



Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 02:29 am BST

PDB ID : 3WDK
Title : Crystal structure of 4-phosphopantoate-beta-alanine ligase complexed with reaction intermediate
Authors : Kishimoto, A.; Kita, A.; Ishibashi, T.; Tomita, H.; Yokooji, Y.; Imanaka, T.; Atomi, H.; Miki, K.
Deposited on : 2013-06-19
Resolution : 2.30 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

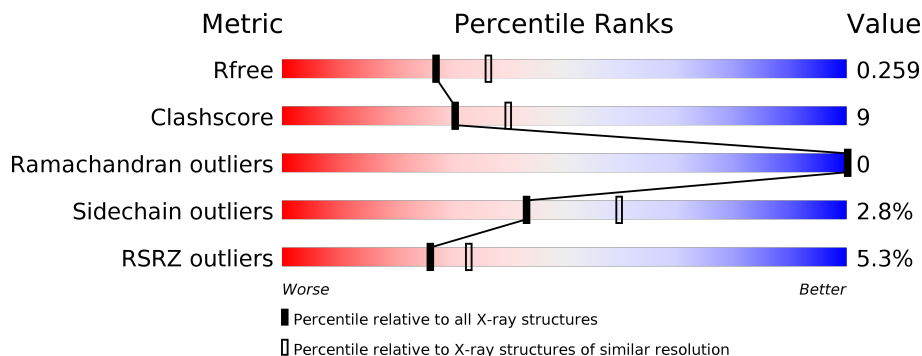
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	261	<div style="display: flex; align-items: center;"> <div style="width: 5%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 77%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 16%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 20px;">5% 77% 16% • 5%</p>
1	B	261	<div style="display: flex; align-items: center;"> <div style="width: 5%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 79%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 15%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 20px;">5% 79% 15% • 5%</p>
1	C	261	<div style="display: flex; align-items: center;"> <div style="width: 4%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 75%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 19%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 20px;">4% 75% 19% • 5%</p>
1	D	261	<div style="display: flex; align-items: center;"> <div style="width: 5%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 73%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 21%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 5%; height: 10px; background-color: grey;"></div> </div> <p style="margin-left: 20px;">5% 73% 21% • •</p>

2 Entry composition [i](#)

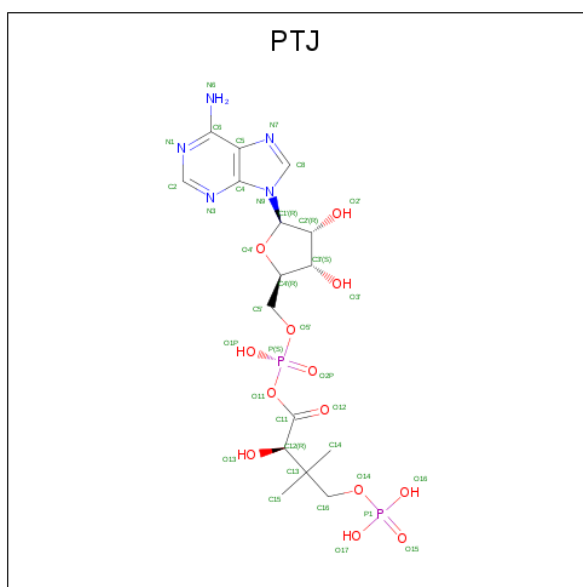
There are 4 unique types of molecules in this entry. The entry contains 8246 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 4-phosphopantoate--beta-alanine ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	249	Total	C	N	O	S	0	0	0
			1956	1239	352	358	7			
1	B	247	Total	C	N	O	S	0	0	0
			1960	1239	350	364	7			
1	C	247	Total	C	N	O	S	0	0	0
			1931	1225	341	358	7			
1	D	250	Total	C	N	O	S	0	0	0
			1961	1243	348	363	7			

- Molecule 2 is 5'-O-[(S)-hydroxy{[(2R)-2-hydroxy-3,3-dimethyl-4-(phosphonoxy)butanoyl]oxy}phosphoryl]adenosine (three-letter code: PTJ) (formula: C₁₆H₂₅N₅O₁₃P₂).



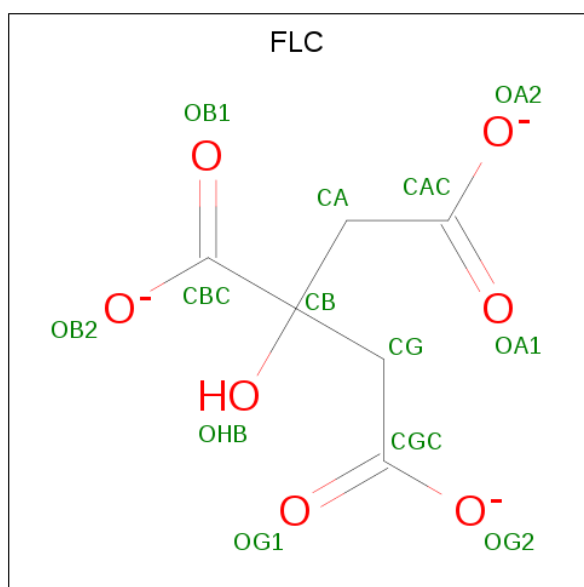
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
2	A	1	Total	C	N	O	P	0	0
			36	16	5	13	2		
2	B	1	Total	C	N	O	P	0	0
			36	16	5	13	2		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	C	1	Total	C	N	O	P	0	0
				36	16	5	13		
2	D	1	Total	C	N	O	P	0	0
				36	16	5	13		

