Full wwPDB X-ray Structure Validation Report (i)

Aug 2, 2022 – 12:09 PM JST

PDB ID	:	7FAC
Title	:	Crystal Structure of C-terminus of the non-structural protein 2 from SARS coronavirus
Authors	:	Li, Y.Y.; Ren, Z.L.; Bao, Z.H.; Ming, Z.H.; Yan, L.M.; Lou, Z.Y.; Rao, Z.H.
Deposited on	:	2021-07-06
Resolution	:	2.71 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 (i)) were used in the production of this report:

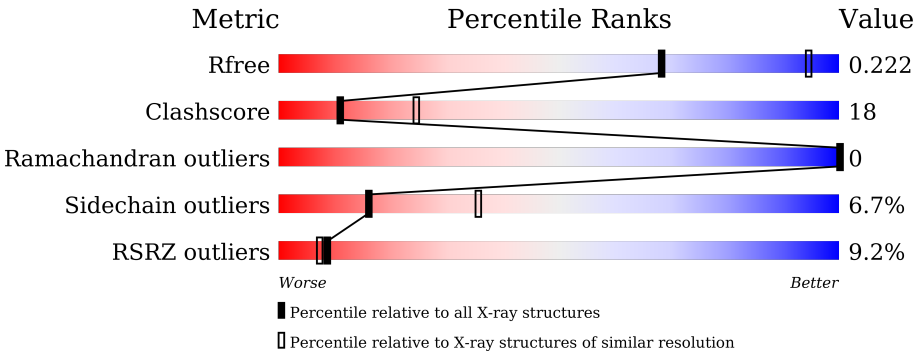
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.29
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.29

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 2.71 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	3359 (2.74-2.70)
Clashscore	141614	3686 (2.74-2.70)
Ramachandran outliers	138981	3622 (2.74-2.70)
Sidechain outliers	138945	3623 (2.74-2.70)
RSRZ outliers	127900	3276 (2.74-2.70)

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 <=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	529	9% 74% 22%

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
2	ZN	A	602	-	-	-	X

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4029 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 Non-structural protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	524	Total	C	N	O	S	0	0	0
			4018	2539	684	766	29			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P0C6U8
A	0	SER	-	expression tag	UNP P0C6U8

- 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	2	Total	Zn	0	0
			2	2		

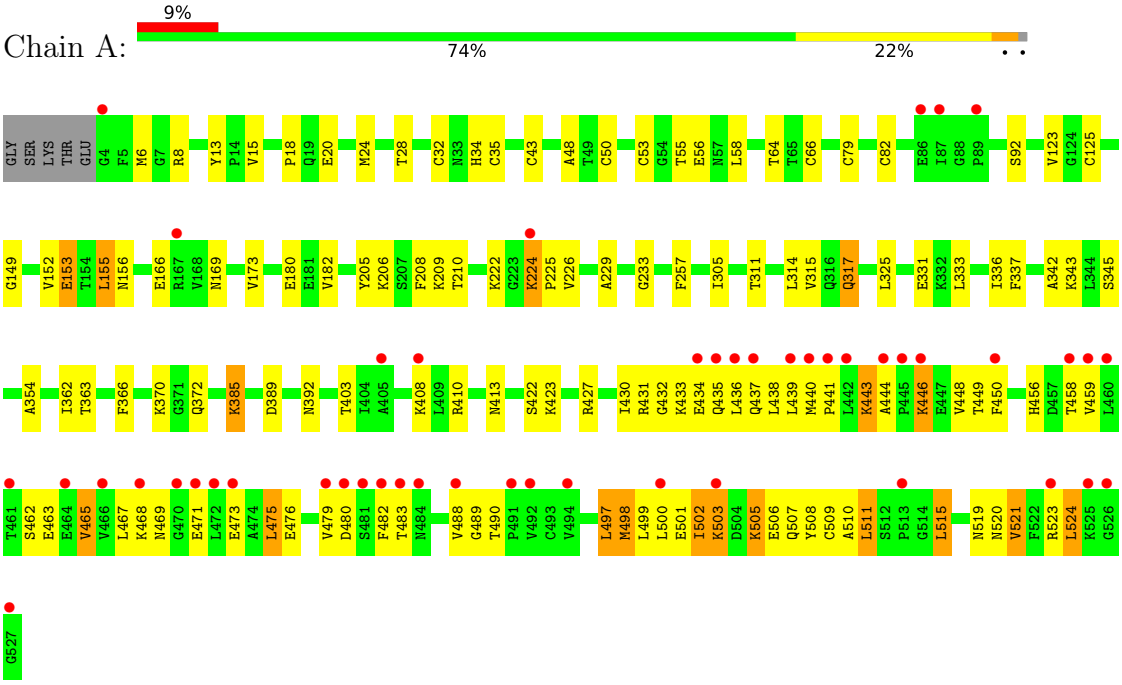
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	9	Total	O	0	0
			9	9		

