Full wwPDB X-ray Structure Validation Report (i)

Mar 18, 2024 – 05:25 PM JST

PDB ID	:	8ITN
Title	:	Crystal structure of USP47apo catalytic domain
Authors	:	Kim, E.E.; Shin, S.C.
Deposited on	:	2023-03-22
Resolution	:	2.60 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 (i) 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 (1)) were used in the production of this report:

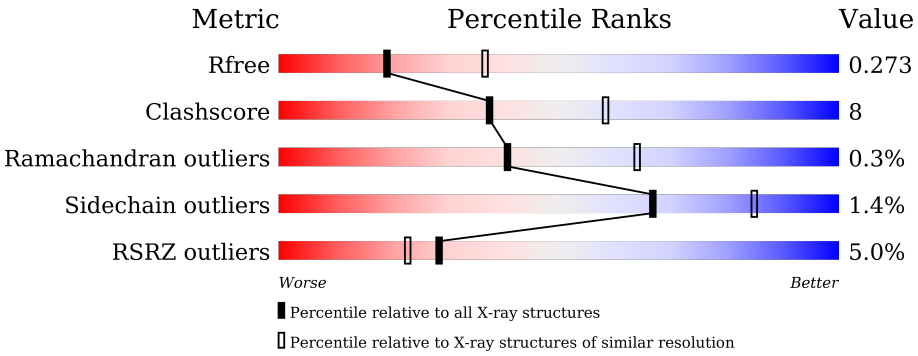
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 <=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	508	2% 56% 12% • 31%
1	B	508	3% 56% 8% • 35%
1	C	508	6% 57% 10% • 32%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 8432 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 Ubiquitin carboxyl-terminal hydrolase 47.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	350	Total	C	N	O	S	0	0	0
			2846	1807	481	539	19			
1	B	329	Total	C	N	O	S	0	0	0
			2678	1708	451	503	16			
1	C	345	Total	C	N	O	S	0	0	0
			2802	1779	472	532	19			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		

- Molecule 3 is water.

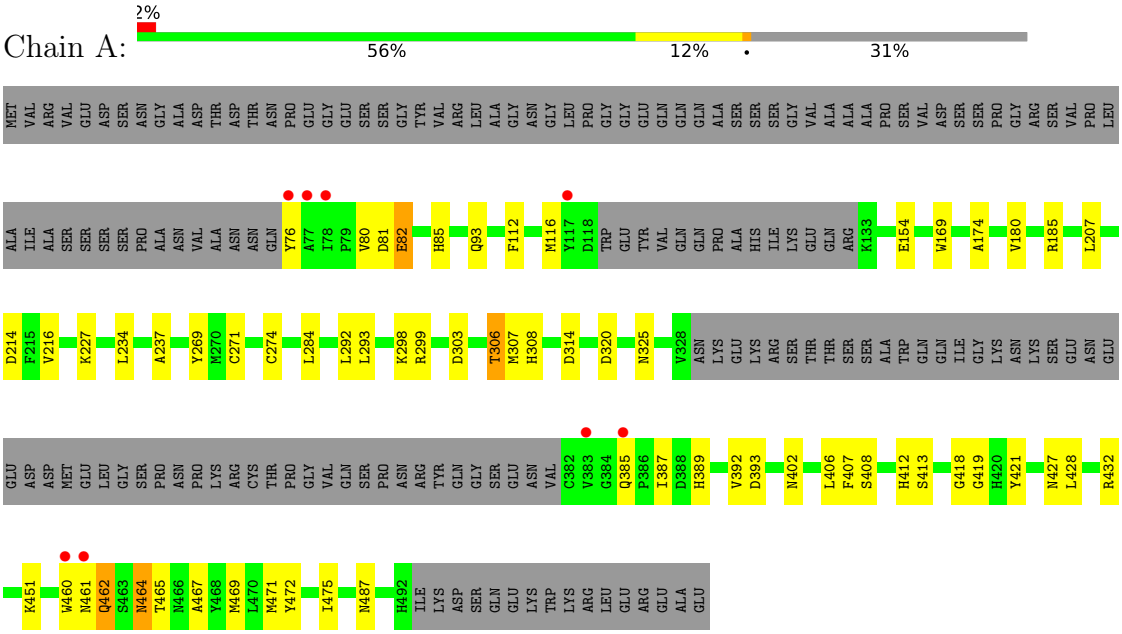
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	76	Total	O	0	0
			76	76		
3	B	11	Total	O	0	0
			11	11		
3	C	17	Total	O	0	0
			17	17		

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.

