



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 20, 2023 – 12:29 AM JST

PDB ID : 7C8J
Title : Structural basis for cross-species recognition of COVID-19 virus spike receptor binding domain to bat ACE2
Authors : Liu, K.F.; Wang, J.; Tan, S.G.; Niu, S.; Wu, L.L.; Zhang, Y.F.; Pan, X.Q.; Meng, Y.M.; Chen, Q.; Wang, Q.H.; Wang, H.W.; Qi, J.X.; Gao, G.F.
Deposited on : 2020-06-01
Resolution : 3.18 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 : 2.36
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

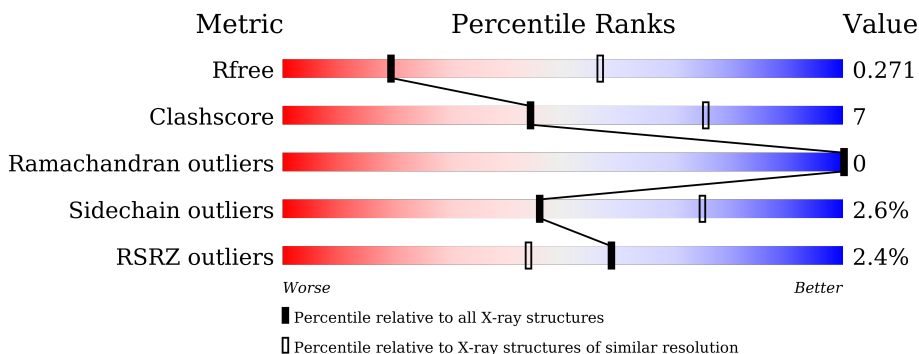
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

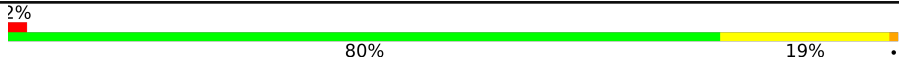

The reported resolution of this entry is 3.18 Å.

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	1467 (3.20-3.16)
Clashscore	141614	1599 (3.20-3.16)
Ramachandran outliers	138981	1574 (3.20-3.16)
Sidechain outliers	138945	1573 (3.20-3.16)
RSRZ outliers	127900	1423 (3.20-3.16)

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	707	
2	B	195	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7317 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 Angiotensin-converting enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	707	5773	3688	965	1087	33	0	0	0

- Molecule 2 is a protein called SARS-CoV-2 Receptor binding domain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	195	1543	989	257	289	8	0	0	0

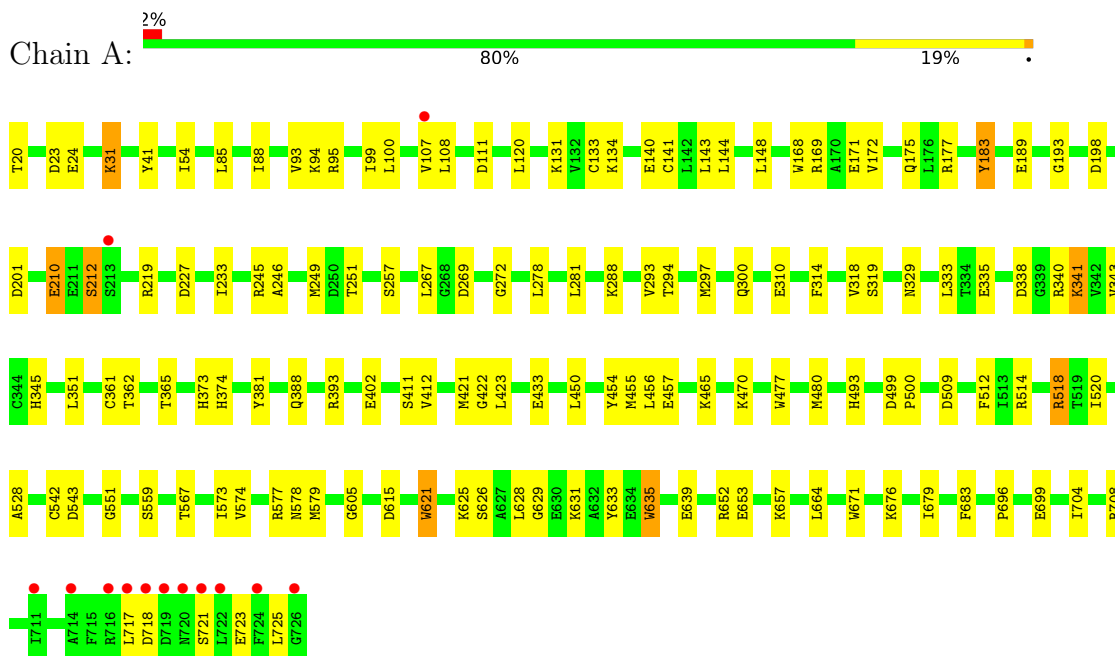
- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

