



# wwPDB X-ray Structure Validation Summary Report ⓘ

May 30, 2020 – 02:46 am BST

PDB ID : 6PI7  
Title : Crystal structure of the TDRD2 extended Tudor domain in complex with an antibody fragment and the PIWIL1 peptide  
Authors : Liu, K.; Min, J.R.; Structural Genomics Consortium (SGC)  
Deposited on : 2019-06-26  
Resolution : 2.80 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](mailto: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.

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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	:	2.11
buster-report	:	1.1.7 (2018)
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)	:	2.11

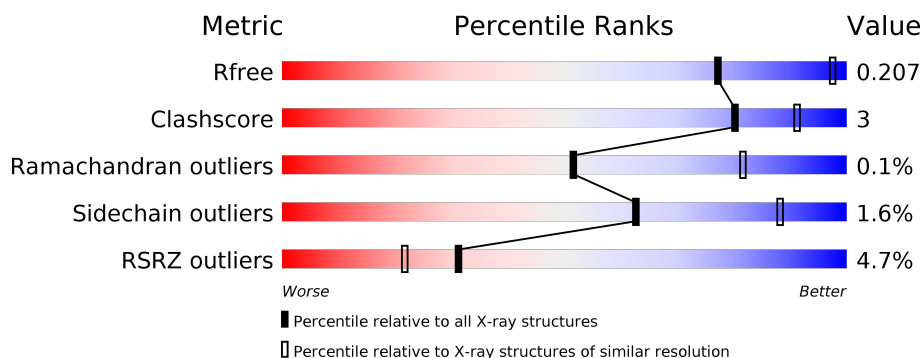
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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  $\geq 3$ , 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	222	<div> <div>76%</div> <div>10% • 13%</div> </div>
1	D	222	<div> <div>4%</div> <div>82%</div> <div>• 14%</div> </div>
2	B	226	<div> <div>11%</div> <div>89%</div> <div>• 7%</div> </div>
2	E	226	<div> <div>4%</div> <div>88%</div> <div>5% 7%</div> </div>
3	C	244	<div> <div>3%</div> <div>83%</div> <div>7% 10%</div> </div>
3	F	244	<div> <div>4%</div> <div>84%</div> <div>6% 10%</div> </div>

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Mol	Chain	Length	Quality of chain
4	G	16	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	UNX	A	602	-	-	-	X
5	UNX	A	604	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8998 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 Tudor and KH domain-containing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	193	Total	C	N	O	S	0	0	1
			1490	951	248	287	4			
1	D	192	Total	C	N	O	S	0	0	0
			1382	878	232	270	2			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	304	GLY	-	expression tag	UNP Q9Y2W6
D	304	GLY	-	expression tag	UNP Q9Y2W6

- Molecule 2 is a protein called Uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	211	Total	C	N	O	S	0	0	0
			1392	869	242	278	3			
2	E	211	Total	C	N	O	S	0	0	1
			1468	921	250	292	5			

- Molecule 3 is a protein called Fab antigen-binding fragment.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	219	Total	C	N	O	S	0	0	0
			1596	1018	266	307	5			
3	F	219	Total	C	N	O	S	0	0	0
			1627	1042	268	312	5			

- Molecule 4 is a protein called Piwi-like protein 1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	G	6	Total	C	N	O	0	0	1
			38	21	12	5			

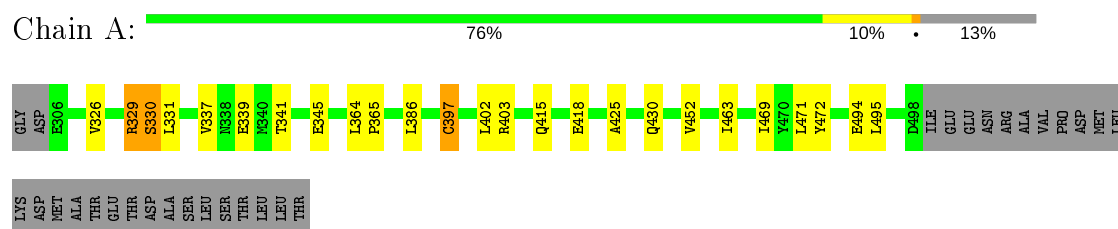
- Molecule 5 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X) (labeled as "Ligand of Interest" by author).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	4	Total	X	0	0
			4	4		
5	D	1	Total	X	0	0
			1	1		