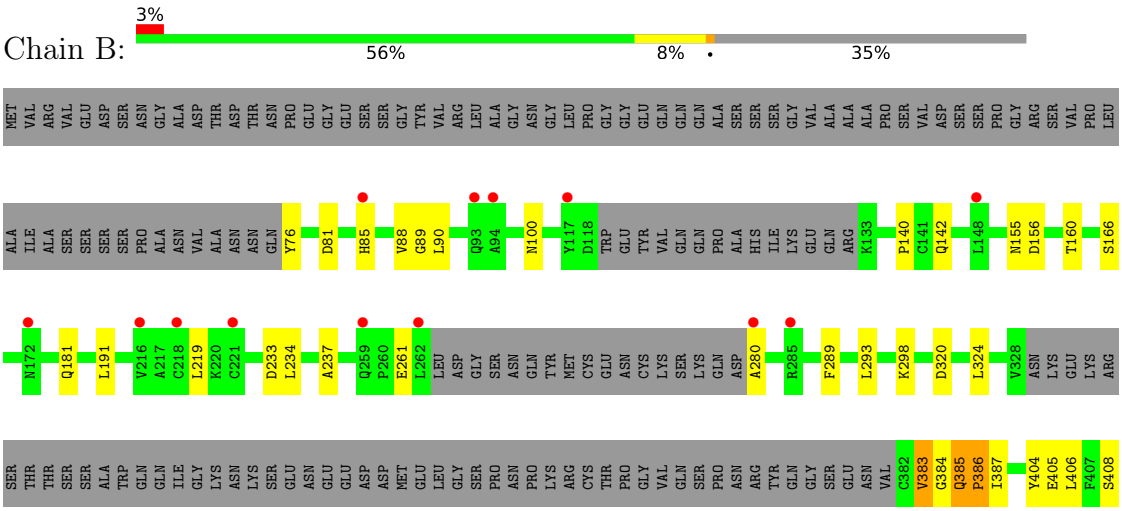
• Molecule 1: Ubiquitin carboxyl-terminal hydrolase 47

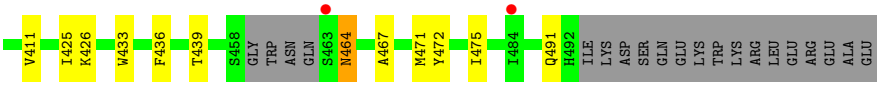
Chain A:



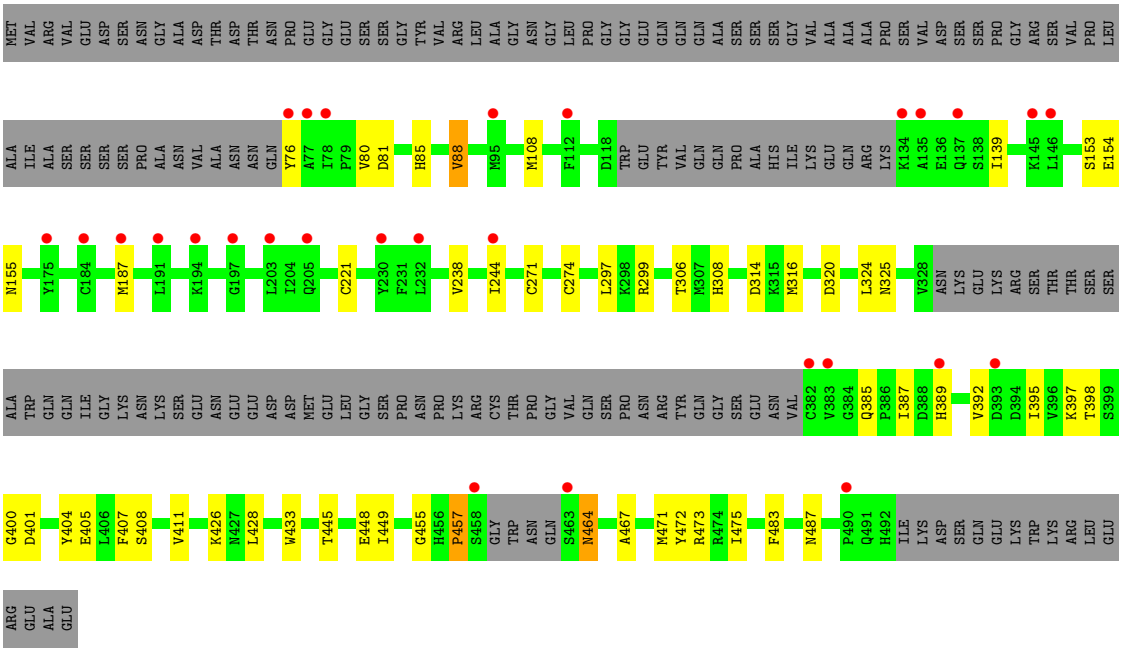
• Molecule 1: Ubiquitin carboxyl-terminal hydrolase 47

