEU	7.5
1	E	510	LEU	7.5
1	E	573	PHE	7.3
1	E	513	PHE	7.1
1	A	612	LEU	6.8
1	E	570	LYS	6.6
1	E	569	GLY	6.4
1	E	611	TYR	6.3
1	E	572	GLY	6.2
1	E	598	ILE	6.0
1	E	576	TRP	5.8
1	E	502	THR	5.8

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Mol	Chain	Res	Type	RSRZ
1	E	612	LEU	5.7
1	E	465	GLY	5.5
1	E	515	PRO	5.2
1	E	514	ALA	5.2
1	B	611	TYR	5.0
1	E	501	LEU	4.8
1	E	613	GLU	4.7
1	E	565	TRP	4.6
1	E	481	SER	4.5
1	E	602	GLY	4.4
1	E	575	VAL	4.4
1	E	543	LYS	4.3
1	E	498	ASP	4.3
1	E	601	LEU	4.3
1	E	418	TYR	4.1
1	E	441	VAL	4.1
1	E	482	GLY	3.9
1	E	458	TYR	3.9
1	E	512	CYS	3.8
1	E	542	GLY	3.8
1	E	597	ARG	3.8
1	E	417	HIS	3.7
1	A	466[A]	TYR	3.7
1	E	604	THR	3.7
1	B	494	GLU	3.7
1	E	541	GLY	3.7
1	B	466[A]	TYR	3.6
1	E	466	TYR	3.6
1	E	530	GLY	3.5
1	E	434	VAL	3.5
1	E	574	LEU	3.4
1	E	456	GLY	3.3
1	E	504	THR	3.3
1	E	596	ASP	3.2
1	E	521	GLY	3.1
1	E	516	ILE	3.1
1	E	426	VAL	3.0
1	E	520	GLU	3.0
1	E	506	ARG	3.0
1	A	483	GLY	2.9
1	E	539	VAL	2.9
1	E	463	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
1	E	419	GLY	2.9
1	E	564	TYR	2.9
1	A	610	GLY	2.9
1	E	568	LYS	2.8
1	E	444	PRO	2.8
1	E	600	LYS	2.8
1	E	599	LYS	2.7
1	E	508	LEU	2.7
1	E	603	LEU	2.6
1	E	436	VAL	2.6
1	E	605	MET	2.6
1	E	519	GLN	2.5
1	B	613	GLU	2.5
1	E	499	GLN	2.5
1	A	421	ILE	2.5
1	A	457	ALA	2.4
1	E	425	PRO	2.4
1	E	561	VAL	2.3
1	E	478	TYR	2.3
1	B	482	GLY	2.3
1	E	450	HIS	2.3
1	A	611	TYR	2.3
1	A	482	GLY	2.3
1	E	503	ASN	2.3
1	E	544	ASN	2.3
1	E	507	ALA	2.2
1	E	606	GLN	2.2
1	E	451	GLY	2.2
1	E	453	SER	2.1
1	E	505	ASN	2.1
1	E	430	TRP	2.1
1	E	480	GLY	2.1
1	E	460	LEU	2.1
1	E	526	ASP	2.1
1	E	533	VAL	2.1
1	E	609	GLU	2.1
2	C	1	DG	2.0
1	E	589	PRO	2.0
1	E	448	GLY	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, 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	UNX	A	711	1/1	0.72	0.25	29,29,29,29	0
4	UNX	E	708	1/1	0.78	0.26	22,22,22,22	1
4	UNX	E	704	1/1	0.81	0.24	41,41,41,41	0
4	UNX	E	709	1/1	0.81	0.46	31,31,31,31	1
4	UNX	E	705	1/1	0.82	0.13	40,40,40,40	0
4	UNX	B	703	1/1	0.83	0.39	38,38,38,38	0
4	UNX	B	725	1/1	0.83	0.32	25,25,25,25	0
4	UNX	A	706	1/1	0.83	0.27	26,26,26,26	0
4	UNX	A	702	1/1	0.85	0.33	38,38,38,38	0
4	UNX	A	729	1/1	0.85	0.29	33,33,33,33	0
4	UNX	B	701	1/1	0.85	0.13	34,34,34,34	0
4	UNX	B	717	1/1	0.86	0.57	11,11,11,11	1
4	UNX	B	712	1/1	0.86	0.15	26,26,26,26	0