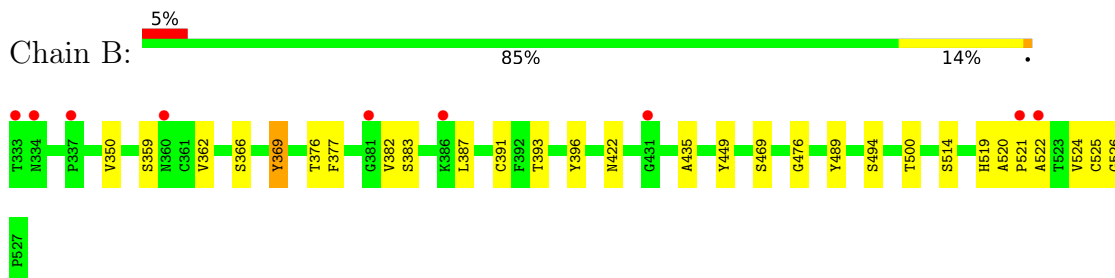
3 Residue-property plots

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: Angiotensin-converting enzyme



- Molecule 2: SARS-CoV-2 Receptor binding domain



4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α , β , γ	163.20Å 163.20Å 211.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.10 – 3.18 48.10 – 3.18	Depositor EDS
% Data completeness (in resolution range)	90.7 (48.10-3.18) 90.7 (48.10-3.18)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 3.19Å)	Xtrriage
Refinement program	PHENIX 1.16_3549	Depositor
R, R_{free}	0.218 , 0.271 0.218 , 0.271	Depositor DCC
R_{free} test set	1108 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	65.4	Xtrriage
Anisotropy	0.064	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 21.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	7317	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.73% of the height of the origin peak. No significant pseudotranslation is detected.*

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:
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	0.25	0/5933	0.46	3/8042 (0.0%)
2	B	0.26	0/1587	0.46	0/2161
All	All	0.25	0/7520	0.46	3/10203 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
2	B	0	1
All	All	0	4

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	635	TRP	CA-CB-CG	6.31	125.69	113.70
1	A	635	TRP	CB-CA-C	-5.77	98.86	110.40
1	A	31	LYS	CD-CE-NZ	5.52	124.40	111.70

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	210	GLU	Peptide
1	A	212	SER	Peptide
1	A	626	SER	Peptide

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Mol	Chain	Res	Type	Group
2	B	519	HIS	Peptide

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	5773	0	5539	81	0
2	B	1543	0	1460	17	0
3	A	1	0	0	0	0
All	All	7317	0	6999	94	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 7.