- Molecule 3 is CITRATE ANION (three-letter code: FLC) (formula: $C_6H_5O_7^-$).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
3	A	1	Total	C	O	0	0
				13	6		
3	C	1	Total	C	O	0	0
				13	6		
3	D	1	Total	C	O	0	0
				13	6		

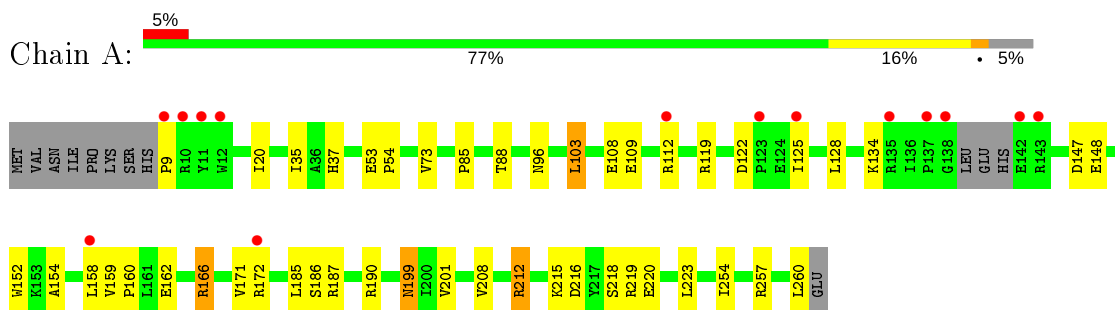
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	57	Total	O	0	0
				57		
4	B	70	Total	O	0	0
				70		
4	C	63	Total	O	0	0
				63		
4	D	65	Total	O	0	0
				65		

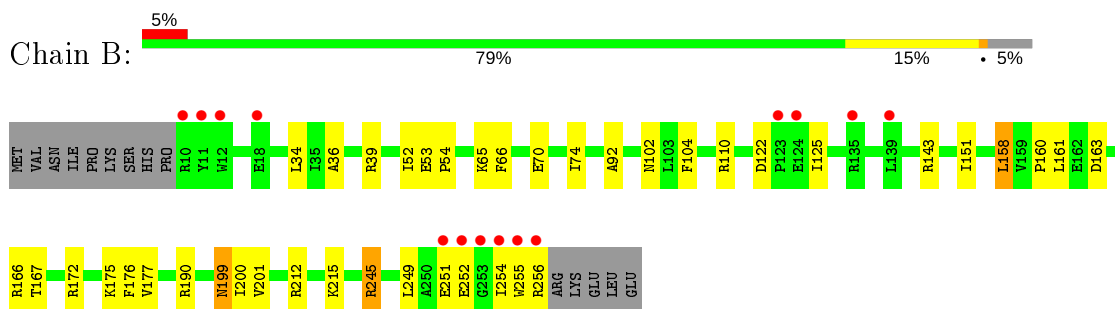
3 Residue-property plots [i](#)

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.

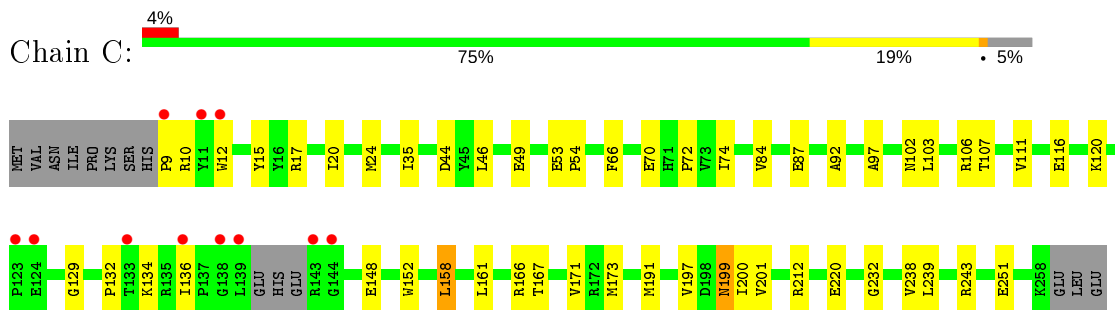
- Molecule 1: 4-phosphopantoate--beta-alanine ligase



