



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 5, 2026 – 02:10 AM UTC

PDB ID : 9SAT / pdb_00009sat
Title : Monoclonal Antibodies from COVID-19 Convalescent Patients Target Cryptic Epitopes for Universal SARS-CoV-2 Neutralization
Authors : Dessau, M.; Harit, A.
Deposited on : 2025-08-07
Resolution : 2.56 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 : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

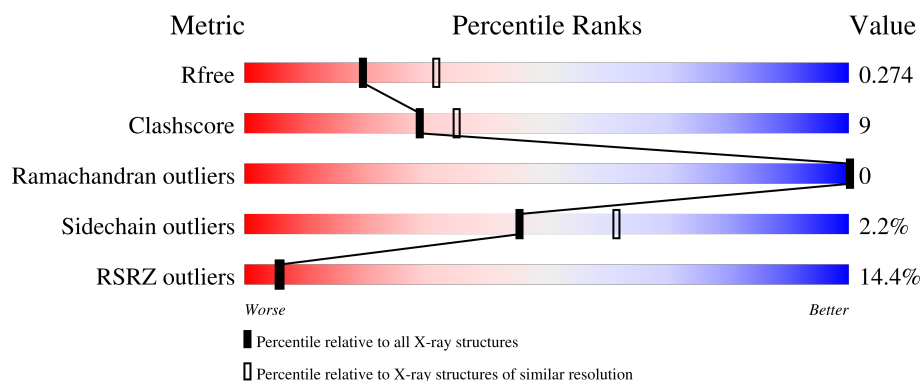
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.56 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}	180053	1853 (2.58-2.54)
Clashscore	190562	1897 (2.58-2.54)
Ramachandran outliers	187476	1875 (2.58-2.54)
Sidechain outliers	187428	1875 (2.58-2.54)
RSRZ outliers	180081	1853 (2.58-2.54)

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	H	225	<div> <div>11%</div> <div>82%</div> <div>14%</div> <div>• •</div> </div>
2	L	216	<div> <div>22%</div> <div>73%</div> <div>21%</div> <div>5%</div> <div>•</div> </div>
3	R	266	<div> <div>7%</div> <div>61%</div> <div>12%</div> <div>27%</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5097 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 TAU-1109 Fab Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	219	Total	C	N	O	S	0	0	0
			1654	1038	279	328	9			

- Molecule 2 is a protein called TAU-1109 Fab Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	213	Total	C	N	O	S	0	0	0
			1642	1032	282	324	4			

- Molecule 3 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	R	195	Total	C	N	O	S	0	1	0
			1546	991	257	290	8			

There are 43 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	542	GLY	-	expression tag	UNP P0DTC2
R	543	GLY	-	expression tag	UNP P0DTC2
R	544	ARG	-	expression tag	UNP P0DTC2
R	545	LEU	-	expression tag	UNP P0DTC2
R	546	GLU	-	expression tag	UNP P0DTC2
R	547	VAL	-	expression tag	UNP P0DTC2
R	548	LEU	-	expression tag	UNP P0DTC2
R	549	PHE	-	expression tag	UNP P0DTC2
R	550	GLN	-	expression tag	UNP P0DTC2
R	551	GLY	-	expression tag	UNP P0DTC2
R	552	PRO	-	expression tag	UNP P0DTC2
R	553	GLY	-	expression tag	UNP P0DTC2
R	554	SER	-	expression tag	UNP P0DTC2
R	555	ALA	-	expression tag	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
R	556	TRP	-	expression tag	UNP P0DTC2
R	557	SER	-	expression tag	UNP P0DTC2
R	558	HIS	-	expression tag	UNP P0DTC2
R	559	PRO	-	expression tag	UNP P0DTC2
R	560	GLN	-	expression tag	UNP P0DTC2
R	561	PHE	-	expression tag	UNP P0DTC2
R	562	GLU	-	expression tag	UNP P0DTC2
R	563	LYS	-	expression tag	UNP P0DTC2
R	564	GLY	-	expression tag	UNP P0DTC2
R	565	GLY	-	expression tag	UNP P0DTC2
R	566	GLY	-	expression tag	UNP P0DTC2
R	567	SER	-	expression tag	UNP P0DTC2
R	568	GLY	-	expression tag	UNP P0DTC2
R	569	GLY	-	expression tag	UNP P0DTC2
R	570	GLY	-	expression tag	UNP P0DTC2
R	571	GLY	-	expression tag	UNP P0DTC2
R	572	SER	-	expression tag	UNP P0DTC2
R	573	GLY	-	expression tag	UNP P0DTC2
R	574	GLY	-	expression tag	UNP P0DTC2
R	575	SER	-	expression tag	UNP P0DTC2
R	576	ALA	-	expression tag	UNP P0DTC2
R	577	TRP	-	expression tag	UNP P0DTC2
R	578	SER	-	expression tag	UNP P0DTC2
R	579	HIS	-	expression tag	UNP P0DTC2
R	580	PRO	-	expression tag	UNP P0DTC2
R	581	GLN	-	expression tag	UNP P0DTC2
R	582	PHE	-	expression tag	UNP P0DTC2
R	583	GLU	-	expression tag	UNP P0DTC2
R	584	LYS	-	expression tag	UNP P0DTC2

