



Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2020 – 07:17 pm BST

PDB ID : 6A9K
Title : Crystal structure of the complex of the hydrolytic antibody Fab 9C10 with a transition-state analog
Authors : Tsuchiya, Y.; Fujii, I.; Tada, T.; Yamaguchi, A.; Tsumuraya, T.; Kumon, A.
Deposited on : 2018-07-13
Resolution : 1.90 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
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

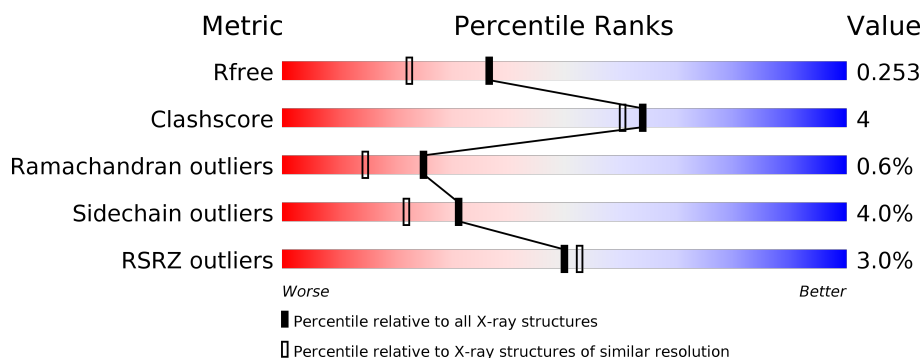
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 ≥ 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	219	<div> <div>2%</div> <div> <div></div> <div>86%</div> <div>11%</div> <div>.</div> </div> </div>
1	L	219	<div> <div>%</div> <div> <div></div> <div>86%</div> <div>12%</div> <div>.</div> </div> </div>
2	B	220	<div> <div>5%</div> <div> <div></div> <div>90%</div> <div>10%</div> </div> </div>
2	H	220	<div> <div>4%</div> <div> <div></div> <div>91%</div> <div>8%</div> <div>.</div> </div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7157 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.

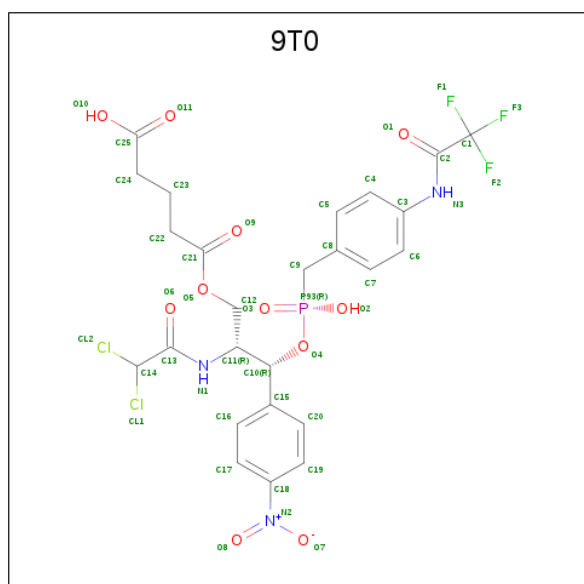
- Molecule 1 is a protein called IMMUNOGLOBULIN 9C10 L CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	219	Total	C	N	O	S	0	0	0
			1696	1060	286	343	7			
1	A	219	Total	C	N	O	S	0	0	0
			1696	1060	286	343	7			

- Molecule 2 is a protein called IMMUNOGLOBULIN 9C10 H CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	220	Total	C	N	O	S	0	0	0
			1681	1064	276	332	9			
2	B	220	Total	C	N	O	S	0	0	0
			1681	1064	276	332	9			

- Molecule 3 is 5-[(2R,3R)-2-[2,2-bis(chloranyl)ethanoylamino]-3-(4-nitrophenyl)-3-[oxidanyl-[4-[2,2,2-tris(fluoranyl)ethanoylamino]phenyl]methyl]phosphoryl]oxy-propoxy]-5-oxidanylide ne-pentanoic acid (three-letter code: 9T0) (formula: C₂₅H₂₅Cl₂F₃N₃O₁₁P).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
3	H	1	Total 45	C 25	Cl 2	F 3	N 3	O 11	P 1	0	0
3	B	1	Total 45	C 25	Cl 2	F 3	N 3	O 11	P 1	0	0