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: Non-structural protein 2



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α, β, γ	112.83Å 112.83Å 91.08Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	36.93 – 2.71 34.23 – 2.71	Depositor EDS
% Data completeness (in resolution range)	99.6 (36.93-2.71) 99.7 (34.23-2.71)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.39 (at 2.72Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.197 , 0.257 0.215 , 0.222	Depositor DCC
R_{free} test set	853 reflections (4.75%)	wwPDB-VP
Wilson B-factor (Å^2)	68.5	Xtriage
Anisotropy	0.196	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 59.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.055 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	4029	wwPDB-VP
Average B, all atoms (Å^2)	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.01% 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	0.55	0/4089	0.72	0/5544

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

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	4018	0	4037	146	0
2	A	2	0	0	0	0
3	A	9	0	0	0	0
All	All	4029	0	4037	146	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 18.

All (146) 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:35:CYS:SG	1:A:53:CYS:HB2	1.83	1.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:438:LEU:CD2	1:A:463:GLU:HB3	1.77	1.13
1:A:224:LYS:HG3	1:A:225:PRO:HD3	1.28	1.13
1:A:433:LYS:O	1:A:440:MET:HE3	1.58	1.03
1:A:433:LYS:HB3	1:A:440:MET:HE2	1.44	0.98
1:A:438:LEU:HD21	1:A:463:GLU:CB	1.92	0.98
1:A:28:THR:HG22	1:A:64:THR:HG22	1.44	0.97
1:A:438:LEU:HD21	1:A:463:GLU:HB3	0.98	0.96
1:A:53:CYS:SG	1:A:55:THR:HG23	2.08	0.92
1:A:35:CYS:SG	1:A:53:CYS:CB	2.57	0.92
1:A:173:VAL:O	1:A:224:LYS:HA	1.74	0.86
1:A:35:CYS:HG	1:A:53:CYS:HB2	1.39	0.85
1:A:224:LYS:CG	1:A:225:PRO:HD3	2.06	0.84
1:A:53:CYS:SG	1:A:55:THR:CG2	2.66	0.84
1:A:433:LYS:O	1:A:440:MET:CE	2.28	0.82
1:A:15:VAL:HG23	1:A:20:GLU:HB2	1.64	0.80
1:A:449:THR:H	1:A:497:LEU:HA	1.46	0.80
1:A:35:CYS:HG	1:A:53:CYS:CB	1.93	0.78
1:A:471:GLU:O	1:A:524:LEU:HD13	1.83	0.78
1:A:515:LEU:N	1:A:515:LEU:HD13	2.01	0.75
1:A:450:PHE:CE2	1:A:498:MET:SD	2.81	0.74
1:A:433:LYS:HD2	1:A:446:LYS:HA	1.69	0.73
1:A:325:LEU:HD22	1:A:366:PHE:CZ	2.24	0.73
1:A:498:MET:HB2	1:A:511:LEU:HD13	1.70	0.72
1:A:446:LYS:NZ	1:A:446:LYS:HB2	2.05	0.71
1:A:149:GLY:N	1:A:152:VAL:HG11	2.06	0.70
1:A:471:GLU:O	1:A:524:LEU:CD1	2.41	0.68
1:A:441:PRO:HD3	1:A:465:VAL:CG2	2.24	0.68
1:A:506:GLU:N	1:A:506:GLU:OE1	2.27	0.67
1:A:433:LYS:HB3	1:A:440:MET:CE	2.23	0.66