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	H	1	Total Zn 1 1	0	0
4	L	2	Total Zn 2 2	0	0

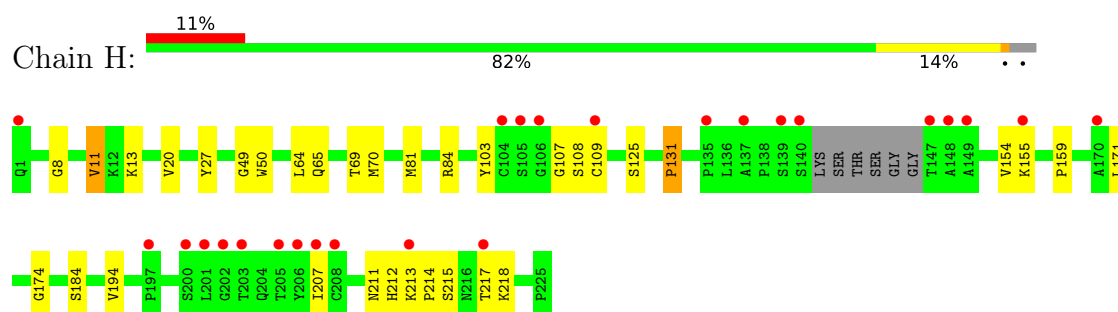
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	86	Total 86	O 86	0	0
5	L	83	Total 83	O 83	0	0
5	R	83	Total 83	O 83	0	0

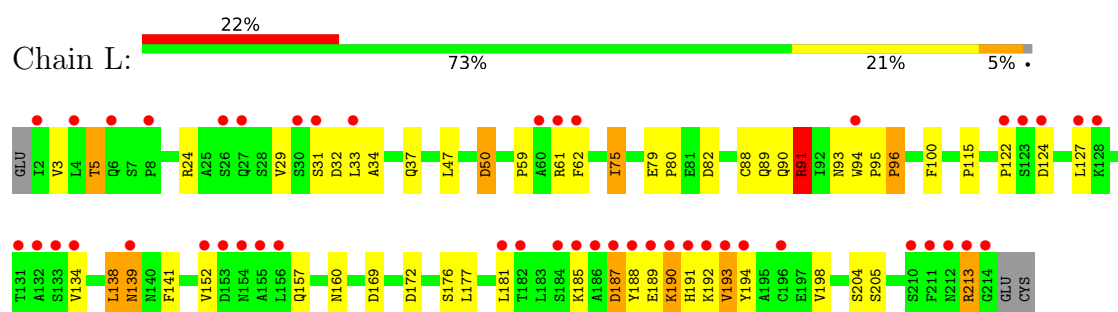
3 Residue-property plots [i](#)

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.