Chain B:





• Molecule 1: Ubiquitin carboxyl-terminal hydrolase 47



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	94.08Å 58.91Å 251.93Å 90.00° 96.69° 90.00°	Depositor
Resolution (Å)	35.50 – 2.60 35.50 – 2.59	Depositor EDS
% Data completeness (in resolution range)	96.0 (35.50-2.60) 96.0 (35.50-2.59)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.66 (at 2.58Å)	Xtriage
Refinement program	PHENIX 1.20.1-4487	Depositor
R, R_{free}	0.258 , 0.269 0.258 , 0.273	Depositor DCC
R_{free} test set	1999 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å^2)	43.2	Xtriage
Anisotropy	0.471	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.26 , 27.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	8432	wwPDB-VP
Average B, all atoms (Å^2)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.36% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	A	0.26	0/2913	0.47	0/3941
1	B	0.28	0/2740	0.48	1/3706 (0.0%)
1	C	0.24	0/2866	0.46	0/3876
All	All	0.26	0/8519	0.47	1/11523 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	383	VAL	CB-CA-C	-6.14	99.73	111.40

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	2846	0	2732	57	0
1	B	2678	0	2587	34	0
1	C	2802	0	2691	42	0
2	A	1	0	0	0	0
2	C	1	0	0	0	0
3	A	76	0	0	2	0
3	B	11	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	17	0	0	0	0
All	All	8432	0	8010	126	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 8.