All (94) 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:120:LEU:HD21	1:A:183:TYR:HE1	1.52	0.74
1:A:198:ASP:OD2	1:A:465:LYS:HG3	1.90	0.72
2:B:520:ALA:HB1	2:B:521:PRO:HD2	1.73	0.70
1:A:183:TYR:OH	1:A:509:ASP:OD2	2.10	0.69
1:A:54:ILE:HD11	1:A:343:VAL:HG23	1.75	0.69
1:A:177:ARG:NH1	1:A:470:LYS:O	2.25	0.69
1:A:251:THR:HG21	1:A:281:LEU:HD22	1.75	0.69
1:A:31:LYS:HE2	2:B:489:TYR:HB3	1.77	0.66
1:A:210:GLU:O	1:A:210:GLU:HG3	1.95	0.66
1:A:653:GLU:OE1	1:A:657:LYS:NZ	2.26	0.66
1:A:573:ILE:HG23	1:A:574:VAL:HG13	1.79	0.65
1:A:85:LEU:O	1:A:88:ILE:HG22	1.98	0.64
2:B:396:TYR:HB2	2:B:514:SER:HB2	1.80	0.64
1:A:635:TRP:HB3	1:A:639:GLU:HB2	1.83	0.61
1:A:54:ILE:HB	1:A:341:LYS:HB3	1.82	0.61
1:A:95:ARG:O	1:A:99:ILE:HG12	2.01	0.60
1:A:120:LEU:HD21	1:A:183:TYR:CE1	2.36	0.60
1:A:134:LYS:NZ	1:A:140:GLU:OE2	2.36	0.59
1:A:293:VAL:HG11	1:A:423:LEU:HD13	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:319:SER:O	1:A:319:SER:OG	2.23	0.57
1:A:133:CYS:HA	1:A:141:CYS:HA	1.88	0.56
2:B:383:SER:H	2:B:387:LEU:HD12	1.68	0.56
2:B:366:SER:HA	2:B:369:TYR:CD2	2.40	0.56
1:A:696:PRO:HG2	1:A:699:GLU:HG3	1.87	0.55
1:A:293:VAL:HG12	1:A:297:MET:HG3	1.87	0.55
1:A:246:ALA:HA	1:A:249:MET:HE3	1.89	0.54
1:A:294:THR:HG23	1:A:365:THR:HA	1.89	0.54
1:A:201:ASP:OD1	1:A:219:ARG:NE	2.40	0.53
1:A:131:LYS:HB3	1:A:143:LEU:HD12	1.90	0.53
1:A:233:ILE:HD13	1:A:450:LEU:HD13	1.91	0.53
1:A:456:LEU:HD12	1:A:477:TRP:HH2	1.73	0.53
2:B:391:CYS:HA	2:B:525:CYS:HA	1.92	0.52
1:A:288:LYS:NZ	1:A:433:GLU:OE1	2.38	0.51
1:A:493:HIS:ND1	1:A:499:ASP:OD2	2.31	0.51
1:A:31:LYS:CE	2:B:489:TYR:HB3	2.40	0.51
1:A:388:GLN:O	1:A:393:ARG:NE	2.43	0.51
1:A:629:GLY:O	1:A:631:LYS:HG2	2.11	0.50
1:A:456:LEU:HD22	1:A:512:PHE:CD2	2.46	0.50
1:A:615:ASP:OD1	1:A:615:ASP:N	2.45	0.50
2:B:366:SER:HA	2:B:369:TYR:CE2	2.46	0.50
1:A:168:TRP:O	1:A:172:VAL:HG12	2.12	0.49
2:B:393:THR:HA	2:B:522:ALA:HA	1.93	0.49
2:B:350:VAL:HG22	2:B:422:ASN:HB3	1.94	0.49
1:A:542:CYS:SG	1:A:543:ASP:N	2.86	0.48
1:A:314:PHE:O	1:A:318:VAL:HG23	2.13	0.48
1:A:108:LEU:HD21	1:A:189:GLU:OE2	2.14	0.47
1:A:318:VAL:HG12	1:A:551:GLY:HA3	1.97	0.47
1:A:683:PHE:HZ	1:A:704:ILE:HD11	1.80	0.47
1:A:107:VAL:HG21	1:A:193:GLY:HA3	1.98	0.46
1:A:514:ARG:O	1:A:518:ARG:HB3	2.16	0.46
1:A:577:ARG:NH2	1:A:578:ASN:OD1	2.49	0.46
2:B:449:TYR:O	2:B:494:SER:OG	2.33	0.46
1:A:20:THR:O	1:A:24:GLU:HG2	2.15	0.45
1:A:24:GLU:OE1	2:B:476:GLY:HA2	2.17	0.45
1:A:455:MET:HE2	1:A:480:MET:HB2	1.98	0.45
1:A:318:VAL:O	1:A:551:GLY:HA3	2.16	0.45
2:B:359:SER:HA	2:B:524:VAL:CG2	2.47	0.45
1:A:457:GLU:HG2	1:A:512:PHE:HB3	1.99	0.45
1:A:335:GLU:HB2	1:A:361:CYS:SG	2.57	0.45
1:A:374:HIS:CE1	1:A:402:GLU:OE1	2.70	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:717:LEU:HB3	1:A:721:SER:OG	2.18	0.44
1:A:718:ASP:H	1:A:721:SER:HG	1.63	0.44
1:A:88:ILE:HD11	1:A:93:VAL:HG23	2.00	0.44
2:B:382:VAL:HG22	2:B:387:LEU:HD12	1.99	0.44
1:A:144:LEU:HA	1:A:148:LEU:HB2	1.98	0.44
1:A:351:LEU:HD12	1:A:351:LEU:H	1.82	0.44
1:A:628:LEU:HD12	1:A:628:LEU:HA	1.70	0.44
1:A:227:ASP:OD2	1:A:454:TYR:OH	2.24	0.44
1:A:621:TRP:CZ3	1:A:725:LEU:HD22	2.52	0.43
1:A:520:ILE:HG21	1:A:579:MET:HG2	2.00	0.43
1:A:621:TRP:HZ3	1:A:725:LEU:HB2	1.82	0.43
1:A:269:ASP:OD1	1:A:272:GLY:N	2.41	0.43
1:A:171:GLU:O	1:A:175:GLN:NE2	2.37	0.43
1:A:621:TRP:HB2	1:A:723:GLU:HG3	2.01	0.43
1:A:267:LEU:HA	1:A:278:LEU:HD11	2.00	0.43
1:A:293:VAL:HG13	1:A:423:LEU:HB3	2.02	0.42
1:A:671:TRP:O	1:A:683:PHE:HA	2.19	0.42
1:A:41:TYR:HH	2:B:500:THR:HG1	1.54	0.42
1:A:676:LYS:HB3	1:A:679:ILE:HB	2.02	0.42
1:A:245:ARG:NH2	1:A:605:GLY:O	2.52	0.42
1:A:373:HIS:CD2	1:A:412:VAL:HG21	2.55	0.42
1:A:652:ARG:NH2	1:A:664:LEU:HB3	2.34	0.42
1:A:300:GLN:NE2	1:A:422:GLY:O	2.40	0.41
1:A:333:LEU:O	1:A:362:THR:HG22	2.20	0.41
1:A:528:ALA:HB2	1:A:574:VAL:HG12	2.01	0.41
1:A:100:LEU:HD12	1:A:100:LEU:HA	1.83	0.41
2:B:376:THR:HB	2:B:435:ALA:HB3	2.03	0.41
1:A:477:TRP:CZ3	1:A:500:PRO:HB3	2.55	0.41
1:A:635:TRP:HB3	1:A:639:GLU:CB	2.50	0.41
1:A:625:LYS:HB3	1:A:625:LYS:HE3	1.85	0.41
2:B:362:VAL:HG13	2:B:526:GLY:HA2	2.03	0.41
1:A:567:THR:HB	1:A:577:ARG:HG3	2.03	0.40
1:A:310:GLU:OE2	1:A:421:MET:HE1	2.20	0.40
1:A:704:ILE:O	1:A:708:ARG:N	2.54	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	705/707 (100%)	699 (99%)	6 (1%)	0	100	100
2	B	193/195 (99%)	191 (99%)	2 (1%)	0	100	100
All	All	898/902 (100%)	890 (99%)	8 (1%)	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	625/630 (99%)	607 (97%)	18 (3%)	42	72
2	B	168/168 (100%)	165 (98%)	3 (2%)	59	81
All	All	793/798 (99%)	772 (97%)	21 (3%)	46	75