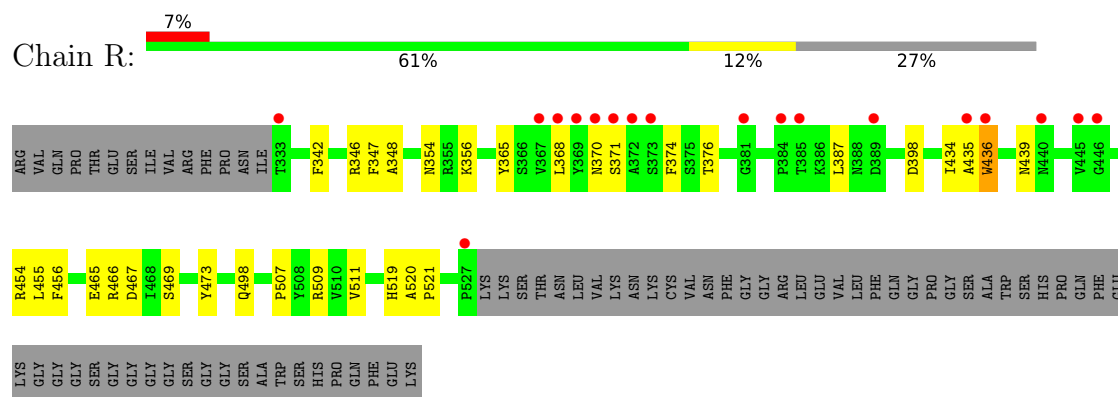
• Molecule 1: TAU-1109 Fab Heavy Chain



• Molecule 2: TAU-1109 Fab Light Chain



• Molecule 3: Spike protein S1



4 Data and refinement statistics

Property	Value	Source
Space group	I 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	83.26Å 103.00Å 225.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	93.69 – 2.56 93.69 – 2.56	Depositor EDS
% Data completeness (in resolution range)	90.7 (93.69-2.56) 90.7 (93.69-2.56)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.11 (at 2.55Å)	Xtriage
Refinement program	PHENIX v1.21	Depositor
R, R_{free}	0.231 , 0.275 0.230 , 0.274	Depositor DCC
R_{free} test set	1416 reflections (4.47%)	wwPDB-VP
Wilson B-factor (Å ²)	21.8	Xtriage
Anisotropy	0.076	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 44.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	5097	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.08% 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

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	H	0.64	0/1695	0.94	4/2311 (0.2%)
2	L	0.76	0/1681	1.15	8/2287 (0.3%)
3	R	0.66	0/1593	0.95	0/2169
All	All	0.69	0/4969	1.02	12/6767 (0.2%)

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
2	L	0	2
3	R	0	4
All	All	0	6

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	115	PRO	CB-CA-C	-9.24	102.99	111.40
2	L	96	PRO	N-CA-C	7.83	127.11	111.69
2	L	115	PRO	N-CA-C	7.52	122.54	110.21
2	L	75	ILE	O-C-N	6.88	131.16	122.57
2	L	138	LEU	O-C-N	6.16	131.99	122.87
2	L	139	ASN	CA-CB-CG	6.12	118.72	112.60
1	H	131	PRO	N-CA-CB	-5.21	97.78	103.25
1	H	184	SER	CA-C-N	5.18	128.97	120.63
1	H	184	SER	C-N-CA	5.18	128.97	120.63
1	H	155	LYS	N-CA-C	5.16	119.04	111.04
2	L	50	ASP	CA-CB-CG	5.15	117.75	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	L	139	ASN	N-CA-C	5.04	118.02	109.76

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	L	213	ARG	Sidechain
2	L	91	ARG	Sidechain
3	R	346	ARG	Sidechain
3	R	436	TRP	Mainchain
3	R	466	ARG	Sidechain
3	R	509	ARG	Sidechain

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	H	1654	0	1601	21	0
2	L	1642	0	1603	43	1
3	R	1546	0	1465	22	1
4	H	1	0	0	0	0
4	L	2	0	0	0	0
5	H	86	0	0	3	0
5	L	83	0	0	5	1
5	R	83	0	0	3	0
All	All	5097	0	4669	83	2

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 9.