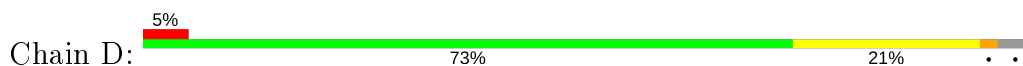
- Molecule 1: 4-phosphopantoate--beta-alanine ligase

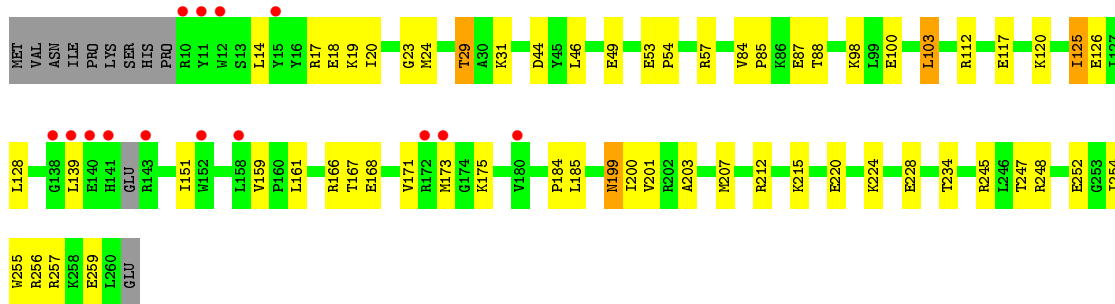


- Molecule 1: 4-phosphopantoate--beta-alanine ligase



- Molecule 1: 4-phosphopantoate--beta-alanine ligase





4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	123.61Å 123.61Å 187.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.49 – 2.30 29.49 – 2.30	Depositor EDS
% Data completeness (in resolution range)	93.3 (29.49-2.30) 93.4 (29.49-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.35 (at 2.31Å)	Xtrriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.216 , 0.264 0.210 , 0.259	Depositor DCC
R_{free} test set	3043 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	25.5	Xtrriage
Anisotropy	0.192	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 44.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8246	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.74% of the height of the origin peak. No significant pseudotranslation is detected.*

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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FLC, PTJ

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	0.31	0/1985	0.57	1/2682 (0.0%)
1	B	0.33	0/1989	0.57	0/2684
1	C	0.32	0/1961	0.56	0/2652
1	D	0.32	0/1990	0.56	0/2689
All	All	0.32	0/7925	0.57	1/10707 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	9	PRO	N-CA-CB	5.53	109.94	103.30

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	1956	0	1981	41	0
1	B	1960	0	2002	42	0
1	C	1931	0	1945	38	0
1	D	1961	0	1980	47	0
2	A	36	0	24	0	0
2	B	36	0	24	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	36	0	24	0	0
2	D	36	0	24	1	0
3	A	13	0	5	0	0
3	C	13	0	5	1	0
3	D	13	0	5	1	0
4	A	57	0	0	1	0
4	B	70	0	0	1	0
4	C	63	0	0	0	0
4	D	65	0	0	0	0
All	All	8246	0	8019	147	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 9.