1:A:498:MET:HG3	1:A:511:LEU:HB2	1.77	0.66
1:A:305:ILE:H	1:A:305:ILE:HD12	1.59	0.65
1:A:498:MET:HB2	1:A:511:LEU:CD1	2.27	0.64
1:A:173:VAL:O	1:A:224:LYS:CA	2.46	0.64
1:A:497:LEU:O	1:A:497:LEU:HG	1.98	0.62
1:A:438:LEU:CD2	1:A:463:GLU:CB	2.66	0.62
1:A:441:PRO:HD3	1:A:465:VAL:HG21	1.81	0.62
1:A:433:LYS:CD	1:A:446:LYS:HB3	2.31	0.61
1:A:475:LEU:HB3	1:A:521:VAL:HG12	1.82	0.60
1:A:79:CYS:SG	1:A:82:CYS:SG	3.00	0.60
1:A:206:LYS:NZ	1:A:209:LYS:HE3	2.16	0.60
1:A:153:GLU:HA	1:A:156:ASN:HB2	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:438:LEU:O	1:A:440:MET:SD	2.61	0.58
1:A:82:CYS:SG	1:A:125:CYS:SG	3.02	0.58
1:A:430:ILE:HG12	1:A:449:THR:HG23	1.87	0.57
1:A:433:LYS:C	1:A:440:MET:HE3	2.25	0.57
1:A:450:PHE:CD2	1:A:498:MET:SD	2.98	0.57
1:A:450:PHE:CZ	1:A:498:MET:SD	2.98	0.56
1:A:8:ARG:HD2	1:A:123:VAL:O	2.05	0.56
1:A:438:LEU:C	1:A:438:LEU:HD13	2.27	0.55
1:A:433:LYS:HD2	1:A:446:LYS:HB3	1.88	0.55
1:A:325:LEU:HD22	1:A:366:PHE:CE2	2.42	0.55
1:A:446:LYS:HB2	1:A:446:LYS:HZ3	1.70	0.54
1:A:444:ALA:HB2	1:A:467:LEU:HG	1.91	0.53
1:A:476:GLU:N	1:A:476:GLU:OE1	2.42	0.52
1:A:173:VAL:HG22	1:A:233:GLY:HA2	1.92	0.52
1:A:430:ILE:CG1	1:A:449:THR:HG23	2.40	0.52
1:A:173:VAL:O	1:A:224:LYS:CB	2.58	0.52
1:A:436:LEU:HD11	1:A:450:PHE:HZ	1.75	0.52
1:A:169:ASN:HD22	1:A:229:ALA:HB3	1.74	0.52
1:A:325:LEU:HD22	1:A:366:PHE:HZ	1.71	0.52
1:A:169:ASN:HB3	1:A:229:ALA:CB	2.40	0.51
1:A:166:GLU:H	1:A:166:GLU:CD	2.13	0.51
1:A:515:LEU:N	1:A:515:LEU:CD1	2.73	0.51
1:A:317:GLN:NE2	1:A:317:GLN:N	2.59	0.51
1:A:502:ILE:HG23	1:A:505:LYS:HB2	1.91	0.51
1:A:206:LYS:HD2	1:A:210:THR:HG23	1.92	0.50
1:A:315:VAL:HG13	1:A:337:PHE:CD1	2.47	0.50
1:A:317:GLN:NE2	1:A:317:GLN:H	2.09	0.50
1:A:385:LYS:HE3	1:A:389:ASP:OD2	2.12	0.50
1:A:370:LYS:HD3	1:A:410:ARG:NH2	2.27	0.49
1:A:436:LEU:HD23	1:A:437:GLN:N	2.27	0.49
1:A:433:LYS:HD3	1:A:446:LYS:HB3	1.95	0.49
1:A:459:VAL:CG2	1:A:488:VAL:HG12	2.43	0.49
1:A:180:GLU:HG2	1:A:257:PHE:CD1	2.48	0.48
1:A:433:LYS:HD2	1:A:446:LYS:CB	2.43	0.48
1:A:50:CYS:SG	1:A:53:CYS:HB3	2.53	0.47
1:A:50:CYS:SG	1:A:53:CYS:N	2.78	0.47
1:A:434:GLU:O	1:A:435:GLN:HB2	2.14	0.47
1:A:222:LYS:O	1:A:222:LYS:HG2	2.14	0.47
1:A:342:ALA:O	1:A:345:SER:OG	2.30	0.47
1:A:499:LEU:HD23	1:A:510:ALA:HA	1.95	0.47
1:A:462:SER:H	1:A:490:THR:HG1	1.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:34:HIS:CG	1:A:53:CYS:HG	2.31	0.47
1:A:438:LEU:HD13	1:A:439:LEU:O	2.14	0.47
1:A:433:LYS:CB	1:A:440:MET:HE2	2.32	0.47
1:A:468:LYS:HD3	1:A:469:ASN:N	2.30	0.47
1:A:385:LYS:CE	1:A:389:ASP:OD2	2.64	0.46
1:A:430:ILE:HG12	1:A:449:THR:HA	1.96	0.46