All (83) 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:R:347:PHE:HA	5:R:601:HOH:O	1.70	0.90
1:H:65:GLN:N	5:H:401:HOH:O	2.14	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:211:ASN:HD22	1:H:218:LYS:HG2	1.49	0.77
2:L:187:ASP:HA	2:L:190:LYS:HB3	1.74	0.68
2:L:61:ARG:NH1	2:L:82:ASP:OD1	2.27	0.68
2:L:79:GLU:HG3	2:L:80:PRO:HD2	1.75	0.67
1:H:211:ASN:ND2	1:H:218:LYS:HG2	2.11	0.66
3:R:365:TYR:CD2	3:R:387:LEU:HB3	2.31	0.65
1:H:69:THR:HG23	1:H:84:ARG:HH22	1.61	0.65
2:L:134:VAL:HG23	2:L:181:LEU:HB3	1.78	0.65
3:R:454:ARG:NH2	3:R:469:SER:O	2.32	0.62
1:H:171:LEU:HD21	1:H:194:VAL:HG21	1.82	0.62
1:H:64:LEU:C	5:H:401:HOH:O	2.39	0.61
2:L:94:TRP:HA	2:L:95:PRO:C	2.26	0.61
2:L:205:SER:CA	5:L:409:HOH:O	2.48	0.60
3:R:436:TRP:HH2	3:R:511:VAL:HG23	1.65	0.60
2:L:134:VAL:CG2	2:L:181:LEU:HB3	2.32	0.60
2:L:124:ASP:O	5:L:401:HOH:O	2.17	0.59
3:R:347:PHE:C	5:R:614:HOH:O	2.46	0.58
3:R:368:LEU:O	3:R:374:PHE:HE2	1.86	0.57
2:L:59:PRO:HB2	2:L:61:ARG:HG2	1.86	0.57
1:H:13:LYS:HG3	1:H:125:SER:HA	1.87	0.57
2:L:61:ARG:O	2:L:75:ILE:HA	2.05	0.56
1:H:20:VAL:HG22	1:H:81:MET:HE3	1.86	0.56
2:L:138:LEU:HD21	2:L:198:VAL:HG13	1.87	0.56
2:L:205:SER:C	5:L:409:HOH:O	2.48	0.56
3:R:376:THR:HB	3:R:435:ALA:HB3	1.88	0.56
2:L:127:LEU:N	5:L:401:HOH:O	2.39	0.55
2:L:29:VAL:HG21	2:L:32:ASP:HB3	1.90	0.53
2:L:152:VAL:HG22	2:L:157:GLN:NE2	2.23	0.53
2:L:152:VAL:HA	2:L:193:VAL:O	2.08	0.53
3:R:342:PHE:CZ	3:R:368:LEU:HD21	2.45	0.52
2:L:187:ASP:HB3	2:L:191:HIS:CE1	2.45	0.51
3:R:370:ASN:O	3:R:371:SER:C	2.54	0.50
2:L:33:LEU:HG	2:L:34:ALA:N	2.26	0.50
3:R:520:ALA:HB1	3:R:521:PRO:HD2	1.93	0.50
2:L:189:GLU:HA	2:L:213:ARG:CZ	2.43	0.49
2:L:61:ARG:HD3	2:L:82:ASP:OD2	2.13	0.49
2:L:31:SER:O	2:L:50:ASP:OD1	2.30	0.49
2:L:139:ASN:HA	2:L:176:SER:OG	2.13	0.48
2:L:61:ARG:HD2	2:L:62:PHE:CZ	2.47	0.48
2:L:122:PRO:HD3	2:L:134:VAL:HG12	1.96	0.48
2:L:169:ASP:HB3	2:L:172:ASP:OD1	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:188:TYR:HA	2:L:194:TYR:OH	2.14	0.47
1:H:108:SER:HB2	3:R:465:GLU:HA	1.96	0.47
2:L:204:SER:C	5:L:409:HOH:O	2.58	0.47
1:H:103:TYR:CE1	1:H:107:GLY:HA2	2.49	0.47
1:H:212:HIS:CD2	1:H:214:PRO:HD2	2.50	0.46
1:H:212:HIS:HB3	1:H:217:THR:OG1	2.14	0.46
2:L:187:ASP:OD1	2:L:187:ASP:N	2.47	0.46
3:R:455:LEU:HD23	3:R:456:PHE:CE2	2.50	0.46
3:R:374:PHE:HA	3:R:436:TRP:HB3	1.99	0.45
3:R:354:ASN:O	3:R:398:ASP:HA	2.17	0.45
3:R:456:PHE:HB3	3:R:473:TYR:CD2	2.52	0.45
1:H:50:TRP:CD1	2:L:96:PRO:CG	3.00	0.45
2:L:160:ASN:ND2	2:L:181:LEU:HD11	2.31	0.45
3:R:342:PHE:HZ	3:R:434:ILE:HD12	1.82	0.44
1:H:49:GLY:CA	1:H:70:MET:HE1	2.47	0.44
1:H:213:LYS:N	1:H:214:PRO:CD	2.80	0.44
2:L:37:GLN:HB2	2:L:47:LEU:HD11	1.99	0.44
2:L:185:LYS:HG2	2:L:185:LYS:O	2.17	0.44
2:L:138:LEU:O	2:L:141:PHE:CE2	2.71	0.44
2:L:95:PRO:HD3	3:R:354:ASN:CG	2.43	0.44
2:L:29:VAL:CG2	2:L:32:ASP:HB3	2.47	0.43
1:H:174:GLY:O	1:H:194:VAL:HA	2.18	0.43
2:L:61:ARG:HG3	2:L:62:PHE:N	2.32	0.43
1:H:131:PRO:HB2	1:H:154:VAL:HG13	1.98	0.43
1:H:11:VAL:HB	1:H:159:PRO:HG3	2.01	0.43
1:H:27:TYR:HB2	5:H:419:HOH:O	2.19	0.43
2:L:89:GLN:HG3	2:L:100:PHE:CE1	2.54	0.42
2:L:138:LEU:O	2:L:177:LEU:N	2.50	0.42
3:R:454:ARG:NH1	3:R:467:ASP:O	2.52	0.42
1:H:8:GLY:HA3	1:H:213:LYS:HE2	2.02	0.42
3:R:342:PHE:CZ	3:R:434:ILE:HD12	2.55	0.41
2:L:91:ARG:NH1	2:L:93:ASN:O	2.53	0.41
3:R:439:ASN:HA	3:R:507:PRO:HG2	2.02	0.41
2:L:5:THR:HA	2:L:24:ARG:O	2.21	0.41
2:L:33:LEU:HD12	2:L:90:GLN:HB2	2.03	0.41
2:L:189:GLU:HA	2:L:213:ARG:NH2	2.36	0.41
3:R:348:ALA:N	5:R:614:HOH:O	2.54	0.41
2:L:88:CYS:SG	2:L:88:CYS:O	2.79	0.40
3:R:467:ASP:OD1	3:R:469:SER:OG	2.37	0.40
1:H:215:SER:OG	1:H:217:THR:HG23	2.21	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:L:480:HOH:O	5:L:480:HOH:O[6_655]	2.00	0.20
2:L:79:GLU:OE2	3:R:519:HIS:NE2[6_655]	2.14	0.06