All (147) 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:B:104:PHE:O	1:B:143:ARG:HG2	1.85	0.76
1:B:199:ASN:HD22	1:B:201:VAL:H	1.30	0.76
1:A:159:VAL:HG22	1:A:162:GLU:HB2	1.67	0.74
1:D:125:ILE:HD13	1:D:126:GLU:N	2.03	0.74
1:C:136:ILE:HG12	1:C:173:MET:HE1	1.72	0.70
1:A:171:VAL:HG11	1:B:256:ARG:HH12	1.57	0.70
1:A:190:ARG:HH11	1:B:254:ILE:HB	1.57	0.69
1:C:136:ILE:HG23	1:C:173:MET:CE	2.24	0.68
1:D:248:ARG:O	1:D:252:GLU:HG3	1.95	0.67
1:C:199:ASN:HD22	1:C:201:VAL:H	1.42	0.67
1:A:218:SER:OG	1:A:220:GLU:HG2	1.95	0.67
1:D:199:ASN:HD22	1:D:200:ILE:N	1.92	0.67
1:A:187:ARG:HH12	1:B:254:ILE:HD12	1.60	0.66
1:B:199:ASN:ND2	1:B:201:VAL:H	1.95	0.65
1:A:158:LEU:HD22	1:A:160:PRO:HD3	1.80	0.63
1:B:104:PHE:HD2	1:B:166:ARG:HD3	1.64	0.62
1:A:257:ARG:HD2	1:A:260:LEU:HD23	1.82	0.61
1:D:23:GLY:C	1:D:29:THR:HG23	2.22	0.59
1:A:199:ASN:HD22	1:A:201:VAL:H	1.51	0.59
1:A:219:ARG:O	1:A:223:LEU:HD23	2.03	0.58
1:A:172:ARG:HH11	1:A:172:ARG:HG2	1.68	0.58
1:B:254:ILE:HG22	1:B:255:TRP:N	2.18	0.58
1:C:136:ILE:HG23	1:C:173:MET:HE2	1.85	0.57
1:D:168:GLU:O	1:D:171:VAL:HG22	2.03	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:ASP:O	1:A:125:ILE:HG22	2.04	0.57
1:A:119:ARG:HH11	1:A:119:ARG:HG3	1.68	0.57
1:A:134:LYS:HE2	1:A:152:TRP:CZ2	2.41	0.56
1:D:17:ARG:O	1:D:20:ILE:HG22	2.06	0.56
1:A:53:GLU:HB3	1:A:54:PRO:HD3	1.87	0.56
1:D:139:LEU:HD11	1:D:166:ARG:HA	1.87	0.56
1:C:17:ARG:O	1:C:20:ILE:HG22	2.06	0.56
1:C:191:MET:HE2	1:D:256:ARG:HB2	1.88	0.56
1:B:254:ILE:HG22	1:B:255:TRP:H	1.71	0.55
1:A:85:PRO:O	1:A:88:THR:HG22	2.07	0.55
1:B:151:ILE:O	1:B:175:LYS:HE3	2.06	0.55
1:B:110:ARG:NH2	2:B:901:PTJ:O15	2.37	0.55
1:A:215:LYS:HG3	1:A:216:ASP:N	2.21	0.55
1:D:53:GLU:HB3	1:D:54:PRO:HD3	1.88	0.54
1:A:187:ARG:HH22	1:B:254:ILE:HD12	1.73	0.54
1:D:212:ARG:O	1:D:215:LYS:HG2	2.07	0.54
1:B:122:ASP:O	1:B:125:ILE:HG22	2.08	0.54
1:A:172:ARG:NH1	1:A:172:ARG:HG2	2.23	0.54
1:B:39:ARG:NH1	4:B:1058:HOH:O	2.40	0.54
1:B:256:ARG:HG2	1:B:256:ARG:O	2.08	0.54
1:D:184:PRO:HG2	1:D:185:LEU:HD22	1.90	0.54
1:D:14:LEU:O	1:D:18:GLU:HG3	2.08	0.53
1:A:212:ARG:O	1:A:215:LYS:HG2	2.08	0.53
1:A:254:ILE:O	1:B:190:ARG:HG2	2.09	0.53
1:D:44:ASP:OD1	1:D:49:GLU:HA	2.08	0.53
1:B:245:ARG:O	1:B:249:LEU:HB2	2.09	0.52
1:D:24:MET:C	1:D:24:MET:HE2	2.30	0.52
1:B:143:ARG:NH1	1:D:112:ARG:NH2	2.58	0.52
1:C:9:PRO:HG2	1:C:10:ARG:H	1.73	0.52
1:C:35:ILE:HG21	1:D:17:ARG:NH1	2.25	0.52
1:A:208:VAL:O	1:A:212:ARG:HD3	2.09	0.52
1:C:161:LEU:HD12	1:C:161:LEU:N	2.25	0.51
1:C:72:PRO:HG2	1:C:97:ALA:HA	1.92	0.51
1:B:143:ARG:HH12	1:D:112:ARG:NH2	2.09	0.50
1:C:74:ILE:HD12	1:C:92:ALA:HA	1.93	0.50
1:D:256:ARG:HD2	1:D:259:GLU:OE2	2.10	0.50
1:B:52:ILE:HG13	1:B:54:PRO:HD2	1.94	0.50
1:D:199:ASN:C	1:D:199:ASN:HD22	2.15	0.50
1:D:84:VAL:HB	1:D:87:GLU:HB2	1.94	0.50
1:A:212:ARG:HG2	1:A:212:ARG:HH11	1.77	0.49
1:C:191:MET:CE	1:D:256:ARG:HB2	2.42	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:159:VAL:HG23	4:A:434:HOH:O	2.10	0.49
1:C:199:ASN:ND2	1:C:201:VAL:HG22	2.27	0.49
1:B:199:ASN:ND2	1:B:201:VAL:HG22	2.28	0.49
1:C:53:GLU:HB3	1:C:54:PRO:HD3	1.95	0.49
1:A:187:ARG:HH12	1:B:254:ILE:CD1	2.26	0.48
1:D:224:LYS:O	1:D:228:GLU:HB2	2.13	0.48
1:A:187:ARG:NH1	1:B:254:ILE:HD12	2.26	0.48
1:C:44:ASP:OD1	1:C:49:GLU:HA	2.13	0.48
1:B:143:ARG:NH1	1:D:112:ARG:HH22	2.11	0.47
1:C:46:LEU:HD11	1:D:46:LEU:CD1	2.44	0.47
1:A:186:SER:O	1:A:190:ARG:HG3	2.14	0.47
1:B:104:PHE:CD2	1:B:166:ARG:HD3	2.45	0.47
1:D:220:GLU:HB3	3:D:302:FLC:HG1	1.97	0.47