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	ASP
1	A	94	LYS
1	A	111	ASP
1	A	169	ARG
1	A	183	TYR
1	A	212	SER
1	A	257	SER
1	A	329	ASN

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Mol	Chain	Res	Type
1	A	338	ASP
1	A	340	ARG
1	A	341	LYS
1	A	345	HIS
1	A	381	TYR
1	A	411	SER
1	A	518	ARG
1	A	559	SER
1	A	621	TRP
1	A	633	TYR
2	B	369	TYR
2	B	377	PHE
2	B	469	SER

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 [i](#)

Of 1 ligands modelled in this entry, 1 is 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 [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

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, 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	707/707 (100%)	-0.10	13 (1%) 68 55	29, 57, 95, 176	0
2	B	195/195 (100%)	0.11	9 (4%) 32 19	40, 61, 105, 131	0
All	All	902/902 (100%)	-0.05	22 (2%) 59 44	29, 58, 101, 176	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	721	SER	10.3
1	A	718	ASP	5.7
1	A	720	ASN	5.4
1	A	717	LEU	3.9
1	A	726	GLY	3.9
1	A	724	PHE	3.8
1	A	716	ARG	3.2
2	B	360	ASN	3.1
2	B	381	GLY	3.0
2	B	522	ALA	2.9
2	B	334	ASN	2.8
1	A	719	ASP	2.6
1	A	711	ILE	2.6
1	A	714	ALA	2.6
1	A	722	LEU	2.6
2	B	386	LYS	2.4
2	B	521	PRO	2.4
1	A	107	VAL	2.3
2	B	333	THR	2.3
1	A	213	SER	2.2
2	B	337	PRO	2.1
2	B	431	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](#)