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	H	215/225 (96%)	209 (97%)	6 (3%)	0	100	100
2	L	211/216 (98%)	200 (95%)	11 (5%)	0	100	100
3	R	194/266 (73%)	185 (95%)	9 (5%)	0	100	100
All	All	620/707 (88%)	594 (96%)	26 (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	H	187/191 (98%)	184 (98%)	3 (2%)	55	70
2	L	185/188 (98%)	178 (96%)	7 (4%)	29	42
3	R	169/224 (75%)	167 (99%)	2 (1%)	63	76
All	All	541/603 (90%)	529 (98%)	12 (2%)	45	61

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	11	VAL
1	H	109	CYS
1	H	207	ILE
2	L	3	VAL
2	L	5	THR
2	L	91	ARG
2	L	187	ASP
2	L	190	LYS
2	L	192	LYS
2	L	193	VAL
3	R	356	LYS
3	R	498	GLN

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

Mol	Chain	Res	Type
1	H	62	GLN
1	H	211	ASN
2	L	162	GLN
3	R	334	ASN
3	R	474	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 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, 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	H	219/225 (97%)	0.70	25 (11%)	10 9	8, 30, 73, 89	0
2	L	213/216 (98%)	0.97	47 (22%)	2 2	7, 25, 80, 96	0
3	R	195/266 (73%)	0.57	18 (9%)	14 14	13, 29, 66, 89	1 (0%)
All	All	627/707 (88%)	0.75	90 (14%)	6 6	7, 28, 73, 96	1 (0%)

All (90) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	31	SER	7.1
2	L	60	ALA	6.8
2	L	61	ARG	6.8
2	L	62	PHE	6.6
1	H	106	GLY	6.6
2	L	26	SER	6.1
2	L	2	ILE	5.6
3	R	436	TRP	5.5
1	H	105	SER	5.4
2	L	194	TYR	4.8
2	L	182	THR	4.7
3	R	371	SER	4.6
1	H	139	SER	4.3
2	L	193	VAL	4.3
3	R	367	VAL	4.3
2	L	156	LEU	4.2
3	R	527	PRO	4.2
3	R	369	TYR	4.1
2	L	214	GLY	4.1
2	L	192	LYS	4.1
2	L	186	ALA	4.1
1	H	147	THR	4.0
1	H	203	THR	3.9