All (126) 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:A:462:GLN:HG2	1:A:462:GLN:O	1.64	0.93
1:A:408:SER:HB3	1:A:471:MET:HB2	1.61	0.81
1:B:408:SER:HB3	1:B:471:MET:HB2	1.64	0.78
1:A:461:ASN:HB2	1:A:462:GLN:HA	1.68	0.76
1:B:320:ASP:CG	1:B:384:GLY:O	2.25	0.74
1:A:299:ARG:NH2	1:A:314:ASP:O	2.21	0.73
1:C:408:SER:HB3	1:C:471:MET:HB2	1.69	0.72
1:B:90:LEU:O	1:B:439:THR:HG22	1.89	0.72
1:A:413:SER:HB3	1:A:465:THR:HG22	1.75	0.69
1:B:88:VAL:HG22	1:B:155:ASN:O	1.93	0.68
1:A:306:THR:CB	1:A:308:HIS:H	2.06	0.67
1:C:85:HIS:NE2	1:C:153:SER:O	2.27	0.67
1:C:306:THR:HB	1:C:308:HIS:H	1.61	0.65
1:B:88:VAL:HG12	1:B:89:GLY:N	2.12	0.64
1:C:457:PRO:CG	1:C:464:ASN:HB3	2.28	0.64
1:C:88:VAL:HG13	1:C:155:ASN:O	1.98	0.64
1:A:76:TYR:HD2	1:C:154:GLU:HG3	1.63	0.63
1:A:214:ASP:HB3	1:A:284:LEU:HD23	1.79	0.63
1:B:81:ASP:N	1:B:85:HIS:O	2.25	0.62
1:A:461:ASN:N	1:A:462:GLN:HB3	2.15	0.62
1:B:234:LEU:HD22	1:B:293:LEU:HD11	1.82	0.62
1:B:385:GLN:HB2	1:B:386:PRO:HD3	1.82	0.61
1:C:238:VAL:HG21	1:C:299:ARG:HG2	1.83	0.59
1:B:404:TYR:HB3	1:B:472:TYR:HB3	1.85	0.58
1:A:306:THR:OG1	1:A:307:MET:HA	2.03	0.58
1:C:455:GLY:O	1:C:457:PRO:HD3	2.03	0.58
1:B:88:VAL:HG13	1:B:156:ASP:C	2.25	0.57
1:A:93:GLN:NE2	1:A:421:TYR:O	2.37	0.56
1:A:427:ASN:ND2	3:A:706:HOH:O	2.38	0.56
1:B:405:GLU:HB2	1:B:475:ILE:HD11	1.88	0.56
1:B:219:LEU:HG	1:B:280:ALA:HA	1.88	0.55
1:A:306:THR:HB	1:A:308:HIS:N	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:460:TRP:C	1:A:462:GLN:HB3	2.26	0.55
1:A:462:GLN:H	1:A:462:GLN:HE21	1.55	0.54
1:B:88:VAL:CG2	1:B:155:ASN:O	2.54	0.54
1:C:299:ARG:NH2	1:C:314:ASP:O	2.40	0.54
1:C:404:TYR:HB3	1:C:472:TYR:HB3	1.90	0.54
1:A:306:THR:HB	1:A:308:HIS:H	1.71	0.53
1:A:76:TYR:CD2	1:C:154:GLU:HG3	2.42	0.53
1:A:412:HIS:HE2	1:A:419:GLY:HA3	1.74	0.53
1:B:464:ASN:ND2	1:B:464:ASN:O	2.42	0.53
1:A:462:GLN:O	1:A:462:GLN:CG	2.46	0.53
1:A:464:ASN:HD22	1:A:464:ASN:N	2.04	0.53
1:C:457:PRO:HG3	1:C:464:ASN:HB3	1.91	0.53
1:A:234:LEU:HD22	1:A:293:LEU:HD11	1.90	0.53
1:B:320:ASP:HA	1:B:406:LEU:HB3	1.89	0.53
1:C:389:HIS:HB2	1:C:392:VAL:HG12	1.90	0.52
1:C:81:ASP:N	1:C:85:HIS:O	2.38	0.52
1:A:412:HIS:NE2	1:A:419:GLY:HA3	2.25	0.52
1:A:81:ASP:N	1:A:85:HIS:O	2.35	0.52
1:B:90:LEU:O	1:B:439:THR:CG2	2.58	0.52
1:C:221:CYS:HB3	1:C:274:CYS:SG	2.49	0.52
1:A:325:ASN:ND2	1:A:402:ASN:H	2.08	0.52
1:A:214:ASP:OD2	1:A:227:LYS:NZ	2.38	0.51
1:C:405:GLU:HB2	1:C:475:ILE:HD11	1.91	0.51
1:A:303:ASP:HB3	1:A:306:THR:HG1	1.74	0.51
1:B:387:ILE:HD12	1:B:387:ILE:H	1.77	0.50
1:C:385:GLN:HG3	1:C:449:ILE:HB	1.94	0.50
1:A:81:ASP:HB3	1:A:82:GLU:OE1	2.12	0.50
1:B:90:LEU:HD22	1:B:100:ASN:HA	1.94	0.49
1:A:487:ASN:HB2	1:C:387:ILE:HG12	1.94	0.49
1:A:325:ASN:HD21	1:A:402:ASN:H	1.60	0.49
1:A:464:ASN:O	1:A:464:ASN:ND2	2.45	0.49
1:B:237:ALA:HA	1:B:298:LYS:HB3	1.95	0.49
1:C:411:VAL:HA	1:C:467:ALA:HA	1.93	0.49
1:C:426:LYS:HB2	1:C:433:TRP:CD2	2.48	0.49