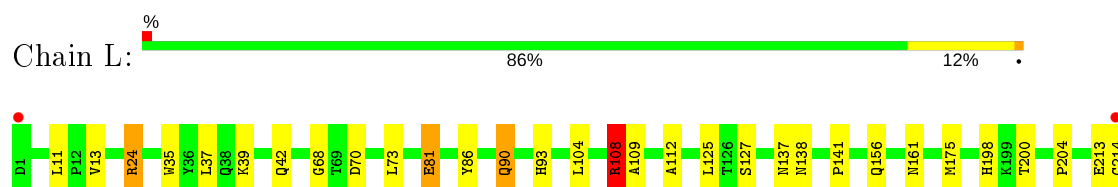
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	L	76	Total 76	O 76	0	0
4	H	121	Total 121	O 121	0	0
4	A	59	Total 59	O 59	0	0
4	B	57	Total 57	O 57	0	0

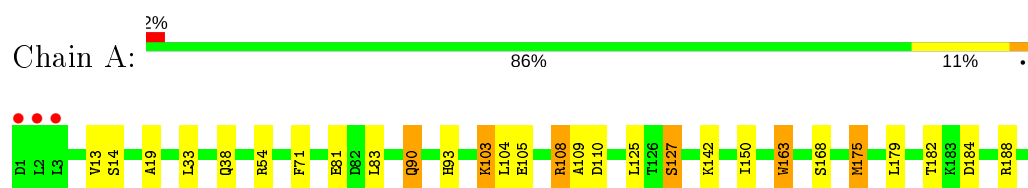
3 Residue-property plots [i](#)

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.

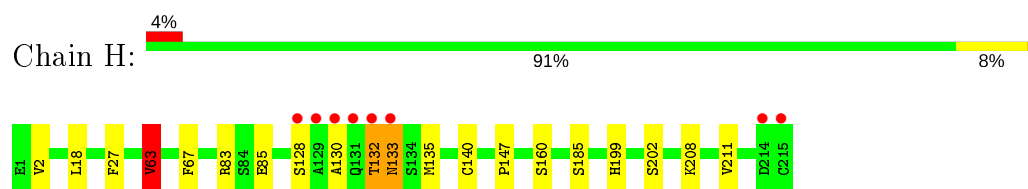
- Molecule 1: IMMUNOGLOBULIN 9C10 L CHAIN



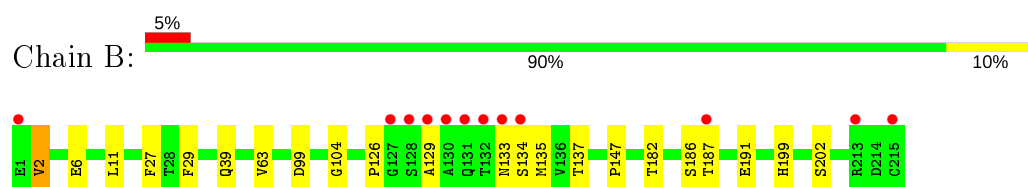
- Molecule 1: IMMUNOGLOBULIN 9C10 L CHAIN



- Molecule 2: IMMUNOGLOBULIN 9C10 H CHAIN



- Molecule 2: IMMUNOGLOBULIN 9C10 H CHAIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	90.99Å 36.55Å 111.99Å 90.00° 91.50° 90.00°	Depositor
Resolution (Å)	50.00 – 1.90 41.75 – 1.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (50.00-1.90) 100.0 (41.75-1.90)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.95 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.194 , 0.249 0.201 , 0.253	Depositor DCC
R_{free} test set	2993 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	22.2	Xtriage
Anisotropy	0.069	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 35.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.022 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7157	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 21.89 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.3764e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² 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: 9T0

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	0.85	0/1735	0.89	3/2353 (0.1%)
1	L	0.83	0/1735	0.92	2/2353 (0.1%)
2	B	0.82	0/1724	0.86	1/2355 (0.0%)
2	H	0.91	1/1724 (0.1%)	0.94	2/2355 (0.1%)
All	All	0.85	1/6918 (0.0%)	0.90	8/9416 (0.1%)