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Mol	Chain	Res	Type	RSRZ
1	H	205	THR	3.8
1	H	202	GLY	3.7
2	L	181	LEU	3.6
2	L	211	PHE	3.6
1	H	208	CYS	3.6
2	L	127	LEU	3.4
1	H	109	CYS	3.4
2	L	132	ALA	3.4
2	L	6	GLN	3.3
3	R	372	ALA	3.3
1	H	201	LEU	3.2
2	L	213	ARG	3.2
1	H	140	SER	3.2
3	R	435	ALA	3.1
3	R	333	THR	3.1
3	R	445	VAL	3.1
2	L	153	ASP	3.0
2	L	190	LYS	2.9
2	L	27	GLN	2.9
3	R	373	SER	2.9
2	L	131	THR	2.9
2	L	155	ALA	2.8
2	L	123	SER	2.8
2	L	30	SER	2.8
2	L	191	HIS	2.8
2	L	184	SER	2.6
1	H	207	ILE	2.6
2	L	210	SER	2.6
1	H	170	ALA	2.6
2	L	187	ASP	2.6
2	L	33	LEU	2.5
2	L	154	ASN	2.5
1	H	200	SER	2.5
1	H	217	THR	2.5
2	L	152	VAL	2.5
2	L	185	LYS	2.5
3	R	389	ASP	2.5
2	L	134	VAL	2.5
2	L	212	ASN	2.4
2	L	133	SER	2.4
3	R	368	LEU	2.4
2	L	139	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
1	H	137	ALA	2.4
1	H	155	LYS	2.4
1	H	206	TYR	2.4
3	R	446	GLY	2.3
1	H	213	LYS	2.3
2	L	8	PRO	2.3
2	L	94	TRP	2.3
1	H	104	CYS	2.3
2	L	122	PRO	2.3
3	R	385	THR	2.3
1	H	149	ALA	2.2
3	R	384	PRO	2.2
3	R	370	ASN	2.2
2	L	4	LEU	2.2
1	H	197	PRO	2.2
1	H	1	GLN	2.1
2	L	124	ASP	2.1
2	L	128	LYS	2.1
2	L	188	TYR	2.1
1	H	135	PRO	2.1
2	L	196	CYS	2.1
1	H	148	ALA	2.0
3	R	440	ASN	2.0
3	R	381	GLY	2.0
2	L	189	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

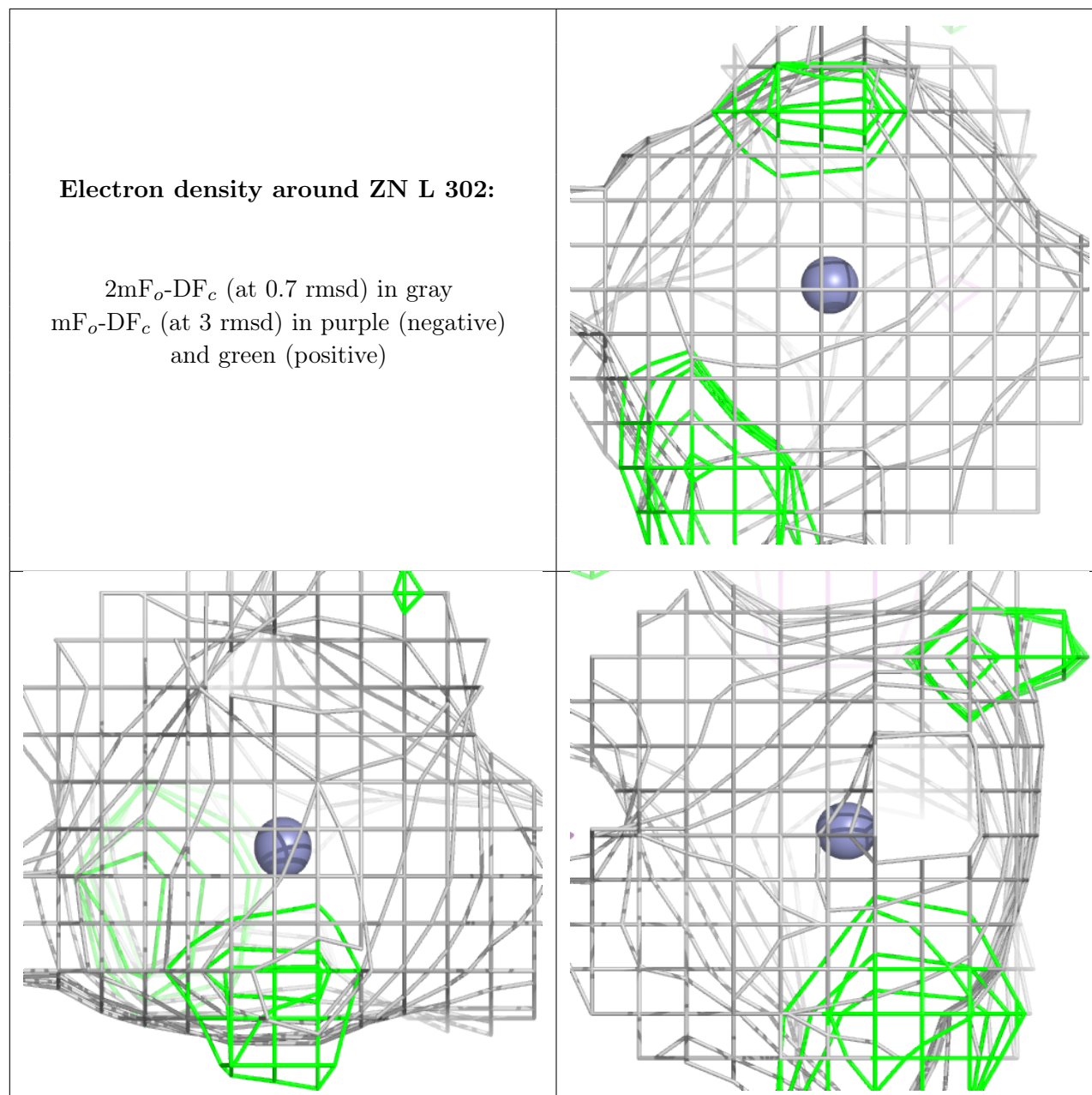
There are no oligosaccharides in this entry.