1:A:180:VAL:HG21	1:A:469:MET:HE1	1.95	0.49
1:B:464:ASN:HD22	1:B:464:ASN:N	2.11	0.48
1:A:407:PHE:HB3	1:A:428:LEU:HD21	1.96	0.48
1:A:237:ALA:HA	1:A:298:LYS:HB2	1.96	0.48
1:C:407:PHE:HB3	1:C:428:LEU:HD21	1.94	0.48
1:A:462:GLN:HE21	1:A:462:GLN:N	2.12	0.47
1:C:464:ASN:HD22	1:C:464:ASN:N	2.12	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:320:ASP:HA	1:A:406:LEU:HB3	1.97	0.47
1:B:88:VAL:CG1	1:B:89:GLY:N	2.77	0.47
1:B:140:PRO:HG3	1:B:191:LEU:HD23	1.96	0.47
1:C:88:VAL:CG1	1:C:155:ASN:O	2.63	0.46
1:A:464:ASN:HD22	1:A:464:ASN:H	1.63	0.46
1:A:461:ASN:N	1:A:462:GLN:CB	2.79	0.46
1:C:324:LEU:HD13	1:C:404:TYR:CD1	2.51	0.46
1:A:216:VAL:HG11	1:A:269:TYR:CE1	2.51	0.46
1:C:139:ILE:HD12	1:C:187:MET:HG2	1.99	0.45
1:A:387:ILE:HG12	1:C:487:ASN:HB3	1.98	0.45
1:A:393:ASP:OD2	1:A:475:ILE:HG21	2.16	0.45
1:A:464:ASN:N	1:A:464:ASN:ND2	2.64	0.45
1:A:432:ARG:HA	1:A:432:ARG:HD2	1.76	0.44
1:A:234:LEU:HD12	1:A:234:LEU:HA	1.79	0.44
1:B:142:GLN:HG3	1:B:166:SER:HB3	2.00	0.44
1:C:81:ASP:HB2	1:C:85:HIS:H	1.83	0.44
1:C:139:ILE:HD11	1:C:187:MET:HA	2.00	0.44
1:C:457:PRO:HG2	1:C:464:ASN:HB3	1.99	0.44
1:A:385:GLN:H	1:A:385:GLN:CD	2.21	0.44
1:C:428:LEU:HD13	1:C:473:ARG:CZ	2.48	0.44
1:A:169:TRP:HB3	1:A:174:ALA:HB1	2.00	0.43
1:C:271:CYS:HB3	1:C:274:CYS:HB2	2.01	0.43
1:A:306:THR:CB	1:A:308:HIS:N	2.77	0.43
1:C:325:ASN:OD1	1:C:401:ASP:N	2.52	0.43
1:B:261:GLU:HG3	1:C:244:ILE:O	2.18	0.43
1:C:397:LYS:HA	1:C:400:GLY:O	2.19	0.43
1:A:271:CYS:HB3	1:A:274:CYS:HB2	2.01	0.43
1:B:425:ILE:HB	1:B:436:PHE:CE1	2.54	0.43
1:B:426:LYS:HB2	1:B:433:TRP:CD2	2.54	0.43
1:A:80:VAL:HG11	1:C:80:VAL:HG21	2.00	0.43
1:C:108:MET:HA	1:C:483:PHE:HZ	1.84	0.42
1:A:306:THR:CB	1:A:307:MET:HA	2.49	0.42
1:A:299:ARG:HD2	1:A:467:ALA:O	2.19	0.42
1:C:445:THR:HG23	1:C:448:GLU:H	1.84	0.42
1:A:303:ASP:HB3	1:A:306:THR:OG1	2.20	0.41
1:B:289:PHE:CE1	1:B:324:LEU:HD23	2.55	0.41
1:B:406:LEU:HB2	1:B:472:TYR:CE2	2.55	0.41
1:B:90:LEU:HD23	1:B:160:THR:CG2	2.50	0.41
1:B:411:VAL:HA	1:B:467:ALA:HA	2.02	0.41
1:A:207:LEU:HB3	1:A:292:LEU:HD12	2.03	0.41
1:C:297:LEU:HD13	1:C:316:MET:HE3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:387:ILE:H	1:C:387:ILE:HD12	1.85	0.41
1:B:464:ASN:HD22	1:B:464:ASN:H	1.69	0.41
1:A:451:LYS:NZ	3:A:712:HOH:O	2.50	0.41
1:B:181:GLN:NE2	1:B:233:ASP:OD2	2.54	0.41
1:B:405:GLU:OE2	1:B:426:LYS:NZ	2.42	0.41
1:C:405:GLU:OE2	1:C:426:LYS:NZ	2.39	0.41
1:A:389:HIS:HB3	1:A:392:VAL:H	1.85	0.40
1:A:112:PHE:O	1:A:116:MET:HG2	2.21	0.40
1:A:406:LEU:HB2	1:A:472:TYR:CE2	2.57	0.40
1:B:385:GLN:N	1:B:386:PRO:CD	2.84	0.40
1:C:395:ILE:O	1:C:398:THR:OG1	2.29	0.40
1:A:154:GLU:HB3	1:C:76:TYR:HD2	1.87	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	344/508 (68%)	323 (94%)	20 (6%)	1 (0%)	41	64
1	B	319/508 (63%)	302 (95%)	16 (5%)	1 (0%)	41	64
1	C	337/508 (66%)	317 (94%)	19 (6%)	1 (0%)	41	64
All	All	1000/1524 (66%)	942 (94%)	55 (6%)	3 (0%)	41	64