1:B:199:ASN:HD22	1:B:200:ILE:N	2.12	0.47
1:C:24:MET:HE1	1:D:31:LYS:HG2	1.95	0.47
1:B:65:LYS:HE2	1:B:176:PHE:CD2	2.50	0.47
1:C:199:ASN:ND2	1:C:201:VAL:H	2.11	0.46
1:A:103:LEU:O	1:A:166:ARG:NH1	2.48	0.46
1:B:255:TRP:O	1:B:256:ARG:HB2	2.16	0.46
1:B:53:GLU:HB3	1:B:54:PRO:HD3	1.98	0.46
1:D:98:LYS:HD3	1:D:128:LEU:HD11	1.97	0.46
1:D:103:LEU:C	1:D:166:ARG:HH12	2.19	0.46
1:A:148:GLU:HA	1:A:152:TRP:HB3	1.98	0.46
1:A:159:VAL:O	1:A:159:VAL:HG13	2.16	0.46
1:C:220:GLU:HB3	3:C:302:FLC:HG1	1.98	0.46
1:D:46:LEU:O	1:D:245:ARG:HD3	2.15	0.46
1:B:74:ILE:HD12	1:B:92:ALA:HA	1.97	0.46
1:C:129:GLY:O	1:C:132:PRO:HD3	2.16	0.45
1:C:167:THR:O	1:C:171:VAL:HG23	2.16	0.45
1:B:212:ARG:O	1:B:215:LYS:HG2	2.16	0.45
1:B:158:LEU:HD22	1:B:160:PRO:HD3	1.98	0.45
1:B:161:LEU:N	1:B:161:LEU:HD12	2.32	0.45
1:D:159:VAL:O	1:D:159:VAL:HG23	2.17	0.45
1:C:197:VAL:HG11	1:C:238:VAL:HG11	1.99	0.45
1:D:167:THR:O	1:D:171:VAL:HG13	2.17	0.45
1:C:243:ARG:HD2	1:D:247:THR:OG1	2.17	0.45
1:C:134:LYS:HB3	1:C:152:TRP:CE3	2.53	0.44
1:C:66:PHE:CZ	1:C:158:LEU:HB2	2.52	0.44
1:A:109:GLU:OE2	1:A:112:ARG:NH2	2.50	0.44
1:B:102:ASN:OD1	1:B:166:ARG:NH1	2.47	0.44
1:C:148:GLU:HA	1:C:152:TRP:HB3	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:232:GLY:HA2	1:D:255:TRP:HB2	2.00	0.44
1:D:161:LEU:HD12	1:D:161:LEU:N	2.33	0.43
1:D:57:ARG:NH2	1:D:234:THR:HA	2.32	0.43
1:C:84:VAL:HB	1:C:87:GLU:HB2	1.99	0.43
1:B:36:ALA:O	2:B:901:PTJ:H22	2.18	0.43
1:A:20:ILE:HG13	1:A:37:HIS:CG	2.54	0.43
1:D:199:ASN:ND2	2:D:301:PTJ:H25	2.16	0.43
1:B:167:THR:HG23	1:B:177:VAL:HG11	2.00	0.43
1:C:116:GLU:O	1:C:120:LYS:HG3	2.19	0.43
1:C:107:THR:O	1:C:111:VAL:HG23	2.19	0.42
1:D:199:ASN:HD22	1:D:201:VAL:H	1.67	0.42
1:C:46:LEU:HD11	1:D:46:LEU:HD11	2.01	0.42
1:A:128:LEU:HD22	1:A:147:ASP:OD2	2.20	0.42
1:B:172:ARG:HG3	1:B:172:ARG:HH21	1.84	0.42
1:D:117:GLU:O	1:D:120:LYS:HB2	2.18	0.42
1:D:100:GLU:OE1	1:D:151:ILE:HG13	2.19	0.42
1:A:148:GLU:HA	1:A:152:TRP:CB	2.49	0.42
1:A:199:ASN:ND2	1:A:201:VAL:HG22	2.33	0.42
1:A:20:ILE:HG13	1:A:37:HIS:ND1	2.34	0.42
1:A:35:ILE:HD11	1:B:34:LEU:CD1	2.50	0.42
1:C:199:ASN:HD22	1:C:200:ILE:N	2.17	0.42
1:D:125:ILE:HD13	1:D:126:GLU:H	1.80	0.42
1:D:85:PRO:O	1:D:88:THR:HG22	2.20	0.42
1:A:73:VAL:CG2	1:A:154:ALA:HB2	2.50	0.41
1:A:108:GLU:HB3	1:A:112:ARG:NH1	2.35	0.41
1:A:187:ARG:NH2	1:B:254:ILE:HD12	2.35	0.41
1:C:106:ARG:HG2	1:C:107:THR:N	2.35	0.41
1:C:70:GLU:OE1	1:C:70:GLU:HA	2.20	0.41
1:C:239:LEU:HG	1:D:254:ILE:CD1	2.50	0.41
1:C:161:LEU:HD12	1:C:161:LEU:H	1.86	0.41
1:C:102:ASN:OD1	1:C:166:ARG:NH2	2.54	0.41
1:C:12:TRP:HA	1:C:15:TYR:HB3	2.03	0.41
1:D:173:MET:HE3	1:D:175:LYS:HE3	2.02	0.41
1:A:122:ASP:CG	1:A:125:ILE:HB	2.41	0.41
1:B:70:GLU:OE2	1:B:70:GLU:HA	2.19	0.41
1:D:24:MET:N	1:D:29:THR:HG23	2.36	0.41
1:B:66:PHE:CZ	1:B:158:LEU:HB2	2.57	0.40
1:B:199:ASN:HD22	1:B:199:ASN:C	2.25	0.40
1:D:203:ALA:O	1:D:207:MET:HG3	2.22	0.40
1:A:159:VAL:HG22	1:A:162:GLU:CB	2.45	0.40
1:D:255:TRP:CE2	1:D:257:ARG:HB3	2.56	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	245/261 (94%)	243 (99%)	2 (1%)	0	100	100
1	B	245/261 (94%)	239 (98%)	6 (2%)	0	100	100
1	C	243/261 (93%)	240 (99%)	3 (1%)	0	100	100
1	D	246/261 (94%)	244 (99%)	2 (1%)	0	100	100
All	All	979/1044 (94%)	966 (99%)	13 (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	199/222 (90%)	193 (97%)	6 (3%)	41	57
1	B	204/222 (92%)	198 (97%)	6 (3%)	42	58
1	C	197/222 (89%)	192 (98%)	5 (2%)	47	65
1	D	200/222 (90%)	195 (98%)	5 (2%)	47	65
All	All	800/888 (90%)	778 (97%)	22 (3%)	43	60