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	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	85	GLU	CD-OE2	6.78	1.33	1.25

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	108	ARG	NE-CZ-NH1	9.54	125.07	120.30
1	L	108	ARG	NE-CZ-NH2	-8.60	116.00	120.30
2	H	63	VAL	CG1-CB-CG2	7.40	122.73	110.90
1	A	54	ARG	NE-CZ-NH2	5.96	123.28	120.30
2	B	99	ASP	CB-CG-OD1	5.26	123.03	118.30
2	H	140	CYS	CA-CB-SG	-5.23	104.59	114.00
1	A	103	LYS	CD-CE-NZ	5.17	123.60	111.70
1	A	175	MET	CA-CB-CG	5.01	121.81	113.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	186	SER	Peptide

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	1696	0	1638	16	0
1	L	1696	0	1638	19	0
2	B	1681	0	1641	14	0
2	H	1681	0	1641	8	0
3	B	45	0	0	0	0
3	H	45	0	0	0	0
4	A	59	0	0	1	0
4	B	57	0	0	0	0
4	H	121	0	0	0	0
4	L	76	0	0	1	0
All	All	7157	0	6558	53	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 4.

All (53) 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)
2:H:132:THR:O	2:H:133:ASN:HB2	1.68	0.89
1:A:38:GLN:HE22	2:B:39:GLN:HE22	1.23	0.84
1:L:81:GLU:HB3	4:L:374:HOH:O	1.83	0.78
1:L:90:GLN:HE22	1:L:93:HIS:H	1.33	0.75
1:A:90:GLN:HE22	1:A:93:HIS:H	1.38	0.72
2:H:132:THR:O	2:H:133:ASN:CB	2.38	0.71
1:L:108:ARG:HD3	1:L:109:ALA:O	1.91	0.70
1:L:161:ASN:HB3	1:L:175:MET:HE3	1.80	0.62
2:H:199:HIS:HD2	2:H:202:SER:OG	1.81	0.62
2:B:137:THR:OG1	2:B:182:THR:HG22	1.99	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:147:PRO:O	2:B:199:HIS:HE1	1.86	0.58
1:A:33:LEU:HD13	1:A:71:PHE:CD2	2.39	0.57
2:B:199:HIS:HD2	2:B:202:SER:OG	1.88	0.57
2:B:2:VAL:HB	2:B:27:PHE:CD1	2.40	0.56
1:L:13:VAL:HG11	1:L:104:LEU:HD11	1.89	0.55
2:B:126:PRO:HB2	2:B:129:ALA:HB2	1.91	0.53
2:H:147:PRO:O	2:H:199:HIS:HE1	1.91	0.53
1:A:108:ARG:HD3	1:A:109:ALA:O	2.08	0.52
1:L:112:ALA:CB	1:L:200:THR:HG21	2.39	0.52
2:H:208:LYS:NZ	1:A:182:THR:HG21	2.25	0.52
2:B:133:ASN:C	2:B:135:MET:H	2.13	0.52
1:A:38:GLN:HE22	2:B:39:GLN:NE2	2.01	0.51
2:H:63:VAL:HG13	2:H:67:PHE:HB2	1.93	0.51
1:L:141:PRO:O	1:L:198:HIS:HE1	1.94	0.50
2:H:208:LYS:HZ3	1:A:182:THR:HG21	1.77	0.49
1:L:108:ARG:CD	1:L:109:ALA:O	2.60	0.49
1:A:199:LYS:HG3	1:A:200:THR:N	2.28	0.47
1:L:39:LYS:HB2	1:L:42:GLN:HG3	1.96	0.47
2:B:27:PHE:CE2	2:B:29:PHE:HA	2.50	0.47
1:L:112:ALA:HB2	1:L:200:THR:HG21	1.97	0.46
2:H:2:VAL:HG13	2:H:27:PHE:CD1	2.51	0.46
1:A:103:LYS:HE3	4:A:305:HOH:O	2.14	0.46
1:A:13:VAL:HG21	1:A:19:ALA:HB2	1.96	0.46
1:L:198:HIS:HD2	1:L:200:THR:CG2	2.29	0.45
1:A:150:ILE:HD11	1:A:179:LEU:HD21	1.98	0.45
1:L:13:VAL:CG1	1:L:104:LEU:HD11	2.46	0.45
1:A:163:TRP:CZ2	1:A:175:MET:SD	3.11	0.44
1:A:104:LEU:HD23	1:A:105:GLU:N	2.33	0.44
1:L:137:ASN:HB3	1:L:138:ASN:HD22	1.83	0.44
2:B:199:HIS:CD2	2:B:202:SER:OG	2.69	0.43
2:B:133:ASN:O	2:B:135:MET:N	2.51	0.43
1:A:83:LEU:HD12	1:A:83:LEU:C	2.38	0.43
2:B:187:THR:O	2:B:191:GLU:HB2	2.18	0.43
1:L:112:ALA:HA	1:L:200:THR:HG21	2.00	0.43
1:A:127:SER:O	1:A:127:SER:OG	2.34	0.43
1:A:110:ASP:OD1	1:A:199:LYS:HD2	2.19	0.42
1:L:24:ARG:HD3	1:L:70:ASP:OD1	2.19	0.42
1:L:37:LEU:HD13	1:L:86:TYR:CZ	2.55	0.42
2:B:11:LEU:HB2	2:B:147:PRO:HG3	2.02	0.42
1:L:213:GLU:O	1:L:214:CYS:CB	2.68	0.41
2:B:6:GLU:OE2	2:B:104:GLY:HA3	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:35:TRP:CE2	1:L:73:LEU:HB2	2.57	0.40
1:L:137:ASN:HB3	1:L:138:ASN:ND2	2.36	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	217/219 (99%)	207 (95%)	10 (5%)	0	100	100
1	L	217/219 (99%)	213 (98%)	3 (1%)	1 (0%)	29	18
2	B	218/220 (99%)	204 (94%)	13 (6%)	1 (0%)	29	18
2	H	218/220 (99%)	208 (95%)	7 (3%)	3 (1%)	11	3
All	All	870/878 (99%)	832 (96%)	33 (4%)	5 (1%)	25	15