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	386	PRO
1	C	457	PRO
1	A	418	GLY

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	312/444 (70%)	307 (98%)	5 (2%)	62	82
1	B	293/444 (66%)	288 (98%)	5 (2%)	60	81
1	C	308/444 (69%)	305 (99%)	3 (1%)	76	90
All	All	913/1332 (68%)	900 (99%)	13 (1%)	67	85

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	82	GLU
1	A	185	ARG
1	A	306	THR
1	A	462	GLN
1	A	464	ASN
1	B	76	TYR
1	B	383	VAL
1	B	385	GLN
1	B	464	ASN
1	B	491	GLN
1	C	88	VAL
1	C	320	ASP
1	C	464	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	325	ASN
1	A	462	GLN
1	A	464	ASN
1	B	464	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry

Of 2 ligands modelled in this entry, 2 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, 95^{th} 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	350/508 (68%)	-0.11	8 (2%) 60 54	18, 40, 77, 142	0
1	B	329/508 (64%)	0.30	15 (4%) 32 26	59, 94, 136, 203	0
1	C	345/508 (67%)	0.34	28 (8%) 12 8	61, 87, 135, 176	0
All	All	1024/1524 (67%)	0.17	51 (4%) 28 23	18, 79, 131, 203	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	76	TYR	11.0
1	C	458	SER	9.0
1	B	148	LEU	6.4
1	C	191	LEU	5.6
1	C	76	TYR	5.4
1	B	285	ARG	5.1
1	C	78	ILE	4.8
1	C	112	PHE	3.9
1	C	382	CYS	3.8
1	B	262	LEU	3.8
1	B	85	HIS	3.6
1	C	197	GLY	3.6
1	C	134	LYS	3.5
1	C	203	LEU	3.5
1	A	77	ALA	3.5
1	A	383	VAL	3.5
1	A	460	TRP	3.3
1	B	94	ALA	3.2
1	C	205	GLN	3.2
1	C	393	ASP	3.2
1	B	259	GLN	3.1
1	C	77	ALA	3.1
1	B	463	SER	3.1

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Mol	Chain	Res	Type	RSRZ
1	C	463	SER	3.0
1	C	135	ALA	3.0
1	B	218	CYS	2.9
1	C	146	LEU	2.9
1	A	117	TYR	2.8
1	C	383	VAL	2.7
1	C	184	CYS	2.7
1	A	385	GLN	2.7
1	C	145	LYS	2.6
1	B	221	CYS	2.5
1	B	280	ALA	2.5
1	C	389	HIS	2.5
1	B	117	TYR	2.5
1	B	216	VAL	2.5
1	C	95	MET	2.5
1	C	232	LEU	2.4
1	C	137	GLN	2.3
1	C	187	MET	2.3
1	A	78	ILE	2.3
1	C	230	TYR	2.3
1	A	461	ASN	2.1
1	B	172	ASN	2.1
1	C	175	TYR	2.1
1	C	490	PRO	2.1
1	C	244	ILE	2.1
1	B	484	ILE	2.1
1	B	93	GLN	2.1
1	C	194	LYS	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,