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	96	ASN
1	A	103	LEU
1	A	166	ARG
1	A	185	LEU
1	A	199	ASN
1	A	212	ARG
1	B	158	LEU
1	B	163	ASP
1	B	199	ASN
1	B	245	ARG
1	B	251	GLU
1	B	252	GLU
1	C	103	LEU
1	C	158	LEU
1	C	199	ASN
1	C	212	ARG
1	C	251	GLU
1	D	19	LYS
1	D	29	THR
1	D	103	LEU
1	D	125	ILE
1	D	199	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	96	ASN
1	A	199	ASN
1	B	96	ASN
1	B	199	ASN
1	C	96	ASN
1	C	199	ASN
1	D	96	ASN
1	D	199	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](#)

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](#)

7 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	FLC	C	302	-	3,12,12	1.14	0	3,17,17	0.56	0
2	PTJ	D	301	-	32,38,38	1.52	5 (15%)	41,59,59	1.51	3 (7%)
2	PTJ	C	301	-	32,38,38	1.52	4 (12%)	41,59,59	1.49	3 (7%)
3	FLC	D	302	-	3,12,12	1.39	0	3,17,17	0.18	0
2	PTJ	A	301	-	32,38,38	1.52	5 (15%)	41,59,59	1.47	3 (7%)
2	PTJ	B	901	-	32,38,38	1.52	4 (12%)	41,59,59	1.50	3 (7%)
3	FLC	A	302	-	3,12,12	1.09	0	3,17,17	0.67	0

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FLC	C	302	-	-	0/6/16/16	-
2	PTJ	D	301	-	-	2/26/48/48	0/3/3/3
2	PTJ	C	301	-	-	3/26/48/48	0/3/3/3
3	FLC	D	302	-	-	0/6/16/16	-
2	PTJ	A	301	-	-	3/26/48/48	0/3/3/3
2	PTJ	B	901	-	-	2/26/48/48	0/3/3/3

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FLC	A	302	-	-	0/6/16/16	-

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	301	PTJ	C2-N3	5.16	1.40	1.32
2	D	301	PTJ	C2-N3	5.15	1.40	1.32
2	A	301	PTJ	C2-N3	5.13	1.40	1.32
2	B	901	PTJ	C2-N3	5.11	1.40	1.32
2	D	301	PTJ	C2-N1	3.47	1.40	1.33
2	A	301	PTJ	C2-N1	3.47	1.40	1.33
2	C	301	PTJ	C2-N1	3.44	1.40	1.33
2	B	901	PTJ	C2-N1	3.42	1.40	1.33
2	D	301	PTJ	C5-C4	-2.78	1.33	1.40
2	C	301	PTJ	C5-C4	-2.78	1.33	1.40
2	A	301	PTJ	C5-C4	-2.78	1.33	1.40
2	B	901	PTJ	C5-C4	-2.77	1.33	1.40
2	A	301	PTJ	C6-C5	-2.64	1.33	1.43
2	D	301	PTJ	C6-C5	-2.63	1.33	1.43
2	C	301	PTJ	C6-C5	-2.62	1.33	1.43
2	B	901	PTJ	C6-C5	-2.62	1.33	1.43
2	A	301	PTJ	O4'-C1'	2.01	1.43	1.41
2	D	301	PTJ	O4'-C1'	2.00	1.43	1.41

