



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 28, 2023 – 01:58 AM EDT

PDB ID : 3L9M
Title : Crystal structure of PKAB3 (pka triple mutant V123A, L173M, Q181K) with compound 18
Authors : Huang, X.
Deposited on : 2010-01-05
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 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
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35
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) : 2.35

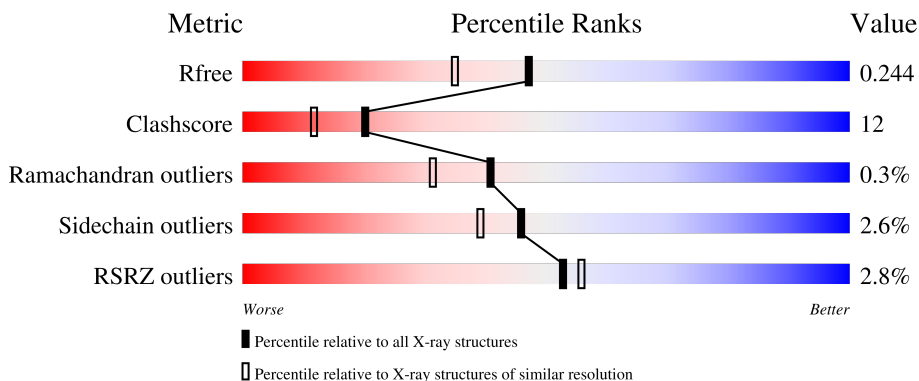
1 Overall quality at a glance

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 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	351	 75% 20% ..
1	B	351	 4% 76% 20% ..
2	C	20	 5% 90% 5% 5%
2	D	20	 5% 80% 10% 10%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6669 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 cAMP-dependent protein kinase catalytic subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	N	O	P				S
1	A	340	Total	C	N	O	P	S	0	0	0
			2778	1802	463	502	2	9			
1	B	338	Total	C	N	O	P	S	0	0	0
			2772	1796	465	500	2	9			

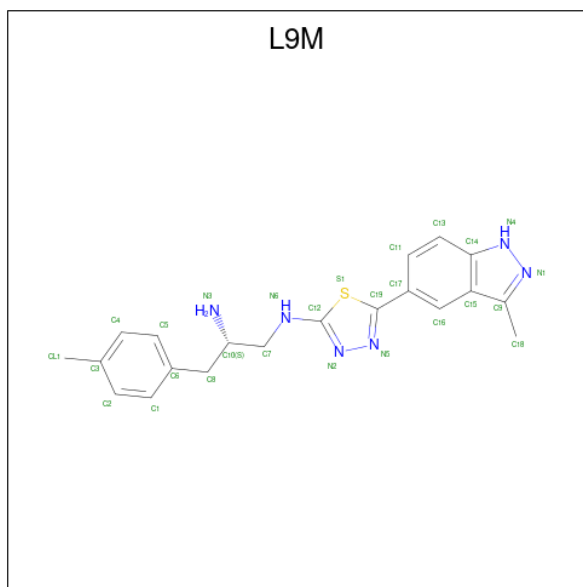
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	123	ALA	VAL	engineered mutation	UNP P17612
A	173	MET	LEU	engineered mutation	UNP P17612
A	181	LYS	GLN	engineered mutation	UNP P17612
B	123	ALA	VAL	engineered mutation	UNP P17612
B	173	MET	LEU	engineered mutation	UNP P17612
B	181	LYS	GLN	engineered mutation	UNP P17612

- Molecule 2 is a protein called cAMP-dependent protein kinase inhibitor alpha.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	19	Total	C	N	O	0	0	0
			148	90	31	27			
2	D	18	Total	C	N	O	0	0	0
			138	84	28	26			

- Molecule 3 is (2S)-N 1 -[5-(3-methyl-1H-indazol-5-yl)-1,3,4-thiadiazol-2-yl]-3-(4-methylphenyl)propane-1,2-diamine (three-letter code: L9M) (formula: C₂₀H₂₂N₆S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	S	0	0
			27	20	6	1		
3	B	1	Total	C	N	S	0	0
			27	20	6	1		

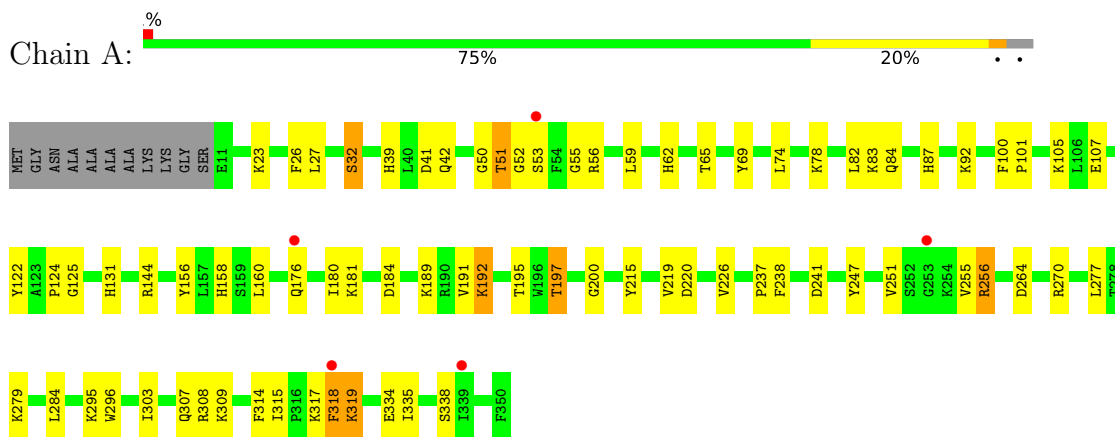
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	349	Total	O	4	0
			349	349		
4	C	40	Total	O	0	0
			40	40		
4	B	350	Total	O	0	0
			350	350		
4	D	40	Total	O	1	0
			40	40		