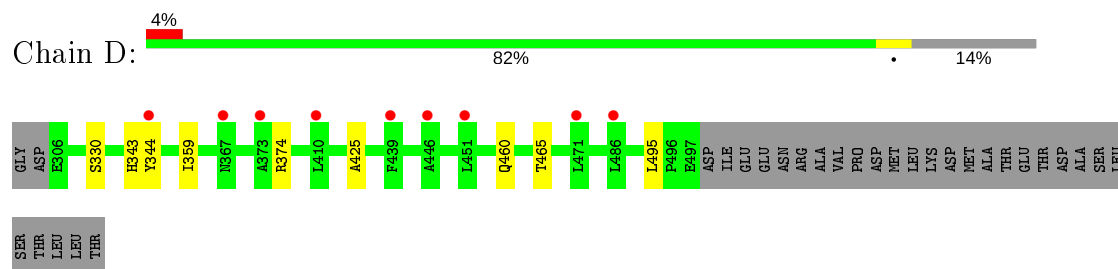
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

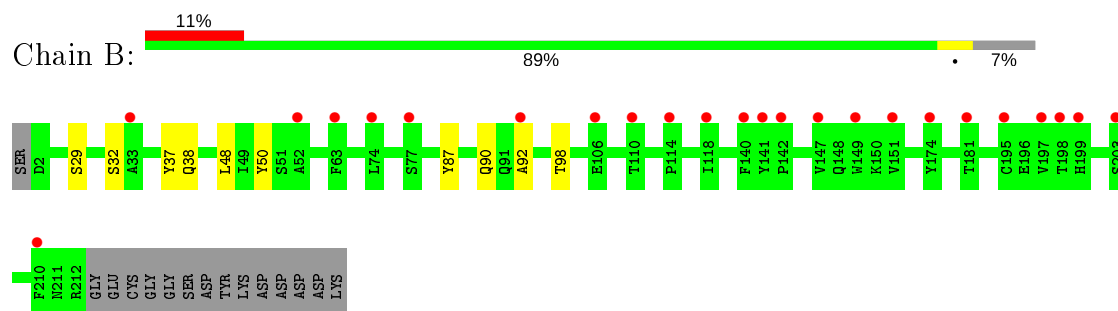
- Molecule 1: Tudor and KH domain-containing protein



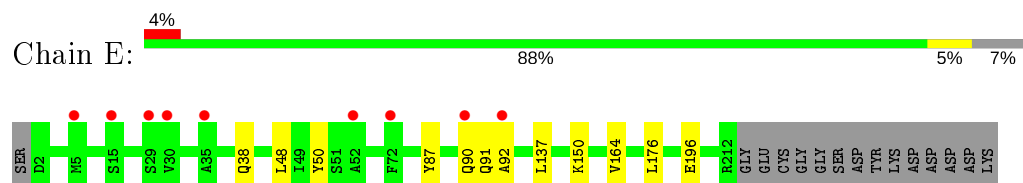
- Molecule 1: Tudor and KH domain-containing protein