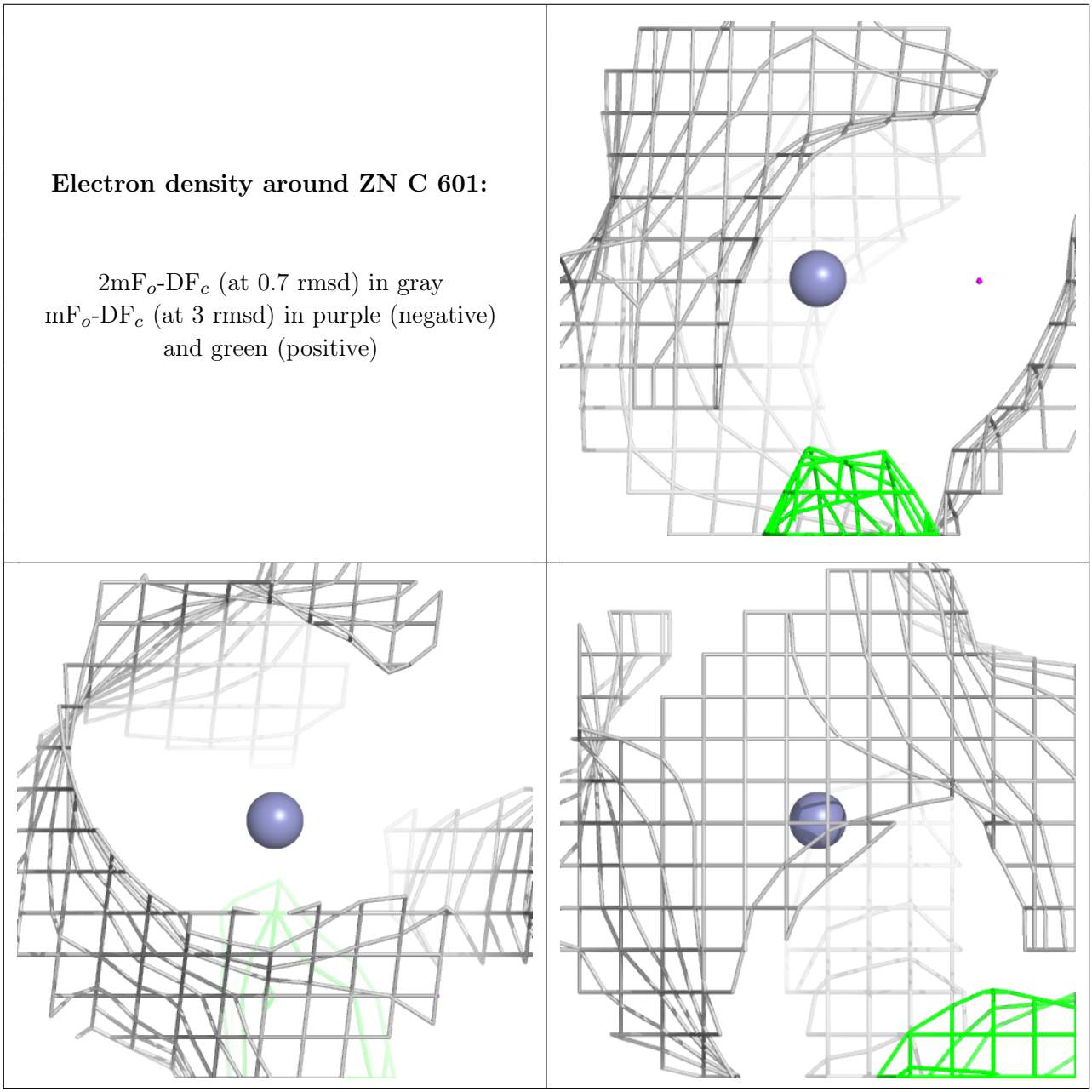
median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	ZN	C	601	1/1	0.96	0.12	71,71,71,71	0
2	ZN	A	601	1/1	0.99	0.16	30,30,30,30	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.