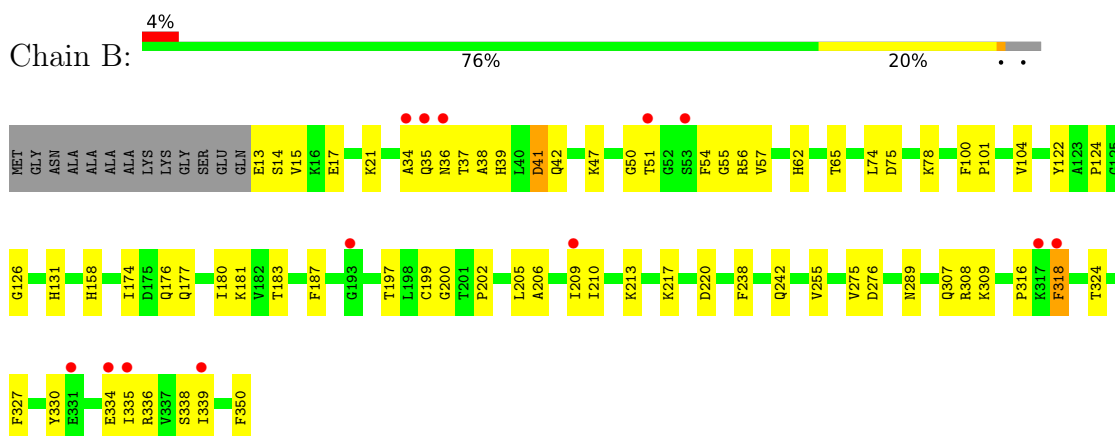
3 Residue-property plots [i](#)

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.

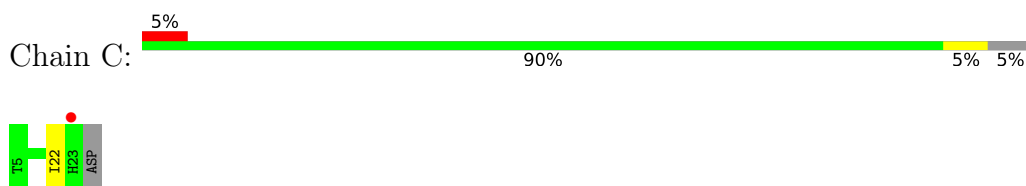
- Molecule 1: cAMP-dependent protein kinase catalytic subunit alpha



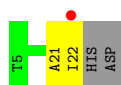
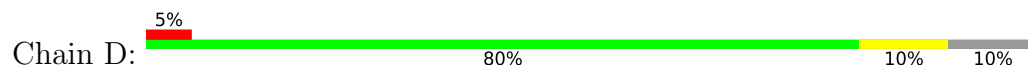
- Molecule 1: cAMP-dependent protein kinase catalytic subunit alpha



- Molecule 2: cAMP-dependent protein kinase inhibitor alpha



- Molecule 2: cAMP-dependent protein kinase inhibitor alpha



4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	117.91Å 114.99Å 72.06Å 90.00° 125.44° 90.00°	Depositor
Resolution (Å)	30.00 – 1.90 29.68 – 1.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-1.90) 97.9 (29.68-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.20 (at 1.89Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.223 , 0.270 0.206 , 0.244	Depositor DCC
R_{free} test set	3049 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	18.4	Xtrriage
Anisotropy	0.295	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 50.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.088 for -h-2*1,-k,l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6669	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.47% 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: TPO, SEP, L9M

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	0.36	0/2828	0.59	0/3811
1	B	0.37	0/2822	0.60	0/3803
2	C	0.37	0/150	0.57	0/201
2	D	0.38	0/139	0.56	0/186
All	All	0.37	0/5939	0.59	0/8001

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 [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	2778	0	2737	63	0
1	B	2772	0	2733	79	0
2	C	148	0	142	1	0
2	D	138	0	135	4	0
3	A	27	0	22	4	0
3	B	27	0	22	1	0
4	A	349	0	0	14	2
4	B	350	0	0	20	0
4	C	40	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	40	0	0	1	0
All	All	6669	0	5791	146	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 12.