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, 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.

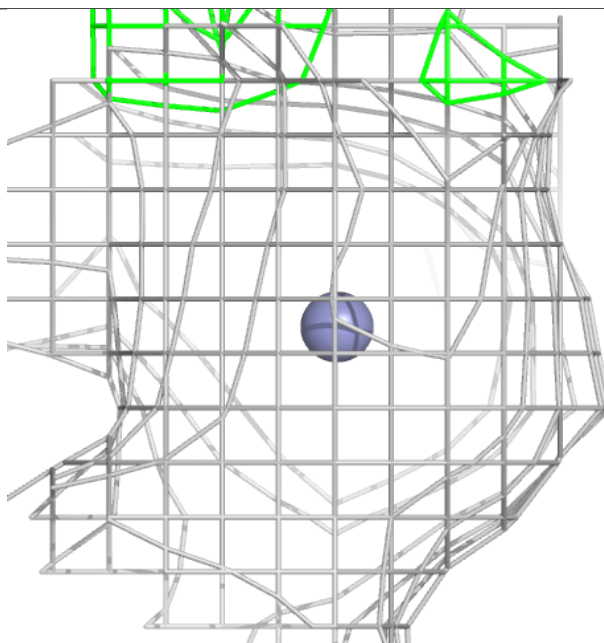
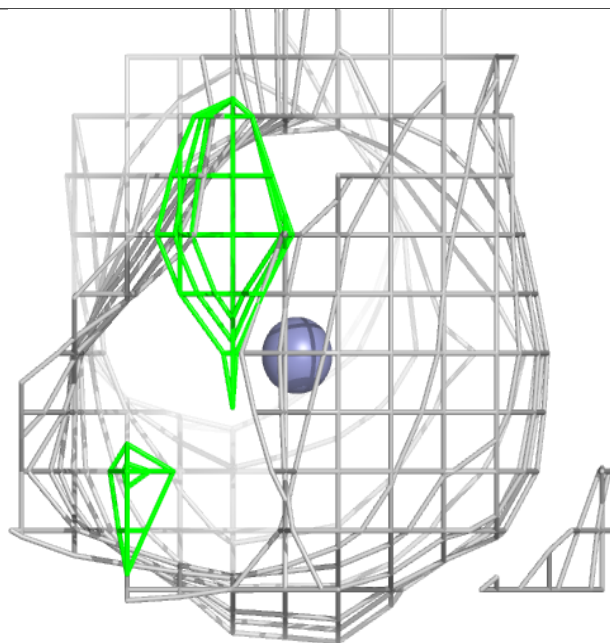
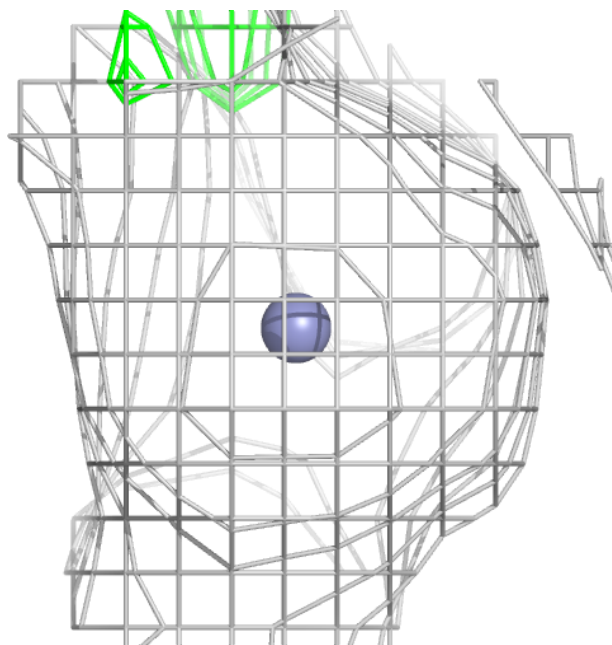
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	ZN	L	302	1/1	0.94	0.06	53,53,53,53	0
4	ZN	H	301	1/1	0.97	0.06	50,50,50,50	0
4	ZN	L	301	1/1	0.99	0.04	5,5,5,5	1