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	133	ASN
2	H	132	THR
2	B	134	SER
1	L	68	GLY
2	H	130	ALA

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	196/196 (100%)	184 (94%)	12 (6%)	18	9
1	L	196/196 (100%)	187 (95%)	9 (5%)	27	17
2	B	191/191 (100%)	189 (99%)	2 (1%)	76	76
2	H	191/191 (100%)	183 (96%)	8 (4%)	30	20
All	All	774/774 (100%)	743 (96%)	31 (4%)	31	22

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	11	LEU
1	L	24	ARG
1	L	81	GLU
1	L	90	GLN
1	L	108	ARG
1	L	125	LEU
1	L	127	SER
1	L	156	GLN
1	L	204	PRO
2	H	18	LEU
2	H	63	VAL
2	H	83	ARG
2	H	128	SER
2	H	135	MET
2	H	160	SER
2	H	185	SER
2	H	211	VAL
1	A	14	SER
1	A	81	GLU
1	A	90	GLN
1	A	108	ARG
1	A	125	LEU
1	A	127	SER
1	A	142	LYS
1	A	163	TRP
1	A	168	SER
1	A	184	ASP
1	A	188	ARG
1	A	199	LYS
2	B	2	VAL
2	B	63	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	90	GLN
1	L	137	ASN
1	L	138	ASN
1	L	190	ASN
1	L	198	HIS
1	L	212	ASN
2	H	164	HIS
2	H	199	HIS
1	A	18	GLN
1	A	90	GLN
1	A	138	ASN
1	A	161	ASN
1	A	210	ASN
1	A	212	ASN
2	B	39	GLN
2	B	164	HIS
2	B	199	HIS

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](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	9T0	H	301	-	42,46,46	2.16	9 (21%)	54,65,65	1.68	7 (12%)
3	9T0	B	301	-	42,46,46	3.21	14 (33%)	54,65,65	1.84	17 (31%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	9T0	H	301	-	-	7/46/51/51	0/2/2/2
3	9T0	B	301	-	-	6/46/51/51	0/2/2/2