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)
3:A:351:L9M:CL1	3:A:351:L9M:C3	1.76	1.58
1:B:206:ALA:O	1:B:209:ILE:HG22	1.65	0.96
1:B:205:LEU:HD22	1:B:209:ILE:HD13	1.46	0.94
1:A:319:LYS:N	1:A:319:LYS:HE3	1.90	0.86
1:B:13:GLU:HG3	1:B:15:VAL:H	1.42	0.80
1:A:41:ASP:HB3	4:A:748:HOH:O	1.83	0.78
1:B:39:HIS:HD2	1:B:41:ASP:H	1.33	0.76
1:B:275:VAL:HG12	4:B:743:HOH:O	1.85	0.76
1:B:39:HIS:H	1:B:42:GLN:NE2	1.84	0.74
1:B:35:GLN:HA	4:B:437:HOH:O	1.87	0.74
1:B:176:GLN:HG3	1:B:318:PHE:HZ	1.52	0.74
1:B:34:ALA:HB1	4:B:959:HOH:O	1.87	0.73
1:B:318:PHE:N	1:B:318:PHE:HD1	1.86	0.73
1:B:36:ASN:ND2	4:B:364:HOH:O	2.21	0.72
1:B:205:LEU:HB3	1:B:209:ILE:HG21	1.71	0.71
1:B:334:GLU:OE1	1:B:336:ARG:HB2	1.91	0.71
1:B:176:GLN:CG	1:B:318:PHE:HZ	2.06	0.69
1:B:318:PHE:N	1:B:318:PHE:CD1	2.59	0.68
1:A:78:LYS:HE2	1:A:82:LEU:HD11	1.73	0.68
1:A:23:LYS:O	1:A:27:LEU:HD23	1.94	0.67
2:D:22:ILE:HA	4:D:607:HOH:O	1.93	0.67
1:A:62:HIS:HD2	1:A:65:THR:H	1.41	0.67
1:A:39:HIS:H	1:A:42:GLN:NE2	1.93	0.66
1:B:35:GLN:HG2	1:B:350:PHE:OXT	1.96	0.66
1:A:264:ASP:CG	1:A:295:LYS:HG2	2.16	0.66
1:A:319:LYS:HE3	1:A:319:LYS:H	1.60	0.66
1:B:39:HIS:N	1:B:42:GLN:NE2	2.44	0.65
1:B:47:LYS:HD3	1:B:324:THR:HG21	1.79	0.65
1:B:205:LEU:HB3	1:B:209:ILE:CG2	2.27	0.64
1:B:187:PHE:HE2	2:D:21:ALA:HB1	1.63	0.64
1:B:13:GLU:HG3	1:B:15:VAL:N	2.12	0.63
1:A:51:THR:HG23	1:A:56:ARG:HB3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:317:LYS:NZ	4:A:1011:HOH:O	2.31	0.63
1:A:51:THR:HG22	1:A:52:GLY:H	1.65	0.62
1:B:335:ILE:O	1:B:335:ILE:HG23	1.99	0.62
1:B:39:HIS:N	1:B:42:GLN:HE21	1.98	0.61
1:B:55:GLY:HA2	4:B:982:HOH:O	2.00	0.60
1:B:47:LYS:HD3	1:B:324:THR:CG2	2.31	0.60
1:B:213:LYS:HE2	4:B:833:HOH:O	2.01	0.59
1:A:189:LYS:HE2	1:A:191:VAL:CG1	2.31	0.59
1:B:17:GLU:O	1:B:21:LYS:HE2	2.03	0.59
1:B:62:HIS:HD2	1:B:65:THR:H	1.49	0.59
1:A:100:PHE:CG	1:A:101:PRO:HD2	2.39	0.58
1:B:62:HIS:CD2	1:B:65:THR:H	2.21	0.58
1:B:39:HIS:H	1:B:42:GLN:HE21	1.52	0.58
3:A:351:L9M:CL1	3:A:351:L9M:C2	2.73	0.58
1:B:316:PRO:HG2	4:B:535:HOH:O	2.05	0.57
1:A:100:PHE:CD1	1:A:101:PRO:HD2	2.39	0.56
1:B:316:PRO:HB3	4:B:601:HOH:O	2.05	0.56
1:A:158:HIS:HE1	1:A:220:ASP:OD2	1.89	0.56
1:B:308:ARG:NH1	4:B:424:HOH:O	2.38	0.56
1:B:37:THR:HG23	4:B:959:HOH:O	2.05	0.56
1:B:74:LEU:N	1:B:74:LEU:HD12	2.21	0.56
1:B:187:PHE:CE2	2:D:21:ALA:HB1	2.41	0.56
1:B:200:GLY:O	2:D:22:ILE:HG12	2.07	0.54
1:A:39:HIS:H	1:A:42:GLN:HE21	1.54	0.54
1:A:74:LEU:HD12	1:A:74:LEU:N	2.23	0.53
1:A:189:LYS:HE2	1:A:191:VAL:HG11	1.91	0.53
1:B:275:VAL:CG1	4:B:743:HOH:O	2.52	0.53
1:A:192:LYS:O	1:A:192:LYS:HG3	2.09	0.52
1:B:209:ILE:HG23	1:B:210:ILE:N	2.23	0.52
1:B:318:PHE:CB	4:B:744:HOH:O	2.58	0.52
1:B:100:PHE:CD1	1:B:101:PRO:HD2	2.45	0.51
1:A:56:ARG:HH22	1:A:335:ILE:HA	1.75	0.51
1:B:176:GLN:HG3	1:B:318:PHE:CZ	2.40	0.51
1:A:303:ILE:HD13	4:A:756:HOH:O	2.11	0.50
1:A:314:PHE:C	1:A:315:ILE:HD12	2.32	0.50
1:A:318:PHE:CD1	1:A:318:PHE:O	2.65	0.50
1:A:122:TYR:O	1:A:124:PRO:HD3	2.11	0.49
1:A:189:LYS:HG2	1:A:191:VAL:HG13	1.92	0.49
1:A:39:HIS:N	1:A:42:GLN:HE21	2.11	0.49
1:A:39:HIS:N	1:A:42:GLN:NE2	2.60	0.49
1:A:335:ILE:HD12	1:A:335:ILE:N	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:318:PHE:HD1	1:B:318:PHE:H	1.59	0.49