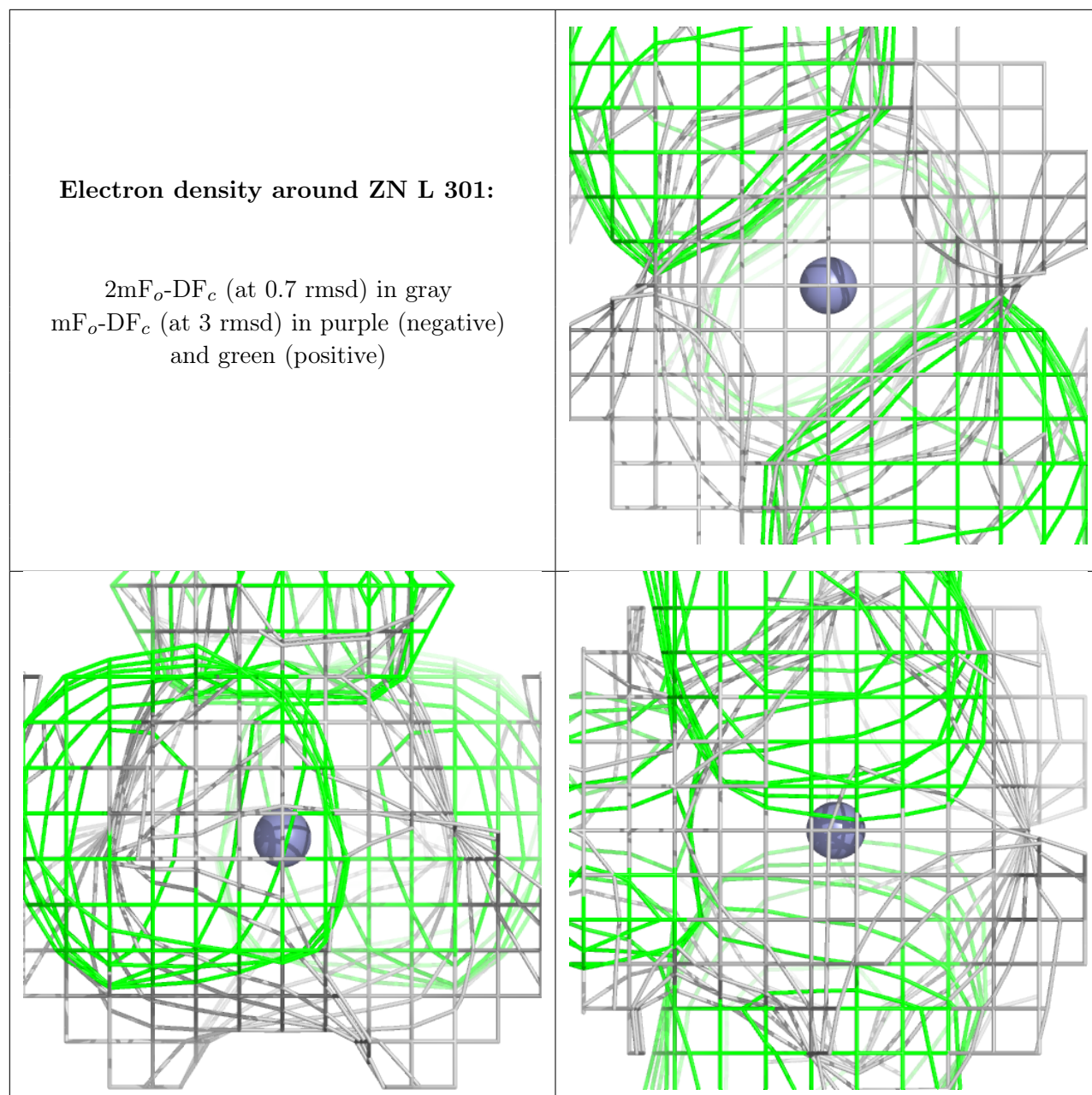
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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



Electron density around ZN H 301:

$2mF_o-DF_c$ (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.