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	301	9T0	O4-C10	-14.73	1.30	1.46
3	H	301	9T0	O4-C10	-8.06	1.37	1.46
3	B	301	9T0	O8-N2	6.10	1.33	1.22
3	B	301	9T0	C15-C10	-5.68	1.41	1.51
3	B	301	9T0	C10-C11	-5.39	1.45	1.53
3	H	301	9T0	C10-C11	-5.30	1.45	1.53
3	H	301	9T0	C15-C10	-4.56	1.43	1.51
3	B	301	9T0	C14-CL2	4.31	1.89	1.76
3	B	301	9T0	C18-N2	-3.84	1.35	1.45
3	B	301	9T0	P93-O2	-3.66	1.47	1.56
3	H	301	9T0	P93-O2	-3.23	1.48	1.56
3	B	301	9T0	F3-C1	-3.03	1.18	1.32
3	H	301	9T0	C14-CL2	2.98	1.85	1.76
3	H	301	9T0	C22-C21	2.65	1.58	1.50
3	H	301	9T0	C20-C19	2.61	1.43	1.38
3	H	301	9T0	P93-O3	-2.57	1.45	1.51
3	B	301	9T0	O5-C21	2.55	1.40	1.33
3	B	301	9T0	C4-C5	2.36	1.43	1.38
3	B	301	9T0	F1-C1	-2.33	1.22	1.32
3	H	301	9T0	C9-C8	-2.22	1.47	1.51
3	B	301	9T0	F2-C1	2.19	1.41	1.32
3	B	301	9T0	C22-C21	2.14	1.57	1.50
3	B	301	9T0	O5-C12	-2.10	1.40	1.45

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	301	9T0	C10-C11-N1	-5.60	100.72	110.23
3	B	301	9T0	O4-C10-C11	5.48	115.86	106.27
3	H	301	9T0	O4-C10-C11	4.72	114.52	106.27
3	B	301	9T0	C10-C11-N1	-4.56	102.47	110.23
3	B	301	9T0	C17-C18-N2	3.83	122.26	119.38
3	H	301	9T0	C15-C10-C11	3.74	117.38	112.61
3	B	301	9T0	C17-C16-C15	3.37	124.59	121.20
3	B	301	9T0	C20-C15-C16	-3.14	114.37	118.29
3	H	301	9T0	O5-C12-C11	-3.02	102.80	108.32
3	B	301	9T0	C12-O5-C21	-2.94	106.24	117.12
3	B	301	9T0	C20-C15-C10	2.71	125.69	120.64
3	B	301	9T0	O4-P93-O3	-2.64	110.88	115.39
3	B	301	9T0	C19-C18-N2	2.40	121.19	119.38
3	H	301	9T0	O2-P93-O3	2.34	117.88	110.07
3	H	301	9T0	C19-C20-C15	-2.31	118.88	121.20
3	B	301	9T0	C13-C14-CL1	-2.23	105.22	109.61
3	B	301	9T0	C3-N3-C2	-2.22	122.76	126.78
3	B	301	9T0	O5-C12-C11	-2.12	104.44	108.32
3	B	301	9T0	O5-C21-C22	2.10	118.50	111.91
3	B	301	9T0	C4-C3-C6	-2.09	116.17	119.03
3	B	301	9T0	C9-C8-C5	2.08	124.39	120.81
3	B	301	9T0	O2-P93-O3	2.06	116.94	110.07
3	H	301	9T0	C3-N3-C2	-2.03	123.10	126.78
3	B	301	9T0	C19-C18-C17	-2.01	116.55	119.86

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	H	301	9T0	C22-C23-C24-C25
3	B	301	9T0	C22-C23-C24-C25
3	H	301	9T0	O9-C21-O5-C12
3	H	301	9T0	C22-C21-O5-C12
3	B	301	9T0	C22-C21-O5-C12
3	B	301	9T0	O9-C21-O5-C12
3	B	301	9T0	C7-C8-C9-P93
3	B	301	9T0	C5-C8-C9-P93
3	H	301	9T0	C5-C8-C9-P93
3	H	301	9T0	C8-C9-P93-O2
3	H	301	9T0	C7-C8-C9-P93
3	B	301	9T0	O5-C21-C22-C23

Continued on next page...