1:A:23:LYS:O	1:A:27:LEU:CD2	2.61	0.49
1:A:180:ILE:CG2	1:A:181:LYS:N	2.76	0.48
1:B:177:GLN:HB2	4:B:395:HOH:O	2.11	0.48
1:A:105:LYS:HE2	4:A:708:HOH:O	2.13	0.48
1:B:174:ILE:HD13	1:B:180:ILE:HD13	1.95	0.48
1:A:26:PHE:HD2	1:A:27:LEU:HD22	1.79	0.47
1:A:192:LYS:O	1:A:192:LYS:HE2	2.15	0.47
1:A:53:SER:C	1:A:55:GLY:H	2.17	0.47
1:A:279:LYS:HA	1:A:284:LEU:HD21	1.96	0.47
1:B:51:THR:HG22	1:B:330:TYR:CD2	2.50	0.47
1:B:104:VAL:HG11	1:B:183:THR:HG22	1.97	0.47
1:B:275:VAL:HG23	1:B:276:ASP:N	2.29	0.47
1:A:180:ILE:HG22	1:A:181:LYS:N	2.30	0.46
1:B:158:HIS:HE1	1:B:220:ASP:OD2	1.97	0.46
1:B:176:GLN:CD	1:B:318:PHE:HZ	2.18	0.46
1:A:158:HIS:HD2	4:A:408:HOH:O	1.97	0.46
1:A:238:PHE:CZ	1:A:255:VAL:HG22	2.51	0.46
1:A:247:TYR:O	1:A:251:VAL:HG22	2.15	0.46
1:B:307:GLN:HE21	1:B:309:LYS:HD2	1.81	0.46
1:B:47:LYS:CD	1:B:324:THR:HG21	2.46	0.46
1:B:335:ILE:HG22	4:B:475:HOH:O	2.16	0.46
1:A:50:GLY:HA3	3:A:351:L9M:H4	1.99	0.45
3:A:351:L9M:CL1	3:A:351:L9M:C4	2.77	0.45
1:B:131:HIS:HB2	4:B:534:HOH:O	2.15	0.45
1:B:238:PHE:CZ	1:B:255:VAL:HG22	2.51	0.45
1:B:318:PHE:HB3	4:B:744:HOH:O	2.16	0.45
1:A:84:GLN:HA	1:A:87:HIS:HD2	1.80	0.45
1:B:75:ASP:HB3	1:B:78:LYS:HD2	1.99	0.45
1:A:195:THR:OG1	1:A:197:TPO:O2P	2.26	0.45
1:B:289:ASN:ND2	4:B:781:HOH:O	2.49	0.45
1:B:177:GLN:NE2	4:B:403:HOH:O	2.50	0.45
1:B:334:GLU:O	1:B:334:GLU:HG3	2.15	0.45
1:B:199:CYS:O	1:B:209:ILE:HD11	2.16	0.44
1:A:144:ARG:NE	1:A:296:TRP:O	2.51	0.44
1:A:105:LYS:HD3	4:A:580:HOH:O	2.17	0.44
1:B:176:GLN:CG	1:B:318:PHE:CZ	2.94	0.44
1:B:209:ILE:CG2	1:B:210:ILE:N	2.80	0.44
1:A:69:TYR:CE1	1:A:107:GLU:HG3	2.52	0.43
1:A:156:TYR:O	1:A:160:LEU:HD13	2.18	0.43
1:A:256:ARG:HG3	4:A:929:HOH:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:308:ARG:HB3	1:A:308:ARG:NH1	2.33	0.43
1:B:55:GLY:CA	4:B:982:HOH:O	2.64	0.43
1:B:180:ILE:CG2	1:B:181:LYS:N	2.81	0.43
1:B:180:ILE:HG22	1:B:181:LYS:N	2.34	0.43
1:B:38:ALA:HA	1:B:42:GLN:HE22	1.84	0.43
1:B:39:HIS:CD2	1:B:41:ASP:H	2.24	0.43
1:B:50:GLY:HA3	3:B:351:L9M:H4	2.01	0.42
1:B:54:PHE:HE2	1:B:57:VAL:HG23	1.83	0.42
1:B:176:GLN:CD	1:B:318:PHE:CZ	2.93	0.42
1:A:307:GLN:HE21	1:A:309:LYS:HD2	1.84	0.42
1:B:13:GLU:HG2	1:B:15:VAL:HB	2.00	0.42
1:B:13:GLU:CG	1:B:15:VAL:HB	2.50	0.42
1:A:83:LYS:NZ	4:A:370:HOH:O	2.53	0.42
1:A:264:ASP:OD1	1:A:295:LYS:HG2	2.19	0.42
1:A:125:GLY:O	1:A:131:HIS:CE1	2.73	0.42
1:A:226:VAL:HG13	1:A:237:PRO:HD2	2.01	0.42
1:A:131:HIS:HD2	4:A:377:HOH:O	2.03	0.41
1:A:315:ILE:HD12	1:A:315:ILE:N	2.34	0.41
1:B:126:GLY:HA2	1:B:327:PHE:CZ	2.55	0.41
1:A:215:TYR:CD2	1:A:219:VAL:HG11	2.55	0.41
1:A:131:HIS:CD2	4:A:377:HOH:O	2.73	0.41
1:B:122:TYR:O	1:B:124:PRO:HD3	2.20	0.41
1:B:339:ILE:HG22	1:B:339:ILE:O	2.19	0.41
1:A:32:SER:HB2	4:A:530:HOH:O	2.20	0.41
1:B:104:VAL:HG13	1:B:181:LYS:HB3	2.02	0.41
1:A:270:ARG:NH2	4:A:465:HOH:O	2.53	0.41
1:A:308:ARG:HD2	4:A:897:HOH:O	2.21	0.41
1:B:176:GLN:NE2	4:B:474:HOH:O	2.54	0.41
1:A:200:GLY:O	2:C:22:ILE:HG12	2.21	0.40
1:A:189:LYS:CE	1:A:191:VAL:HG11	2.51	0.40
1:A:277:LEU:HD13	4:A:485:HOH:O	2.20	0.40
1:B:217:LYS:HE2	1:B:217:LYS:HB3	1.94	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:521:HOH:O	4:A:521:HOH:O[2_555]	1.65	0.55
4:A:792:HOH:O	4:A:792:HOH:O[2_555]	1.77	0.43