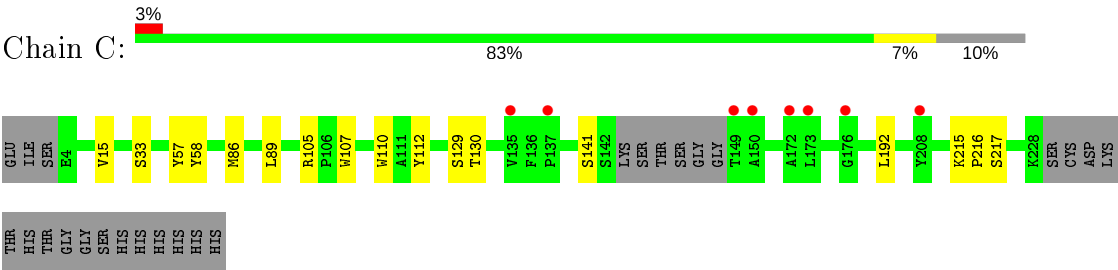
- Molecule 2: Uncharacterized protein



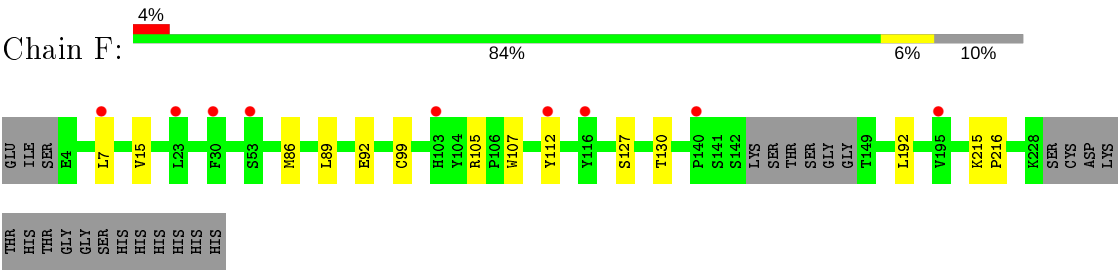
- Molecule 2: Uncharacterized protein



- Molecule 3: Fab antigen-binding fragment



• Molecule 3: Fab antigen-binding fragment



• Molecule 4: Piwi-like protein 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	148.10Å 148.10Å 168.03Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.48 – 2.80 48.48 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.48-2.80) 99.8 (48.48-2.80)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.78 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, $R_{free}$	0.190 , 0.206 0.191 , 0.207	Depositor DCC
$R_{free}$ test set	2561 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	83.0	Xtriage
Anisotropy	0.108	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 72.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.39$ , $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.429 for h,-h-k,-l	Xtriage
Reported twinning fraction	0.565 for H, K, L 0.435 for -K, -H, -L	Depositor
Outliers	0 of 51283 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	8998	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.94% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: 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	1.03	4/1529 (0.3%)	0.76	0/2092
1	D	0.83	0/1421	0.73	0/1953
2	B	0.82	0/1424	0.75	0/1961
2	E	0.85	1/1500 (0.1%)	0.75	0/2051
3	C	0.85	0/1645	0.73	0/2259
3	F	0.82	1/1676 (0.1%)	0.73	0/2298
4	G	1.16	0/37	0.91	0/47
All	All	0.87	6/9232 (0.1%)	0.74	0/12661

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	339	GLU	CD-OE1	9.26	1.35	1.25
1	A	418	GLU	CD-OE1	7.58	1.33	1.25
2	E	196	GLU	CD-OE1	5.95	1.32	1.25
1	A	494	GLU	CD-OE1	5.58	1.31	1.25
3	F	92	GLU	CD-OE2	5.54	1.31	1.25

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	A	1490	0	1384	13	0
1	D	1382	0	1143	5	0
2	B	1392	0	1082	7	0
2	E	1468	0	1246	6	0
3	C	1596	0	1399	15	0
3	F	1627	0	1469	11	0
4	G	38	0	39	0	0
5	A	4	0	0	0	0
5	D	1	0	0	0	0
All	All	8998	0	7762	46	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 3.