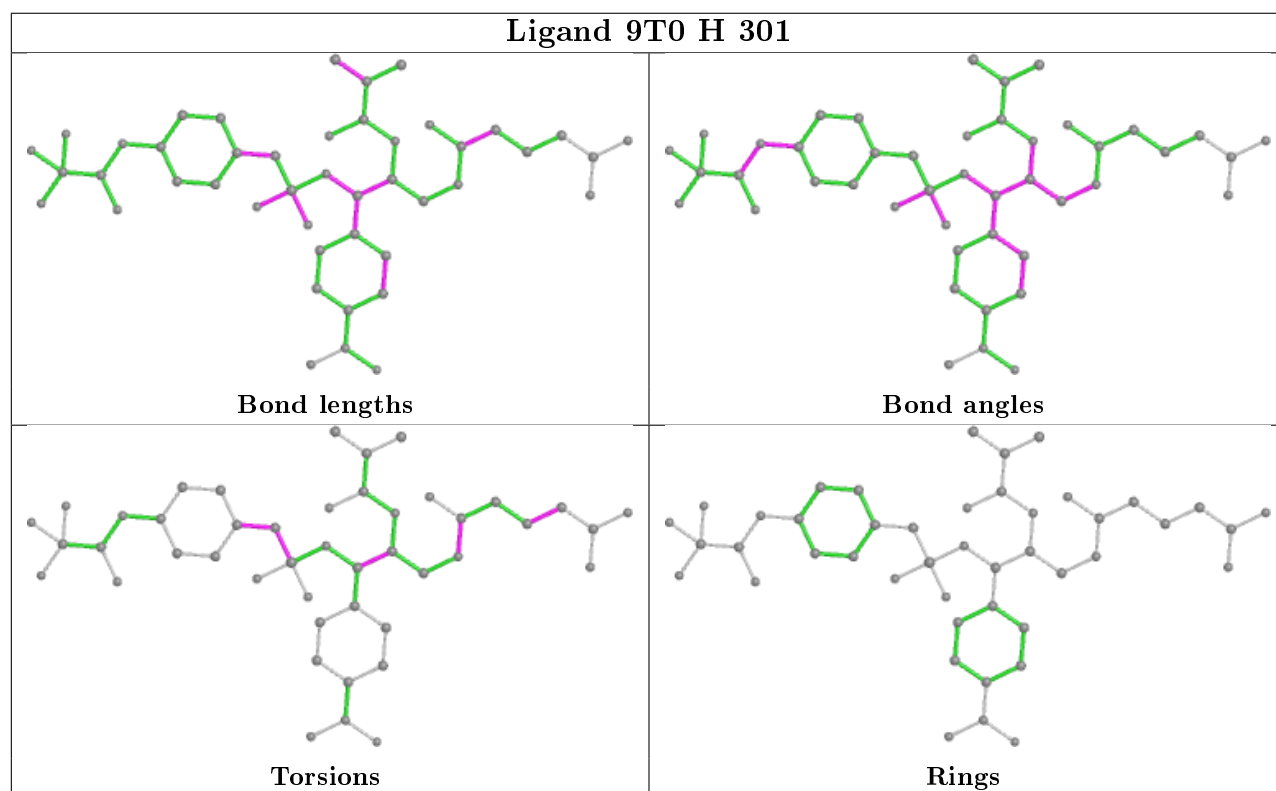
Continued from previous page...