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	336/351 (96%)	326 (97%)	9 (3%)	1 (0%)	41	31
1	B	334/351 (95%)	322 (96%)	11 (3%)	1 (0%)	41	31
2	C	17/20 (85%)	17 (100%)	0	0	100	100
2	D	16/20 (80%)	16 (100%)	0	0	100	100
All	All	703/742 (95%)	681 (97%)	20 (3%)	2 (0%)	41	31

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	184	ASP
1	B	202	PRO

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	291/303 (96%)	280 (96%)	11 (4%)	33	24
1	B	291/303 (96%)	286 (98%)	5 (2%)	60	57
2	C	14/15 (93%)	14 (100%)	0	100	100
2	D	13/15 (87%)	13 (100%)	0	100	100
All	All	609/636 (96%)	593 (97%)	16 (3%)	46	39

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	SER
1	A	51	THR
1	A	59	LEU
1	A	92	LYS
1	A	176	GLN
1	A	192	LYS
1	A	241	ASP
1	A	256	ARG
1	A	318	PHE
1	A	319	LYS
1	A	334	GLU
1	B	14	SER
1	B	41	ASP
1	B	56	ARG
1	B	242	GLN
1	B	318	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	39	HIS
1	A	42	GLN
1	A	62	HIS
1	A	67	ASN
1	A	84	GLN
1	A	113	ASN
1	A	131	HIS
1	A	158	HIS
1	A	271	ASN
1	A	307	GLN
2	C	20	ASN
1	B	35	GLN
1	B	36	ASN
1	B	39	HIS
1	B	42	GLN
1	B	62	HIS
1	B	68	HIS
1	B	84	GLN
1	B	87	HIS
1	B	99	ASN
1	B	113	ASN
1	B	158	HIS
1	B	176	GLN

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Mol	Chain	Res	Type
1	B	242	GLN
1	B	271	ASN
1	B	289	ASN
1	B	307	GLN
2	D	20	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

4 non-standard protein/DNA/RNA residues 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
1	SEP	A	338	1	8,9,10	0.94	0	8,12,14	1.85	1 (12%)
1	TPO	A	197	1	8,10,11	0.95	0	10,14,16	1.09	1 (10%)
1	TPO	B	197	1	8,10,11	0.89	0	10,14,16	1.06	1 (10%)
1	SEP	B	338	1	8,9,10	0.95	0	8,12,14	1.60	1 (12%)

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
1	SEP	A	338	1	-	5/5/8/10	-
1	TPO	A	197	1	-	2/9/11/13	-
1	TPO	B	197	1	-	2/9/11/13	-
1	SEP	B	338	1	-	3/5/8/10	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	338	SEP	OG-CB-CA	4.84	112.86	108.14
1	B	338	SEP	OG-CB-CA	3.74	111.79	108.14
1	A	197	TPO	CG2-CB-CA	-2.45	108.33	113.16
1	B	197	TPO	CG2-CB-CA	-2.25	108.73	113.16

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	338	SEP	N-CA-CB-OG
1	A	338	SEP	CB-OG-P-O1P
1	A	338	SEP	CB-OG-P-O2P
1	A	338	SEP	CB-OG-P-O3P
1	B	197	TPO	O-C-CA-CB
1	B	338	SEP	CB-OG-P-O2P
1	A	197	TPO	CB-OG1-P-O3P
1	B	197	TPO	CB-OG1-P-O3P
1	B	338	SEP	CA-CB-OG-P
1	B	338	SEP	N-CA-CB-OG
1	A	338	SEP	CA-CB-OG-P
1	A	197	TPO	O-C-CA-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	197	TPO	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides 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	L9M	A	351	-	21,30,30	3.32	16 (76%)	22,42,42	2.41	9 (40%)
3	L9M	B	351	-	21,30,30	3.09	15 (71%)	22,42,42	2.65	10 (45%)

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	L9M	A	351	-	-	1/7/13/13	0/4/4/4
3	L9M	B	351	-	-	0/7/13/13	0/4/4/4

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	351	L9M	CL1-C3	6.96	1.76	1.51
3	A	351	L9M	N5-N2	-6.74	1.24	1.37
3	B	351	L9M	N5-N2	-6.58	1.25	1.37
3	B	351	L9M	CL1-C3	5.82	1.71	1.51
3	A	351	L9M	C16-C17	4.51	1.48	1.39
3	B	351	L9M	C16-C17	4.48	1.48	1.39
3	B	351	L9M	C13-C11	3.77	1.45	1.35
3	A	351	L9M	C13-C11	3.59	1.45	1.35
3	A	351	L9M	C18-C9	-3.51	1.47	1.50
3	B	351	L9M	C18-C9	-3.44	1.47	1.50
3	A	351	L9M	C2-C1	3.42	1.45	1.38
3	A	351	L9M	C1-C6	3.29	1.45	1.38
3	B	351	L9M	C16-C15	3.25	1.45	1.40
3	B	351	L9M	C13-C14	3.17	1.47	1.41
3	A	351	L9M	C5-C6	3.16	1.45	1.38
3	A	351	L9M	C16-C15	3.08	1.45	1.40
3	A	351	L9M	C13-C14	2.89	1.46	1.41
3	B	351	L9M	C5-C6	2.87	1.45	1.38
3	B	351	L9M	C5-C4	2.75	1.43	1.38
3	A	351	L9M	C5-C4	2.72	1.43	1.38
3	A	351	L9M	C4-C3	2.59	1.46	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	351	L9M	C2-C1	2.59	1.43	1.38
3	A	351	L9M	C2-C3	2.59	1.46	1.38
3	B	351	L9M	C4-C3	2.49	1.45	1.38
3	B	351	L9M	C15-C14	2.47	1.49	1.42
3	B	351	L9M	C1-C6	2.44	1.44	1.38
3	A	351	L9M	C15-C14	2.32	1.48	1.42
3	B	351	L9M	C2-C3	2.25	1.45	1.38
3	B	351	L9M	N4-N1	-2.13	1.33	1.37
3	A	351	L9M	C7-N6	2.06	1.49	1.45
3	A	351	L9M	C11-C17	2.02	1.46	1.41