1:A:315:VAL:HG13	1:A:337:PHE:HB3	1.98	0.46
1:A:372:GLN:OE1	1:A:392:ASN:HB3	2.16	0.46
1:A:498:MET:HE2	1:A:498:MET:HB3	1.82	0.46
1:A:422:SER:OG	1:A:423:LYS:N	2.49	0.45
1:A:311:THR:O	1:A:314:LEU:HB2	2.16	0.45
1:A:433:LYS:CA	1:A:440:MET:HE3	2.46	0.45
1:A:173:VAL:O	1:A:224:LYS:HB2	2.17	0.45
1:A:35:CYS:SG	1:A:53:CYS:SG	3.11	0.45
1:A:438:LEU:HD13	1:A:439:LEU:N	2.31	0.45
1:A:449:THR:HB	1:A:497:LEU:HB2	1.99	0.45
1:A:439:LEU:HD23	1:A:439:LEU:HA	1.63	0.45
1:A:468:LYS:O	1:A:469:ASN:OD1	2.34	0.45
1:A:224:LYS:N	1:A:225:PRO:CD	2.80	0.44
1:A:433:LYS:HD2	1:A:446:LYS:CA	2.41	0.44
1:A:362:ILE:HG22	1:A:363:THR:HG23	1.98	0.44
1:A:333:LEU:HB3	1:A:336:ILE:HD12	2.00	0.44
1:A:441:PRO:C	1:A:443:LYS:H	2.21	0.44
1:A:13:TYR:O	1:A:15:VAL:HG12	2.17	0.44
1:A:149:GLY:C	1:A:152:VAL:HG13	2.38	0.44
1:A:446:LYS:NZ	1:A:446:LYS:CB	2.73	0.43
1:A:403:THR:OG1	1:A:408:LYS:HG2	2.17	0.43
1:A:53:CYS:SG	1:A:55:THR:HG21	2.56	0.43
1:A:370:LYS:HD3	1:A:410:ARG:HH21	1.83	0.43
1:A:224:LYS:CD	1:A:225:PRO:HD3	2.47	0.43
1:A:343:LYS:HA	1:A:343:LYS:HD2	1.93	0.43
1:A:524:LEU:HD13	1:A:524:LEU:HA	1.69	0.43
1:A:56:GLU:O	1:A:56:GLU:HG2	2.18	0.43
1:A:508:TYR:O	1:A:521:VAL:HG22	2.18	0.43
1:A:24:MET:CE	1:A:66:CYS:HB3	2.49	0.42
1:A:34:HIS:CG	1:A:53:CYS:SG	3.12	0.42
1:A:430:ILE:HG23	1:A:448:VAL:O	2.19	0.42
1:A:6:MET:SD	1:A:18:PRO:HD3	2.60	0.42
1:A:205:TYR:CZ	1:A:222:LYS:HB2	2.55	0.42
1:A:34:HIS:ND1	1:A:34:HIS:C	2.72	0.42
1:A:506:GLU:N	1:A:506:GLU:CD	2.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:489:GLY:HA3	1:A:500:LEU:HD11	2.02	0.42
1:A:24:MET:HE2	1:A:66:CYS:HB3	2.01	0.42
1:A:431:ARG:NE	1:A:431:ARG:HA	2.35	0.42
1:A:35:CYS:HG	1:A:53:CYS:HG	1.65	0.41
1:A:155:LEU:HD13	1:A:155:LEU:HA	1.85	0.41
1:A:449:THR:H	1:A:497:LEU:CA	2.24	0.41
1:A:182:VAL:HG13	1:A:208:PHE:CE1	2.56	0.41
1:A:311:THR:HB	1:A:354:ALA:HB1	2.01	0.41
1:A:436:LEU:HD23	1:A:437:GLN:H	1.84	0.41
1:A:169:ASN:HB3	1:A:229:ALA:HB3	2.01	0.41
1:A:50:CYS:SG	1:A:53:CYS:CB	3.08	0.41
1:A:503:LYS:HA	1:A:503:LYS:HD3	1.45	0.41
1:A:507:GLN:HA	1:A:523:ARG:HG2	2.02	0.41
1:A:500:LEU:HD13	1:A:501:GLU:N	2.35	0.41
1:A:224:LYS:HG3	1:A:225:PRO:CD	2.21	0.40
1:A:413:ASN:OD1	1:A:413:ASN:N	2.53	0.40
1:A:32:CYS:SG	1:A:50:CYS:HB2	2.61	0.40
1:A:432:GLY:HA3	1:A:434:GLU:OE1	2.22	0.40
1:A:456:HIS:CE1	1:A:519:ASN:OD1	2.74	0.40
1:A:43:CYS:HB3	1:A:48:ALA:CB	2.51	0.40
1:A:473:GLU:OE1	1:A:524:LEU:C	2.60	0.40
1:A:433:LYS:HG2	1:A:440:MET:HG2	2.03	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	522/529 (99%)	499 (96%)	23 (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	447/451 (99%)	417 (93%)	30 (7%)	16 35