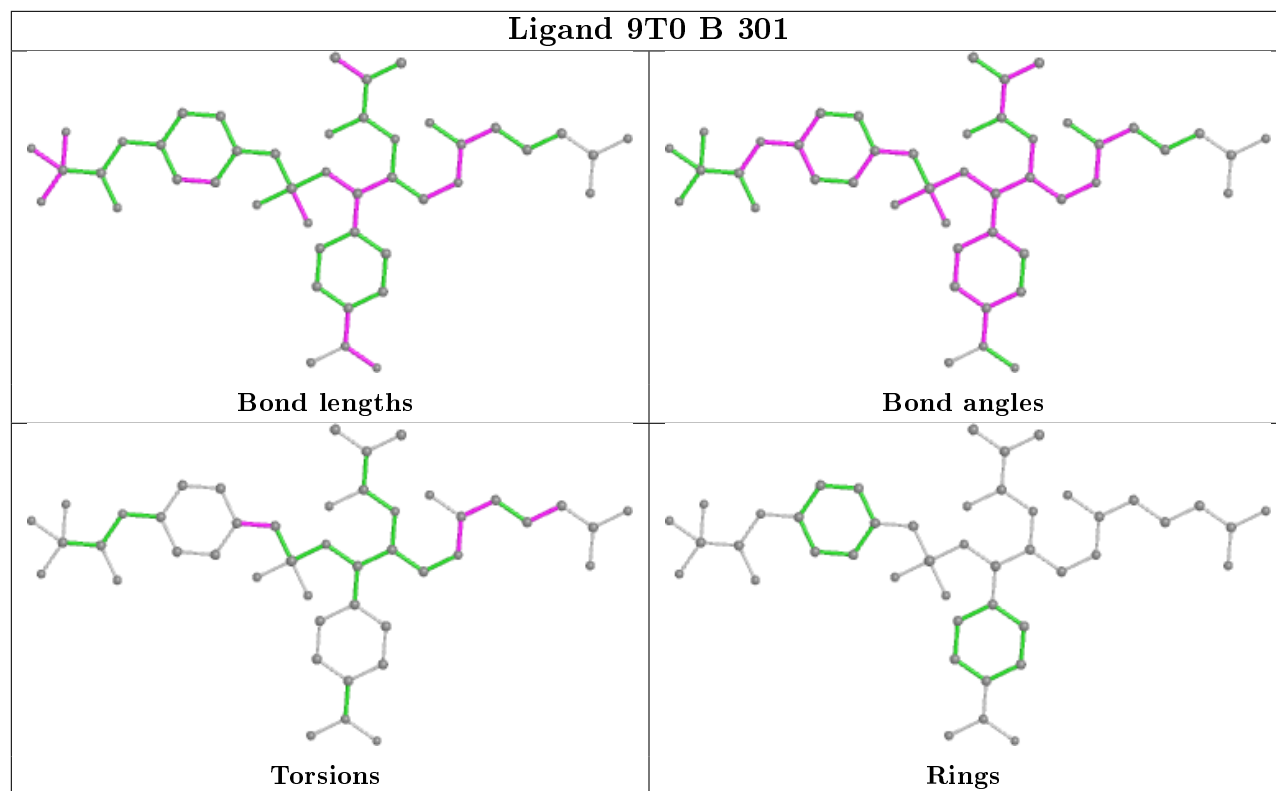
Mol	Chain	Res	Type	Atoms
3	H	301	9T0	O4-C10-C11-C12

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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	219/219 (100%)	-0.03	4 (1%) 68 71	19, 32, 52, 95	0
1	L	219/219 (100%)	-0.19	2 (0%) 84 85	18, 30, 48, 83	0
2	B	220/220 (100%)	0.22	12 (5%) 25 28	21, 32, 82, 136	0
2	H	220/220 (100%)	-0.12	8 (3%) 42 45	17, 25, 45, 97	0
All	All	878/878 (100%)	-0.03	26 (2%) 50 53	17, 30, 53, 136	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	132	THR	10.7
2	B	130	ALA	8.7
2	H	129	ALA	8.7
2	H	133	ASN	7.2
1	A	1	ASP	6.7
2	H	215	CYS	6.5
2	B	128	SER	5.7
2	H	132	THR	5.5
2	B	129	ALA	5.3
2	H	214	ASP	4.4
1	L	1	ASP	4.3
2	B	127	GLY	4.2
2	H	128	SER	4.2
1	L	214	CYS	4.0
2	B	134	SER	3.9
2	B	131	GLN	3.8
2	B	133	ASN	3.7
1	A	214	CYS	3.6
2	B	215	CYS	3.2
2	B	1	GLU	2.9
2	H	131	GLN	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	B	213	ARG	2.7
1	A	3	LEU	2.5
2	H	130	ALA	2.3
1	A	2	LEU	2.3
2	B	187	THR	2.1