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	351	L9M	C7-N6-C12	-6.04	113.03	123.36
3	B	351	L9M	C7-N6-C12	-5.61	113.75	123.36
3	B	351	L9M	C5-C6-C1	4.67	125.51	118.17
3	B	351	L9M	C5-C4-C3	-3.78	116.32	121.38
3	A	351	L9M	C5-C6-C1	3.68	123.94	118.17
3	B	351	L9M	C4-C3-C2	3.60	126.00	118.11
3	A	351	L9M	C16-C17-C11	3.39	122.38	118.15
3	B	351	L9M	C1-C2-C3	-3.37	116.86	121.38
3	B	351	L9M	C13-C14-N4	3.28	135.53	130.19
3	A	351	L9M	C5-C4-C3	-3.11	117.22	121.38
3	A	351	L9M	C4-C3-C2	3.02	124.74	118.11
3	A	351	L9M	C1-C2-C3	-2.89	117.52	121.38
3	B	351	L9M	C18-C9-N1	2.84	125.89	119.65
3	B	351	L9M	C16-C17-C11	2.81	121.65	118.15
3	A	351	L9M	C13-C14-N4	2.69	134.57	130.19
3	B	351	L9M	C2-C1-C6	-2.49	117.60	121.03
3	B	351	L9M	C4-C5-C6	-2.42	117.70	121.03
3	A	351	L9M	C2-C1-C6	-2.33	117.83	121.03
3	A	351	L9M	C18-C9-N1	2.25	124.60	119.65

There are no chirality outliers.

All (1) torsion outliers are listed below:

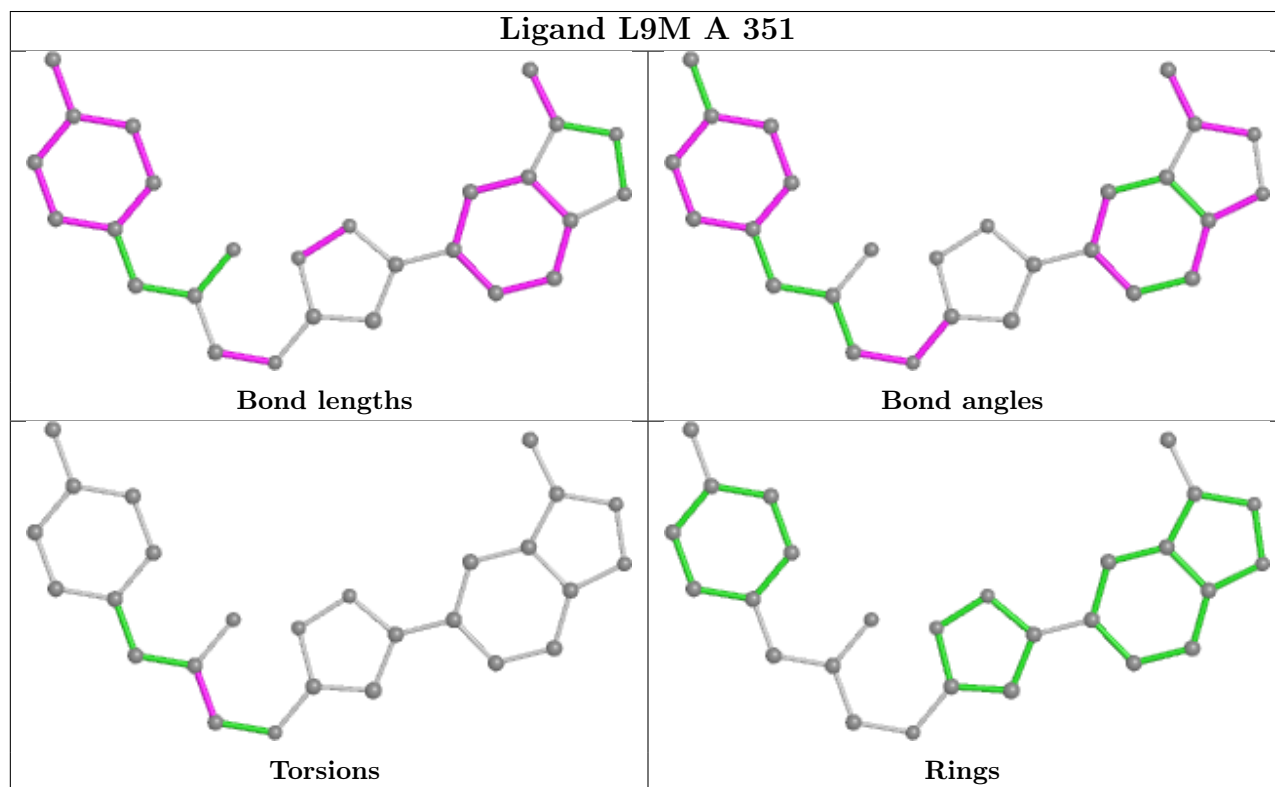
Mol	Chain	Res	Type	Atoms
3	A	351	L9M	N3-C10-C7-N6