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	58	LEU
1	A	92	SER
1	A	153	GLU
1	A	155	LEU
1	A	224	LYS
1	A	226	VAL
1	A	317	GLN
1	A	331	GLU
1	A	385	LYS
1	A	427	ARG
1	A	443	LYS
1	A	446	LYS
1	A	458	THR
1	A	465	VAL
1	A	475	LEU
1	A	479	VAL
1	A	480	ASP
1	A	482	PHE
1	A	483	THR
1	A	497	LEU
1	A	498	MET
1	A	502	ILE
1	A	503	LYS
1	A	505	LYS
1	A	509	CYS
1	A	511	LEU
1	A	515	LEU
1	A	520	ASN
1	A	521	VAL
1	A	524	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	169	ASN
1	A	456	HIS

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	524/529 (99%)	0.39	48 (9%) 9 7	30, 79, 147, 167	0

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	526	GLY	10.4
1	A	459	VAL	5.5
1	A	484	ASN	5.4
1	A	491	PRO	5.4
1	A	224	LYS	5.2
1	A	523	ARG	4.9
1	A	473	GLU	4.8
1	A	436	LEU	4.7
1	A	442	LEU	4.6
1	A	527	GLY	4.6
1	A	435	GLN	4.6
1	A	444	ALA	4.4
1	A	481	SER	4.3
1	A	525	LYS	4.2
1	A	458	THR	4.2
1	A	87	ILE	4.0
1	A	441	PRO	3.9
1	A	492	VAL	3.9
1	A	503	LYS	3.9
1	A	439	LEU	3.7
1	A	460	LEU	3.4
1	A	483	THR	3.3
1	A	470	GLY	3.3
1	A	482	PHE	3.2
1	A	4	GLY	3.2
1	A	440	MET	3.1
1	A	471	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	479	VAL	3.0
1	A	445	PRO	3.0
1	A	405	ALA	3.0
1	A	434	GLU	2.9
1	A	86	GLU	2.8
1	A	472	LEU	2.8
1	A	464	GLU	2.8
1	A	437	GLN	2.8
1	A	500	LEU	2.8
1	A	89	PRO	2.8
1	A	488	VAL	2.7
1	A	408	LYS	2.6
1	A	466	VAL	2.6
1	A	480	ASP	2.5
1	A	494	VAL	2.3
1	A	468	LYS	2.3
1	A	461	THR	2.3
1	A	446	LYS	2.3
1	A	513	PRO	2.2
1	A	167	ARG	2.2
1	A	450	PHE	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)