The worst 5 of 46 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:C:86:MET:HE2	3:C:89:LEU:HD21	1.85	0.59
1:A:469:ILE:HD12	1:A:471:LEU:HD13	1.87	0.57
3:F:86:MET:HE2	3:F:89:LEU:HD21	1.87	0.55
1:A:364:LEU:HB3	1:A:365:PRO:HD3	1.89	0.55
2:B:50:TYR:HB2	3:C:112:TYR:O	2.07	0.54

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	191/222 (86%)	180 (94%)	11 (6%)	0	100	100
1	D	190/222 (86%)	180 (95%)	10 (5%)	0	100	100
2	B	209/226 (92%)	202 (97%)	7 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	209/226 (92%)	203 (97%)	6 (3%)	0	100	100
3	C	215/244 (88%)	209 (97%)	5 (2%)	1 (0%)	29	61
3	F	215/244 (88%)	209 (97%)	6 (3%)	0	100	100
4	G	4/16 (25%)	3 (75%)	1 (25%)	0	100	100
All	All	1233/1400 (88%)	1186 (96%)	46 (4%)	1 (0%)	51	81

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	141	SER

### 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	154/194 (79%)	149 (97%)	5 (3%)	39	73
1	D	120/194 (62%)	119 (99%)	1 (1%)	81	94
2	B	106/198 (54%)	104 (98%)	2 (2%)	57	85
2	E	129/198 (65%)	127 (98%)	2 (2%)	62	88
3	C	150/204 (74%)	148 (99%)	2 (1%)	69	91
3	F	157/204 (77%)	156 (99%)	1 (1%)	86	96
4	G	2/9 (22%)	2 (100%)	0	100	100
All	All	818/1201 (68%)	805 (98%)	13 (2%)	62	88

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	29	SER
2	B	98	THR
2	E	91	GLN
1	A	463	ILE
1	D	330	SER

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

Mol	Chain	Res	Type
1	A	415	GLN
3	C	213	ASN
1	D	460	GLN
1	D	488	HIS
2	E	125	GLN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 5 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 ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	193/222 (86%)	0.47	0 <span>100</span> <span>100</span>	47, 63, 94, 101	0
1	D	192/222 (86%)	0.33	9 (4%) <span>31</span> <span>22</span>	88, 111, 135, 145	0
2	B	211/226 (93%)	0.60	24 (11%) <span>5</span> <span>3</span>	63, 119, 149, 163	0
2	E	211/226 (93%)	0.41	9 (4%) <span>35</span> <span>25</span>	59, 97, 126, 138	0
3	C	219/244 (89%)	0.44	8 (3%) <span>41</span> <span>31</span>	52, 81, 132, 140	0
3	F	219/244 (89%)	0.38	9 (4%) <span>37</span> <span>27</span>	64, 88, 114, 133	0
4	G	6/16 (37%)	0.06	0 <span>100</span> <span>100</span>	62, 73, 89, 92	0
All	All	1251/1400 (89%)	0.44	59 (4%) <span>31</span> <span>22</span>	47, 93, 138, 163	0

The worst 5 of 59 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	197	VAL	5.1
2	B	174	TYR	5.1
2	E	52	ALA	4.7
2	B	147	VAL	4.0
2	B	195	CYS	3.9