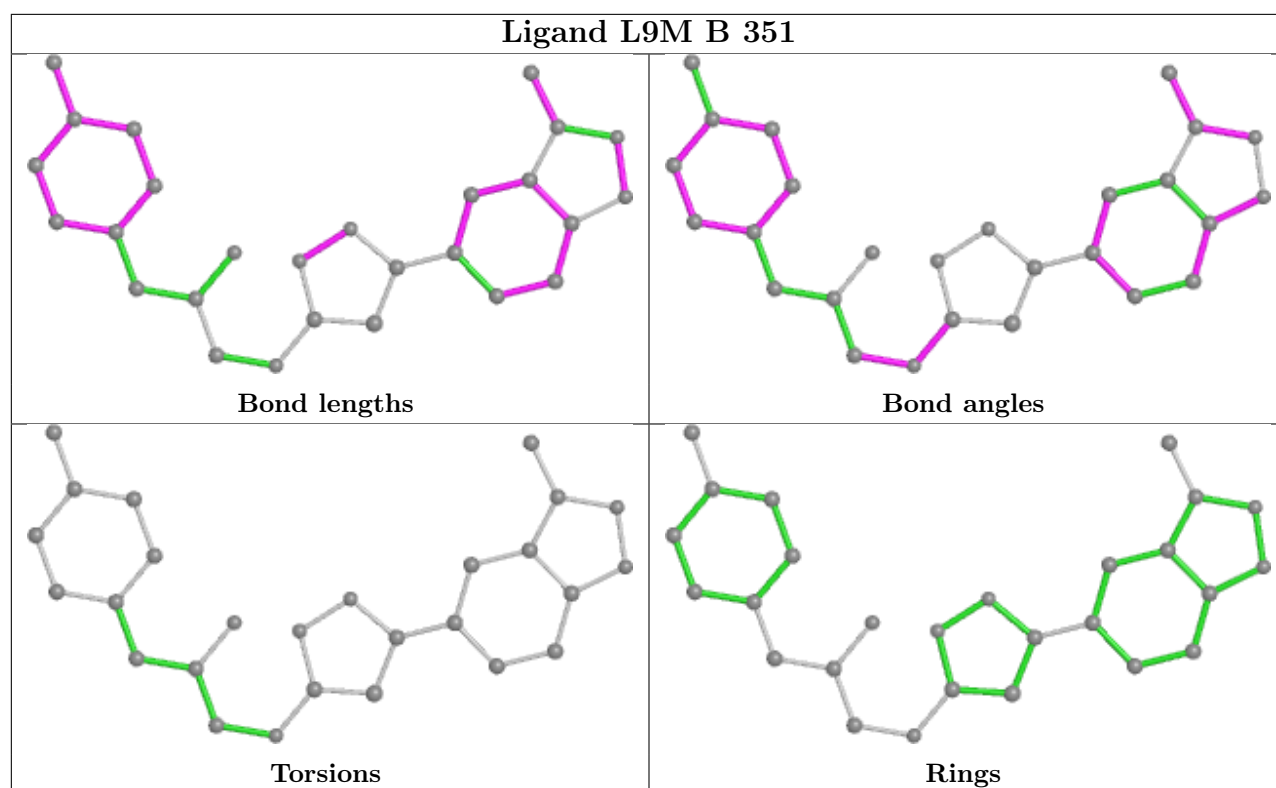
There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	351	L9M	4	0
3	B	351	L9M	1	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	338/351 (96%)	0.04	5 (1%) 73 76	10, 19, 32, 37	0
1	B	336/351 (95%)	0.11	13 (3%) 39 42	11, 18, 32, 41	0
2	C	19/20 (95%)	-0.12	1 (5%) 26 29	13, 17, 28, 37	0
2	D	18/20 (90%)	-0.22	1 (5%) 24 27	12, 16, 25, 33	0
All	All	711/742 (95%)	0.06	20 (2%) 53 56	10, 18, 32, 41	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	318	PHE	7.8
1	B	34	ALA	6.1
1	A	318	PHE	5.6
2	C	23	HIS	5.0
1	A	339	ILE	4.2
2	D	22	ILE	3.2
1	B	193	GLY	2.9
1	A	253	GLY	2.8
1	B	335	ILE	2.8
1	B	36	ASN	2.8
1	A	53	SER	2.7
1	B	339	ILE	2.7
1	B	334	GLU	2.5
1	A	176	GLN	2.5
1	B	35	GLN	2.4
1	B	53	SER	2.4
1	B	51	THR	2.4
1	B	331	GLU	2.2
1	B	317	LYS	2.1
1	B	209	ILE	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	SEP	A	338	10/11	0.89	0.14	33,34,36,36	0
1	SEP	B	338	10/11	0.94	0.08	25,26,27,27	0
1	TPO	B	197	11/12	0.95	0.08	16,18,18,19	0
1	TPO	A	197	11/12	0.96	0.09	14,15,16,17	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