4	UNX	A	707	1/1	0.87	0.23	35,35,35,35	0
4	UNX	A	710	1/1	0.88	0.29	39,39,39,39	0
4	UNX	A	715	1/1	0.88	0.17	23,23,23,23	0
4	UNX	E	710	1/1	0.89	0.16	31,31,31,31	0
4	UNX	E	701	1/1	0.90	0.09	40,40,40,40	0
4	UNX	B	723	1/1	0.90	0.20	31,31,31,31	0
4	UNX	B	702	1/1	0.90	0.25	28,28,28,28	0
4	UNX	A	726	1/1	0.91	0.35	36,36,36,36	0
4	UNX	B	722	1/1	0.91	0.16	26,26,26,26	0
4	UNX	A	727	1/1	0.91	0.20	33,33,33,33	0
4	UNX	A	728	1/1	0.91	0.11	33,33,33,33	0
4	UNX	A	724	1/1	0.91	0.18	26,26,26,26	0
4	UNX	E	711	1/1	0.91	0.10	36,36,36,36	0
4	UNX	B	706	1/1	0.92	0.19	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	UNX	B	710	1/1	0.92	0.17	24,24,24,24	0
4	UNX	A	714	1/1	0.92	0.19	27,27,27,27	0
4	UNX	A	708	1/1	0.92	0.24	29,29,29,29	0
4	UNX	B	719	1/1	0.92	0.21	22,22,22,22	0
4	UNX	E	712	1/1	0.92	0.13	39,39,39,39	0
4	UNX	B	720	1/1	0.93	0.30	22,22,22,22	1
4	UNX	B	705	1/1	0.93	0.19	29,29,29,29	0
4	UNX	B	715	1/1	0.93	0.16	33,33,33,33	0
4	UNX	B	724	1/1	0.93	0.16	36,36,36,36	0
4	UNX	A	705	1/1	0.93	0.21	33,33,33,33	0
4	UNX	A	723	1/1	0.93	0.09	35,35,35,35	0
4	UNX	E	702	1/1	0.93	0.14	35,35,35,35	0
4	UNX	A	717	1/1	0.94	0.10	28,28,28,28	0
4	UNX	A	718	1/1	0.94	0.11	27,27,27,27	0
4	UNX	A	721	1/1	0.94	0.31	23,23,23,23	0
4	UNX	E	707	1/1	0.94	0.13	34,34,34,34	0
4	UNX	B	708	1/1	0.94	0.15	27,27,27,27	0
4	UNX	A	712	1/1	0.94	0.25	27,27,27,27	0
4	UNX	A	716	1/1	0.94	0.14	27,27,27,27	0
4	UNX	A	725	1/1	0.94	0.18	28,28,28,28	0
4	UNX	B	716	1/1	0.94	0.19	27,27,27,27	0
4	UNX	B	704	1/1	0.95	0.16	28,28,28,28	0
4	UNX	A	719	1/1	0.95	0.08	28,28,28,28	0
4	UNX	A	722	1/1	0.95	0.11	37,37,37,37	0
4	UNX	E	703	1/1	0.95	0.15	34,34,34,34	0
4	UNX	B	707	1/1	0.95	0.13	18,18,18,18	0
4	UNX	A	720	1/1	0.95	0.28	20,20,20,20	0
4	UNX	B	718	1/1	0.96	0.33	25,25,25,25	0
4	UNX	A	704	1/1	0.96	0.13	26,26,26,26	0
4	UNX	B	714	1/1	0.96	0.10	26,26,26,26	0
4	UNX	A	709	1/1	0.96	0.12	20,20,20,20	0
4	UNX	B	709	1/1	0.96	0.17	21,21,21,21	0
4	UNX	A	701	1/1	0.96	0.31	18,18,18,18	0
4	UNX	B	721	1/1	0.97	0.56	10,10,10,10	1
4	UNX	E	706	1/1	0.97	0.15	33,33,33,33	0
4	UNX	B	713	1/1	0.97	0.17	32,32,32,32	0
4	UNX	A	713	1/1	0.97	0.17	21,21,21,21	0
4	UNX	A	703	1/1	0.98	0.37	29,29,29,29	0
4	UNX	B	711	1/1	0.98	0.12	21,21,21,21	0

6.5 Other polymers [i](#)

There are no such residues in this entry.