### 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 carbohydrates in this entry.

## 6.4 Ligands

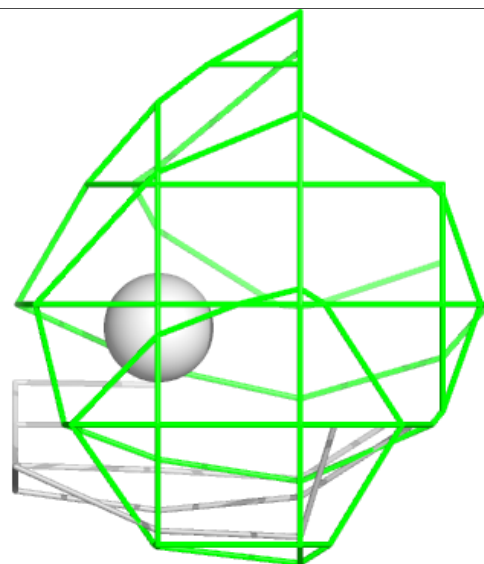
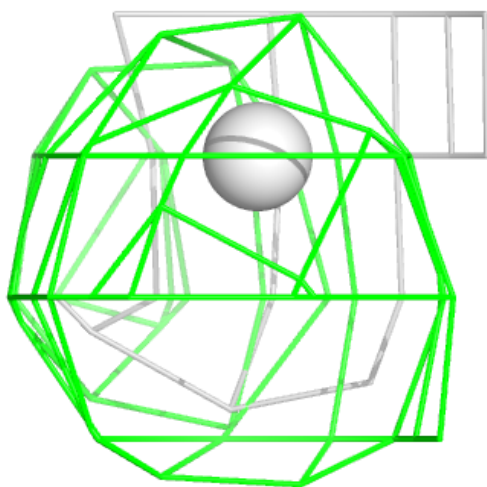
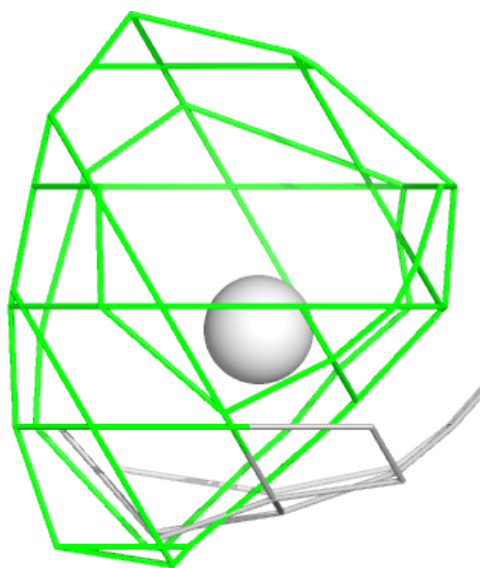
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
5	UNX	A	604	1/1	0.47	0.62	74,74,74,74	0
5	UNX	A	602	1/1	0.69	0.46	51,51,51,51	0
5	UNX	D	601	1/1	0.82	0.42	63,63,63,63	0
5	UNX	A	603	1/1	0.84	0.53	61,61,61,61	0
5	UNX	A	601	1/1	0.90	0.44	59,59,59,59	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around UNX A 604:**