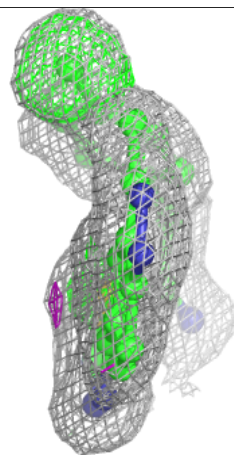
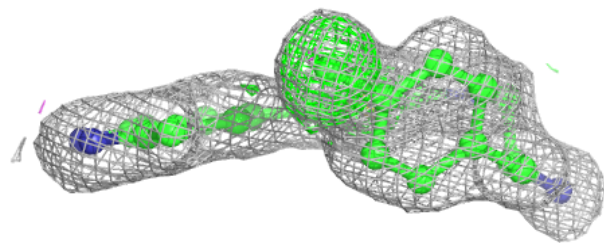
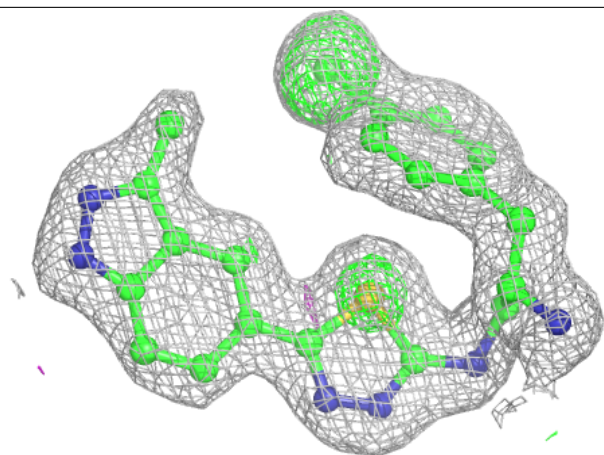
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

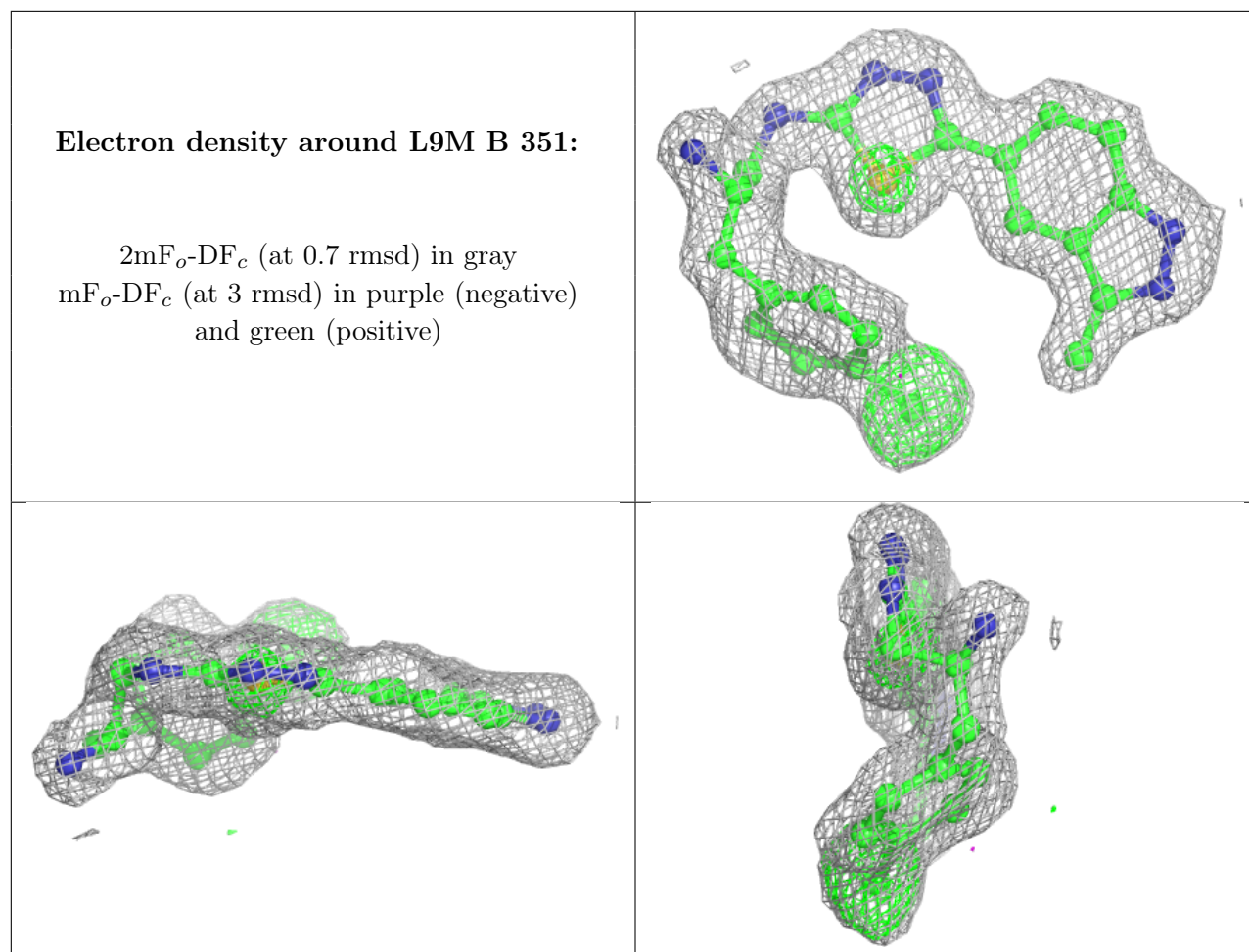
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	L9M	A	351	27/27	0.82	0.17	10,15,20,29	0
3	L9M	B	351	27/27	0.82	0.17	13,15,21,31	0

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 L9M A 351:

$2mF_o-DF_c$ (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.