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	301	PTJ	N3-C2-N1	-7.06	117.65	128.68
2	C	301	PTJ	N3-C2-N1	-6.95	117.82	128.68
2	B	901	PTJ	N3-C2-N1	-6.94	117.83	128.68
2	A	301	PTJ	N3-C2-N1	-6.89	117.90	128.68
2	B	901	PTJ	C5-C6-N6	-2.91	115.93	120.35
2	C	301	PTJ	C5-C6-N6	-2.72	116.22	120.35
2	B	901	PTJ	O4'-C1'-C2'	-2.69	102.99	106.93
2	C	301	PTJ	O4'-C1'-C2'	-2.55	103.20	106.93
2	A	301	PTJ	C5-C6-N6	-2.54	116.50	120.35
2	D	301	PTJ	C5-C6-N6	-2.49	116.57	120.35
2	D	301	PTJ	O4'-C1'-C2'	-2.39	103.43	106.93
2	A	301	PTJ	O4'-C1'-C2'	-2.37	103.46	106.93

There are no chirality outliers.

All (10) torsion outliers are listed below:

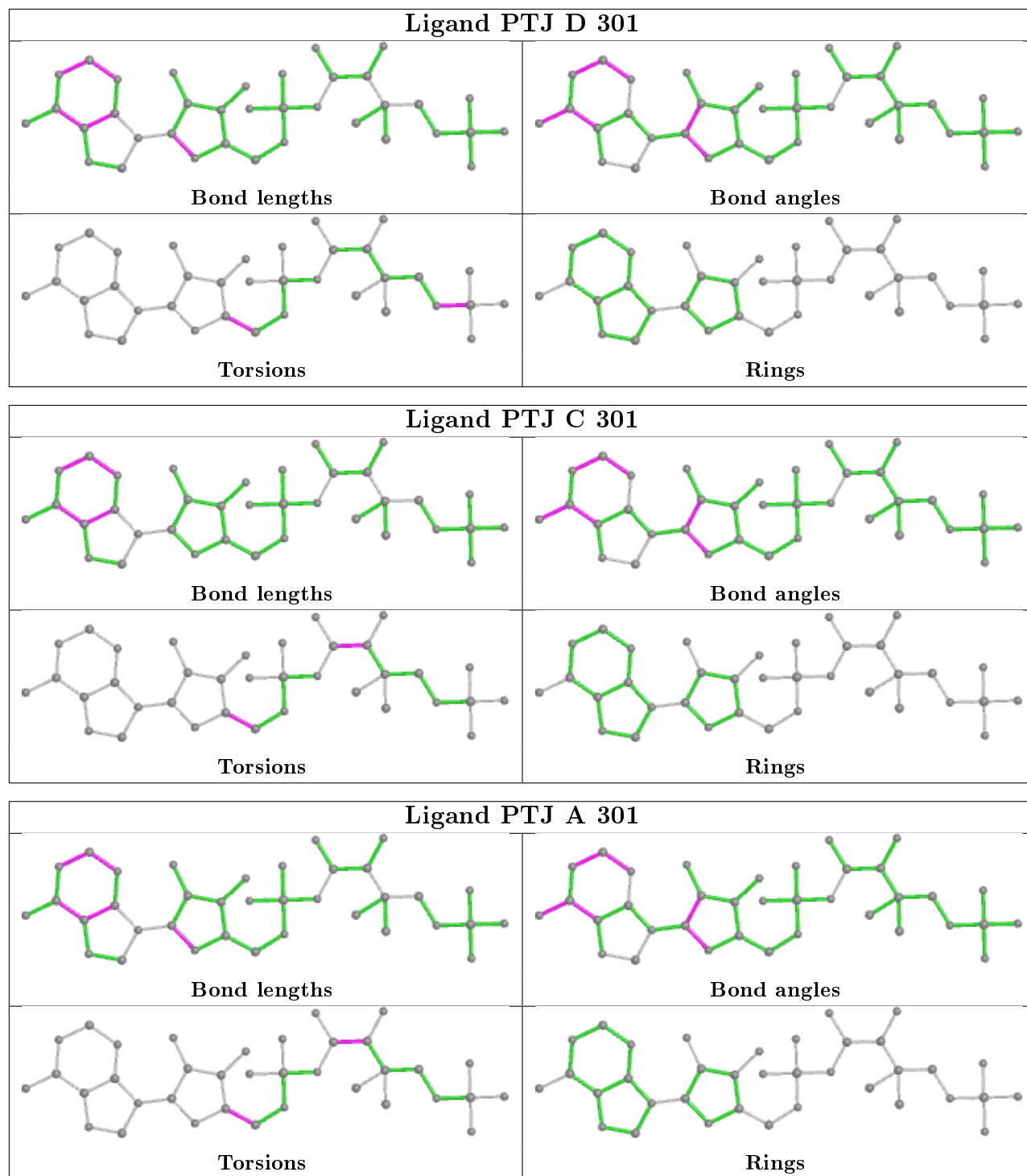
Mol	Chain	Res	Type	Atoms
2	C	301	PTJ	O12-C11-C12-O13
2	C	301	PTJ	O11-C11-C12-O13
2	A	301	PTJ	O12-C11-C12-O13
2	B	901	PTJ	O12-C11-C12-O13
2	A	301	PTJ	O11-C11-C12-O13
2	D	301	PTJ	C16-O14-P1-O17
2	C	301	PTJ	O4'-C4'-C5'-O5'
2	B	901	PTJ	O4'-C4'-C5'-O5'
2	A	301	PTJ	O4'-C4'-C5'-O5'
2	D	301	PTJ	O4'-C4'-C5'-O5'