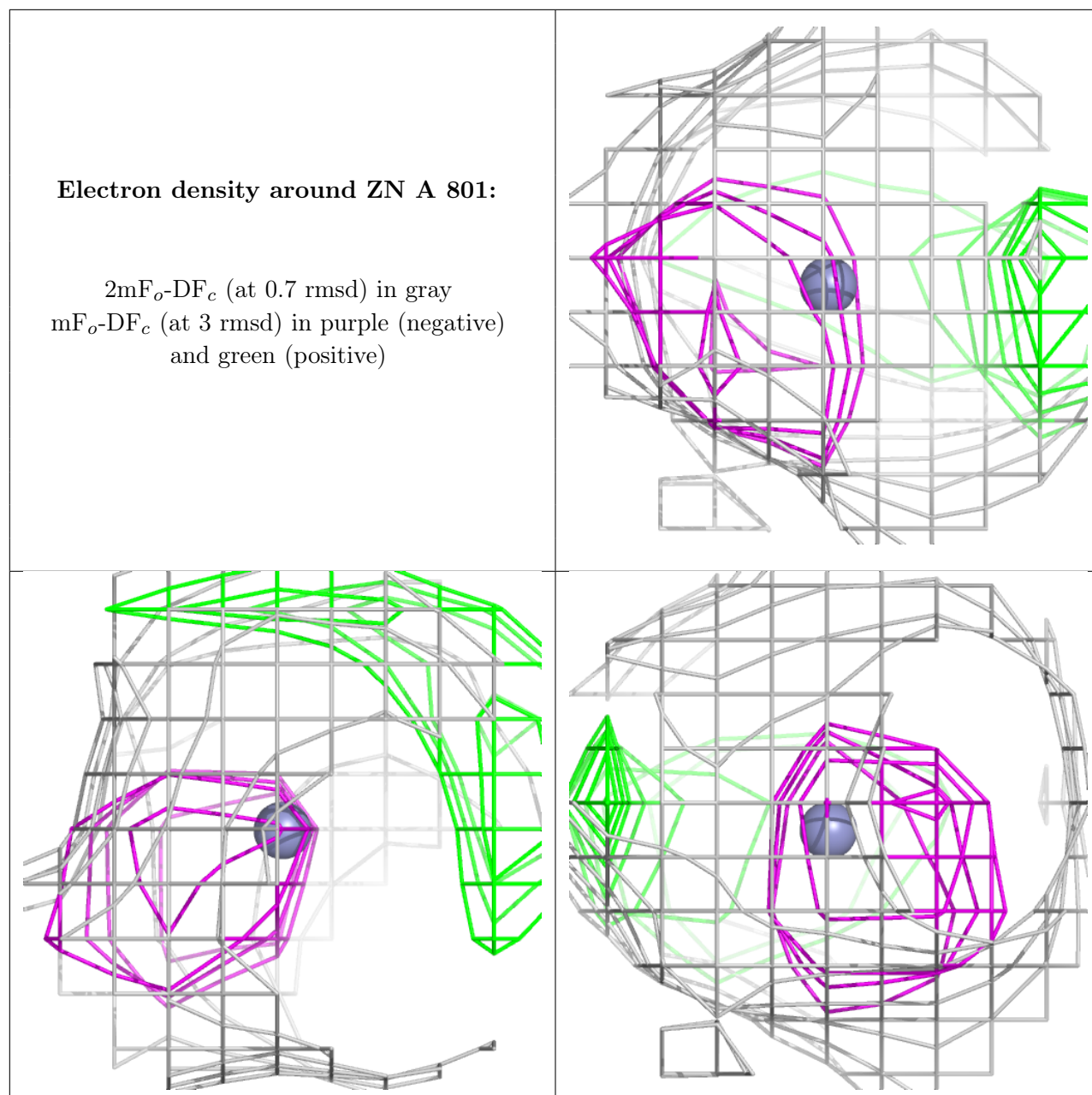
There are no monosaccharides in this entry.

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
3	ZN	A	801	1/1	0.87	0.11	42,42,42,42	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.