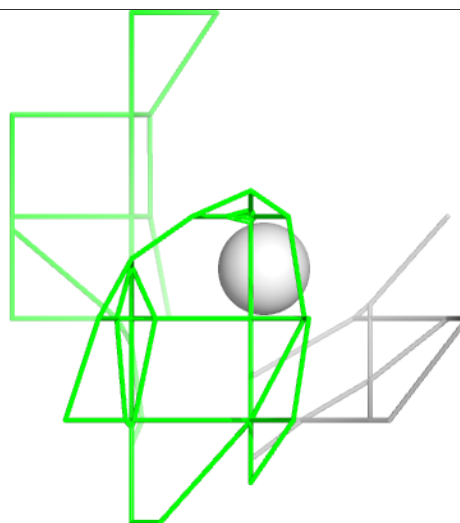
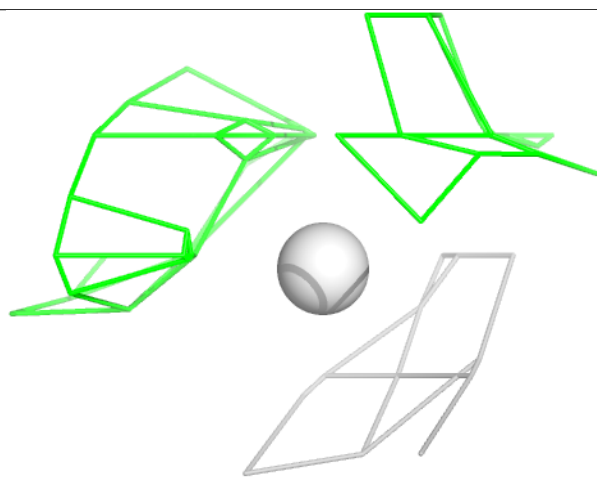
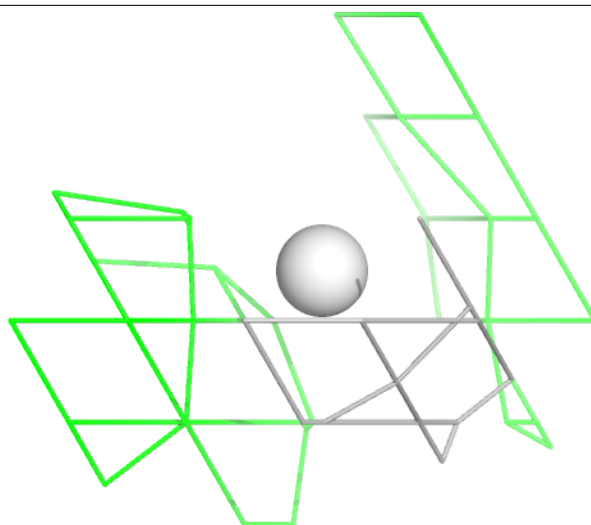
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





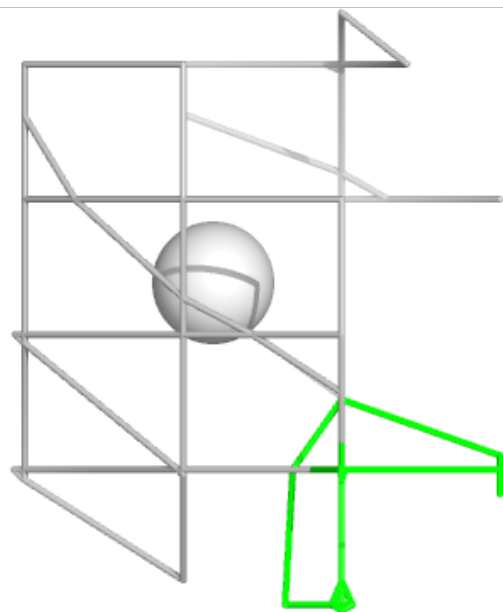
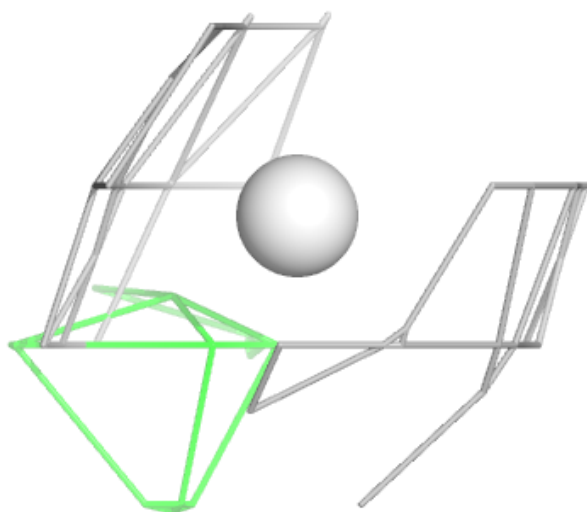
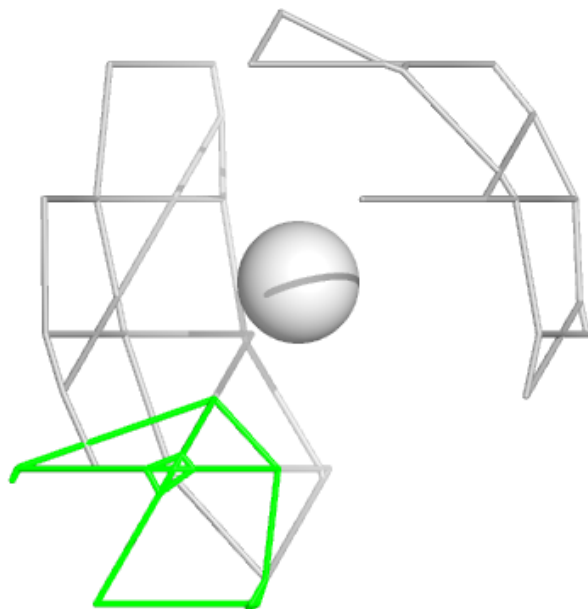
**Electron density around UNX A 602:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