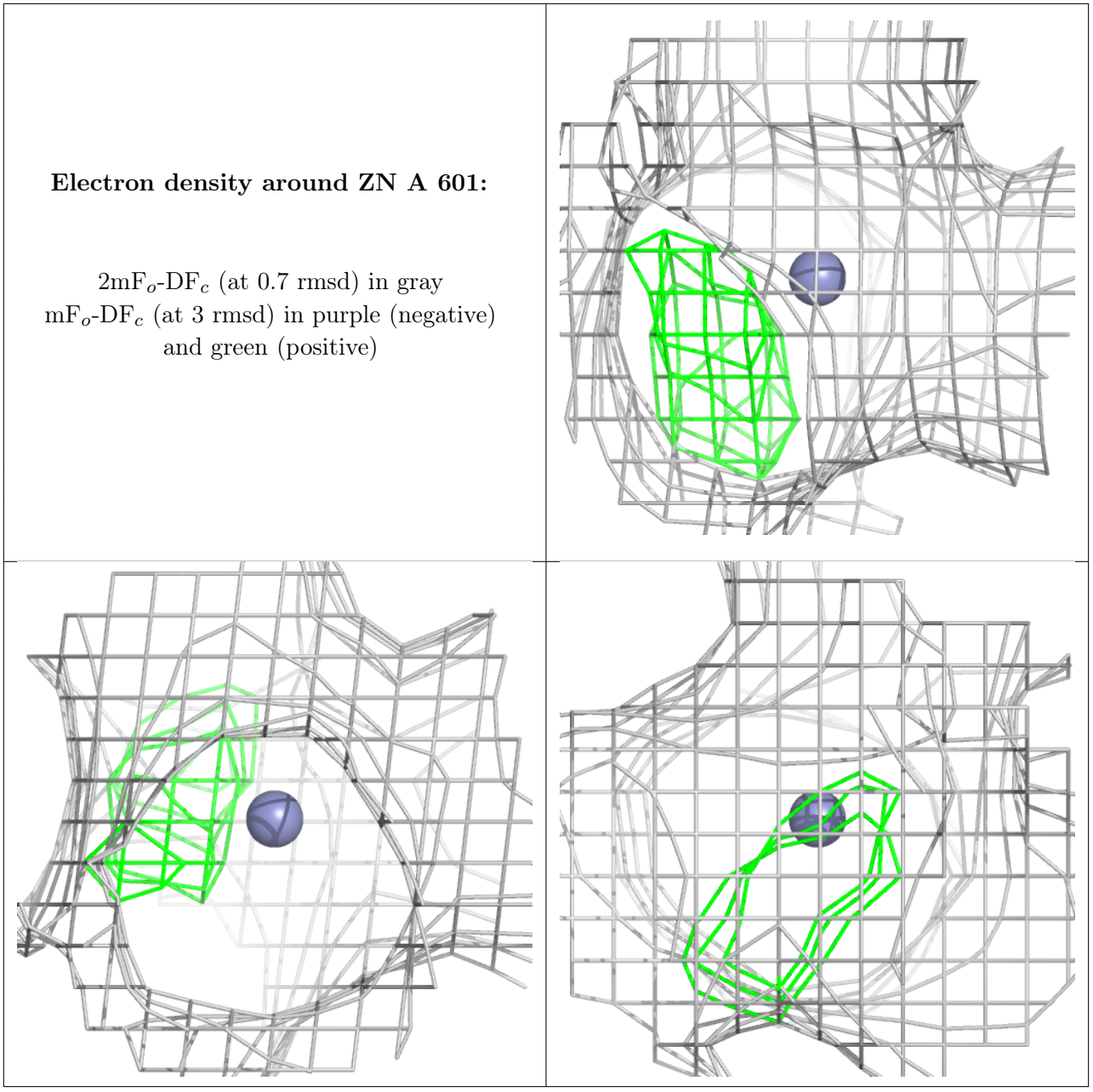
Electron density around ZN C 601:

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



Electron density around ZN A 601:

$2mF_o$-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

There are no such residues in this entry.