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 [i](#)

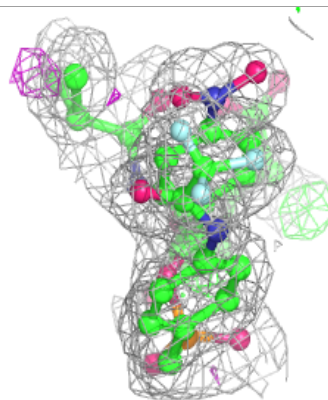
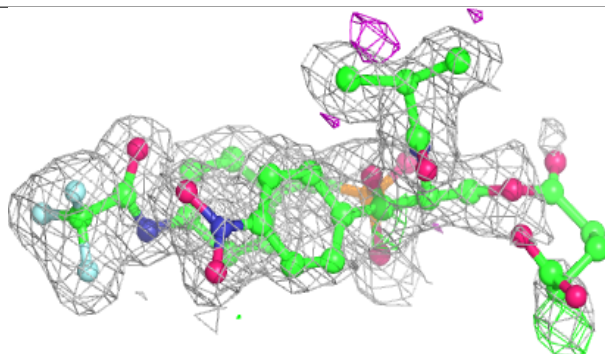
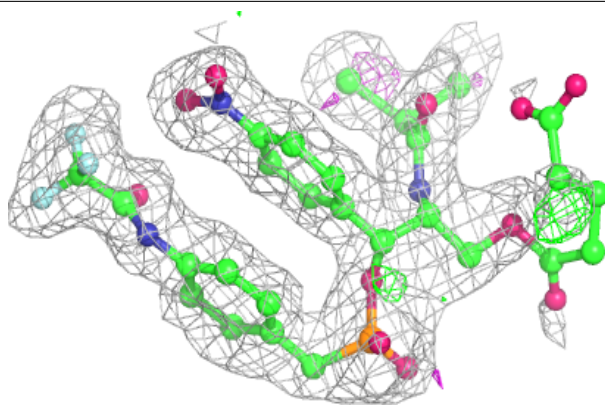
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	9T0	B	301	45/45	0.91	0.15	27,41,77,83	0
3	9T0	H	301	45/45	0.95	0.12	20,25,65,67	0

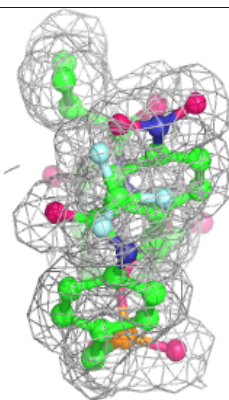
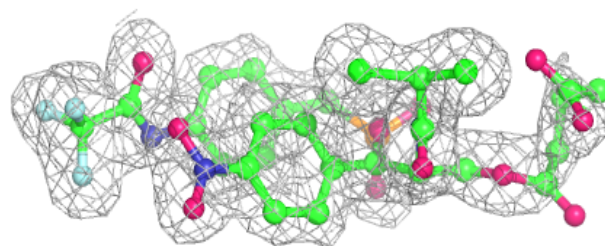
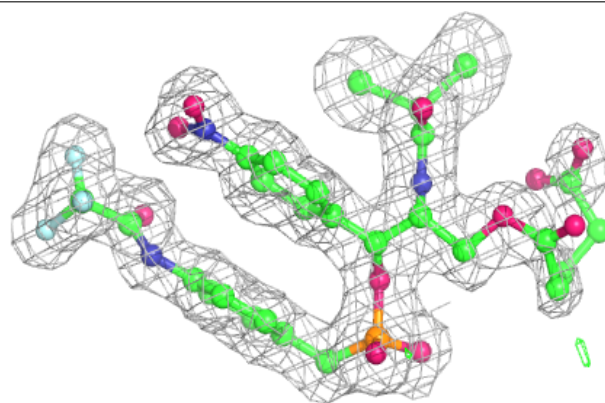
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 9T0 B 301:

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

**Electron density around 9T0 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.