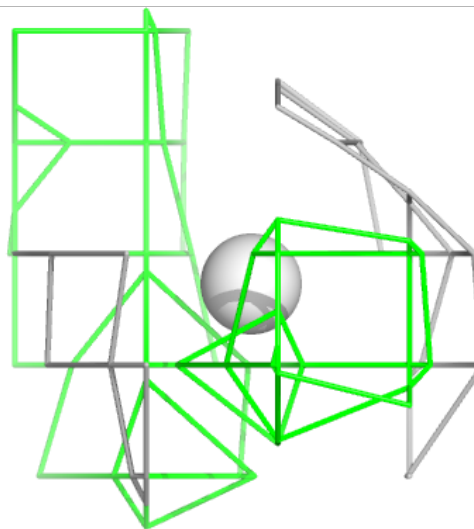
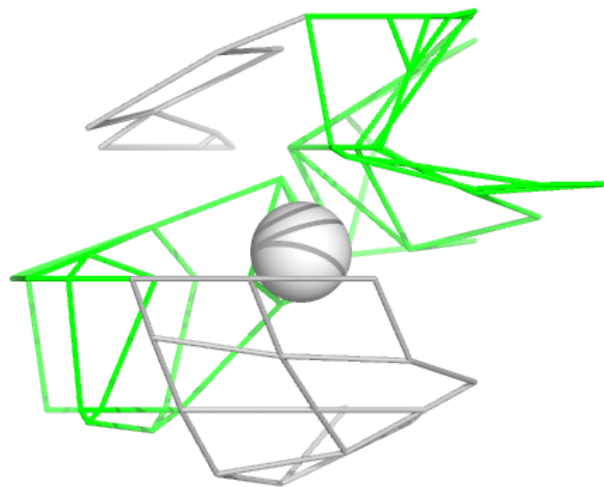
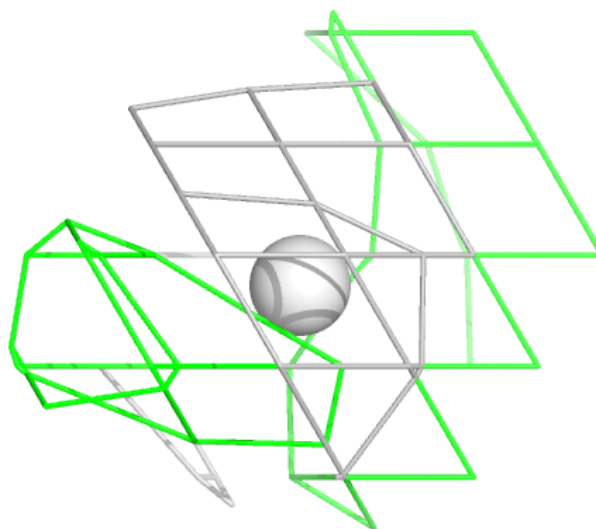
**Electron density around UNX D 601:**