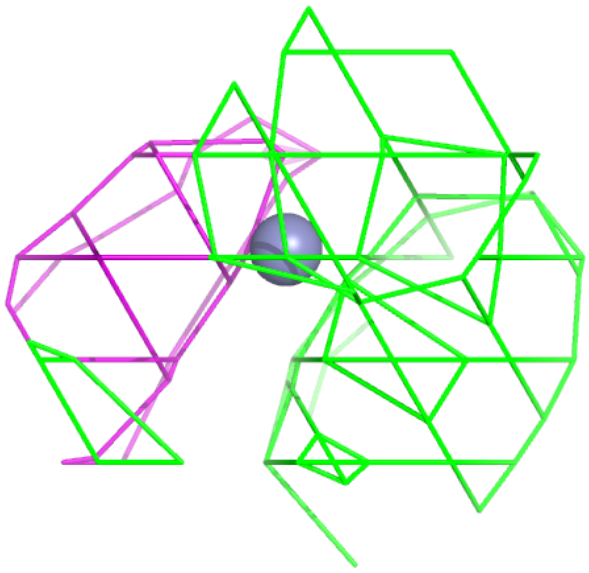
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

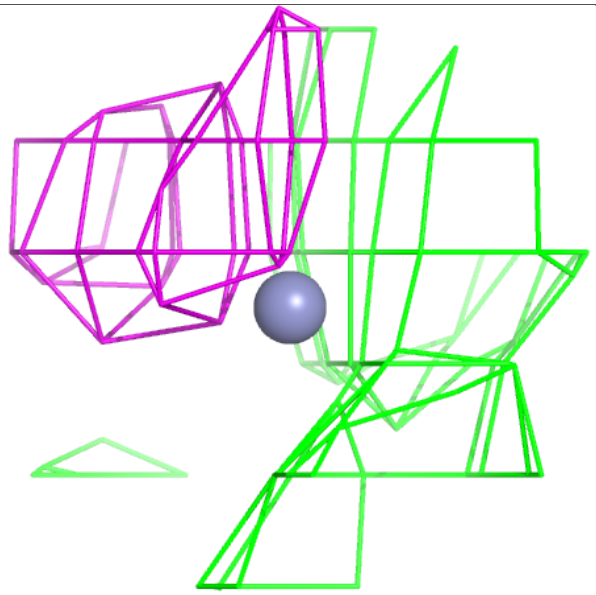
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	ZN	A	601	1/1	0.34	0.15	79,79,79,79	0
2	ZN	A	602	1/1	0.76	0.44	85,85,85,85	0

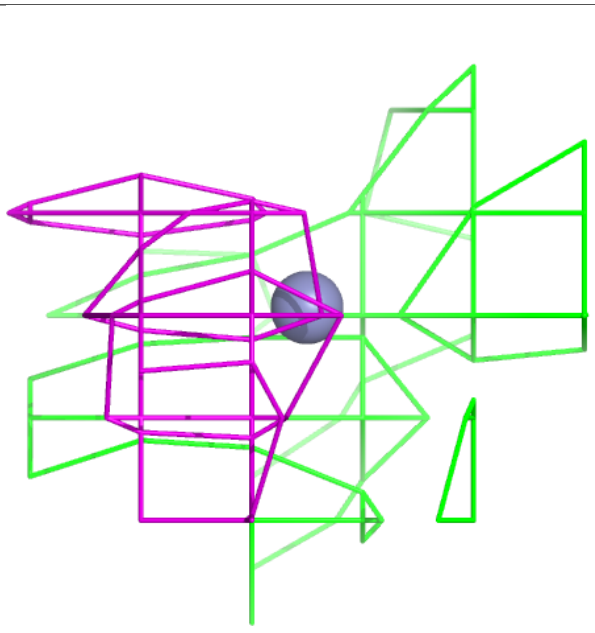
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ZN 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)