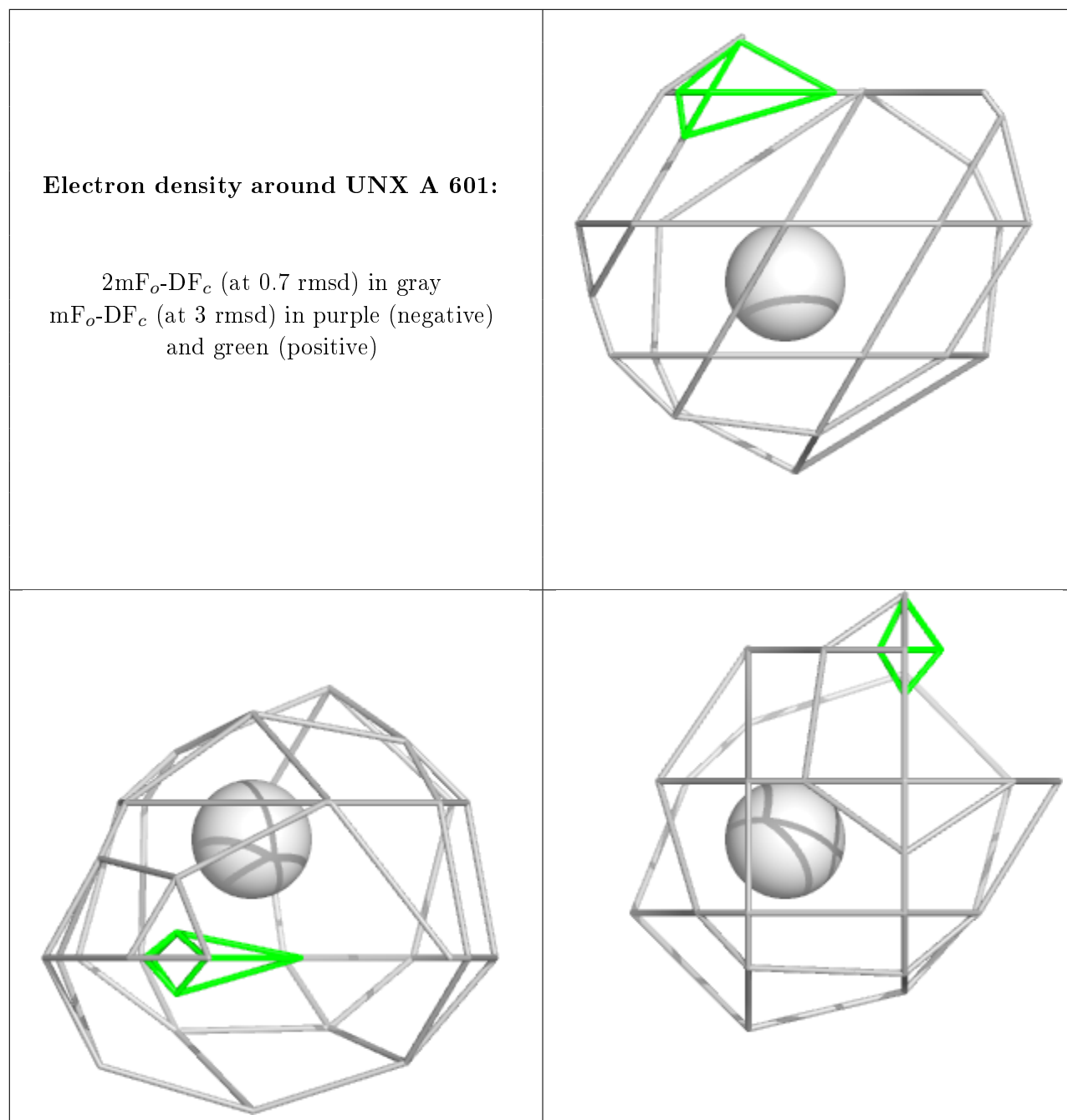
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around UNX A 603:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)





## 6.5 Other polymers [i](#)

There are no such residues in this entry.