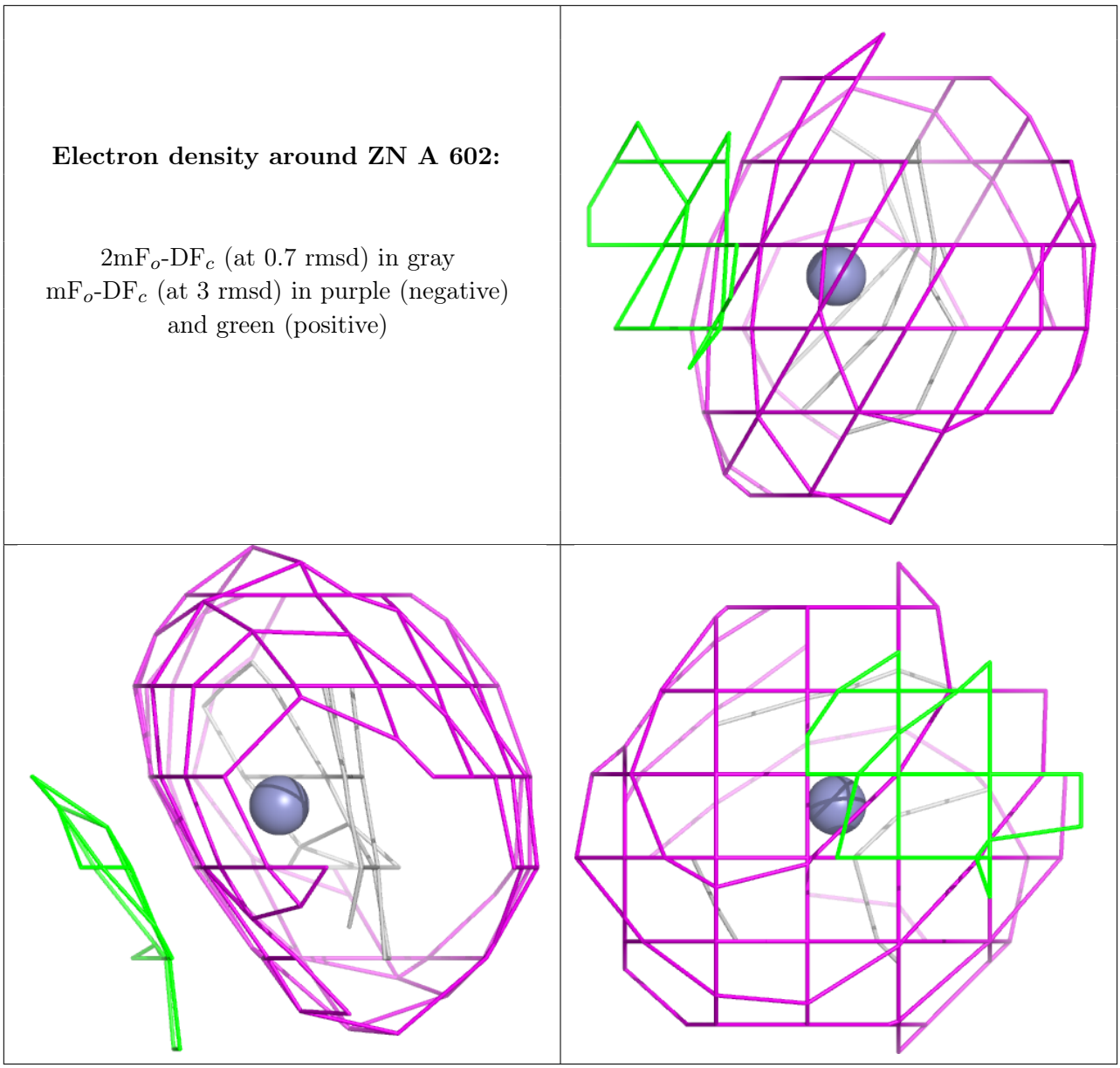






Electron density around ZN A 602:

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



6.5 Other polymers (i)

There are no such residues in this entry.