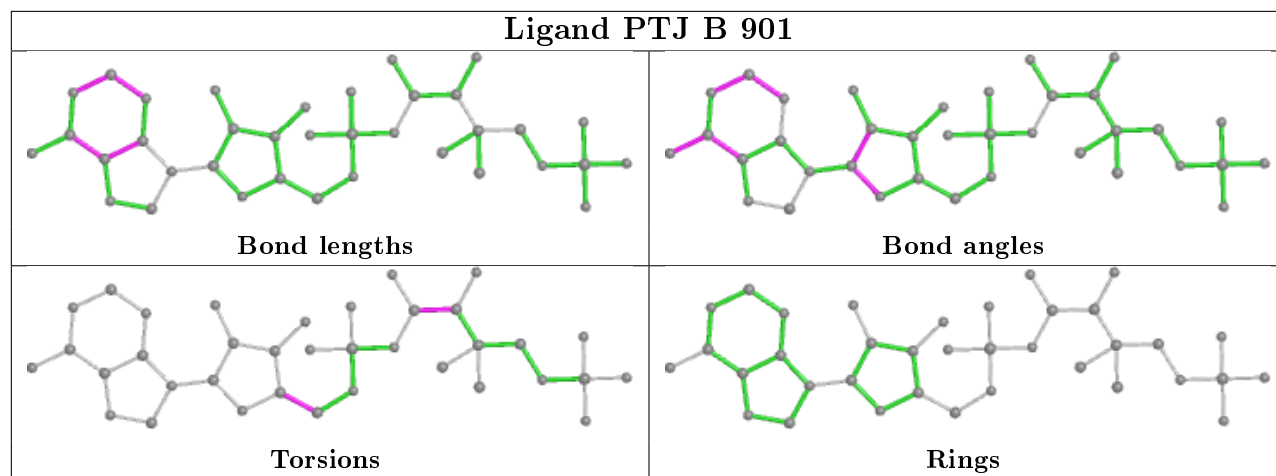
There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	302	FLC	1	0
2	D	301	PTJ	1	0
3	D	302	FLC	1	0
2	B	901	PTJ	2	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

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	249/261 (95%)	0.24	14 (5%) 24 30	14, 30, 59, 80	0
1	B	247/261 (94%)	0.18	14 (5%) 23 30	11, 23, 55, 85	0
1	C	247/261 (94%)	0.21	11 (4%) 33 40	10, 26, 57, 77	0
1	D	250/261 (95%)	0.25	14 (5%) 24 30	12, 27, 54, 79	0
All	All	993/1044 (95%)	0.22	53 (5%) 26 33	10, 27, 59, 85	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	12	TRP	6.1
1	B	252	GLU	6.0
1	C	139	LEU	6.0
1	D	11	TYR	5.7
1	B	254	ILE	5.6
1	C	138	GLY	5.5
1	D	139	LEU	5.4
1	B	253	GLY	5.3
1	C	11	TYR	5.1
1	A	11	TYR	5.0
1	D	141	HIS	4.9
1	B	255	TRP	4.9
1	D	143	ARG	4.6
1	D	140	GLU	4.4
1	C	123	PRO	4.3
1	B	11	TYR	4.2
1	A	123	PRO	3.9
1	A	143	ARG	3.7
1	C	9	PRO	3.7
1	C	12	TRP	3.6
1	A	137	PRO	3.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	138	GLY	3.6
1	A	135	ARG	3.5
1	D	138	GLY	3.4
1	A	10	ARG	3.2
1	B	135	ARG	3.2
1	C	133	THR	3.2
1	B	124	GLU	3.1
1	B	10	ARG	3.0
1	B	12	TRP	3.0
1	A	9	PRO	3.0
1	B	256	ARG	3.0
1	C	124	GLU	2.9
1	A	125	ILE	2.9
1	A	12	TRP	2.8
1	D	15	TYR	2.8
1	D	10	ARG	2.8
1	C	136	ILE	2.7
1	C	143	ARG	2.7
1	D	152	TRP	2.7
1	B	139	LEU	2.6
1	B	251	GLU	2.6
1	D	173	MET	2.5
1	B	123	PRO	2.5
1	A	142	GLU	2.5
1	D	172	ARG	2.3
1	A	172	ARG	2.3
1	D	180	VAL	2.3
1	B	18	GLU	2.2
1	A	158	LEU	2.2
1	A	112	ARG	2.1
1	D	158	LEU	2.1
1	C	144	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](#)

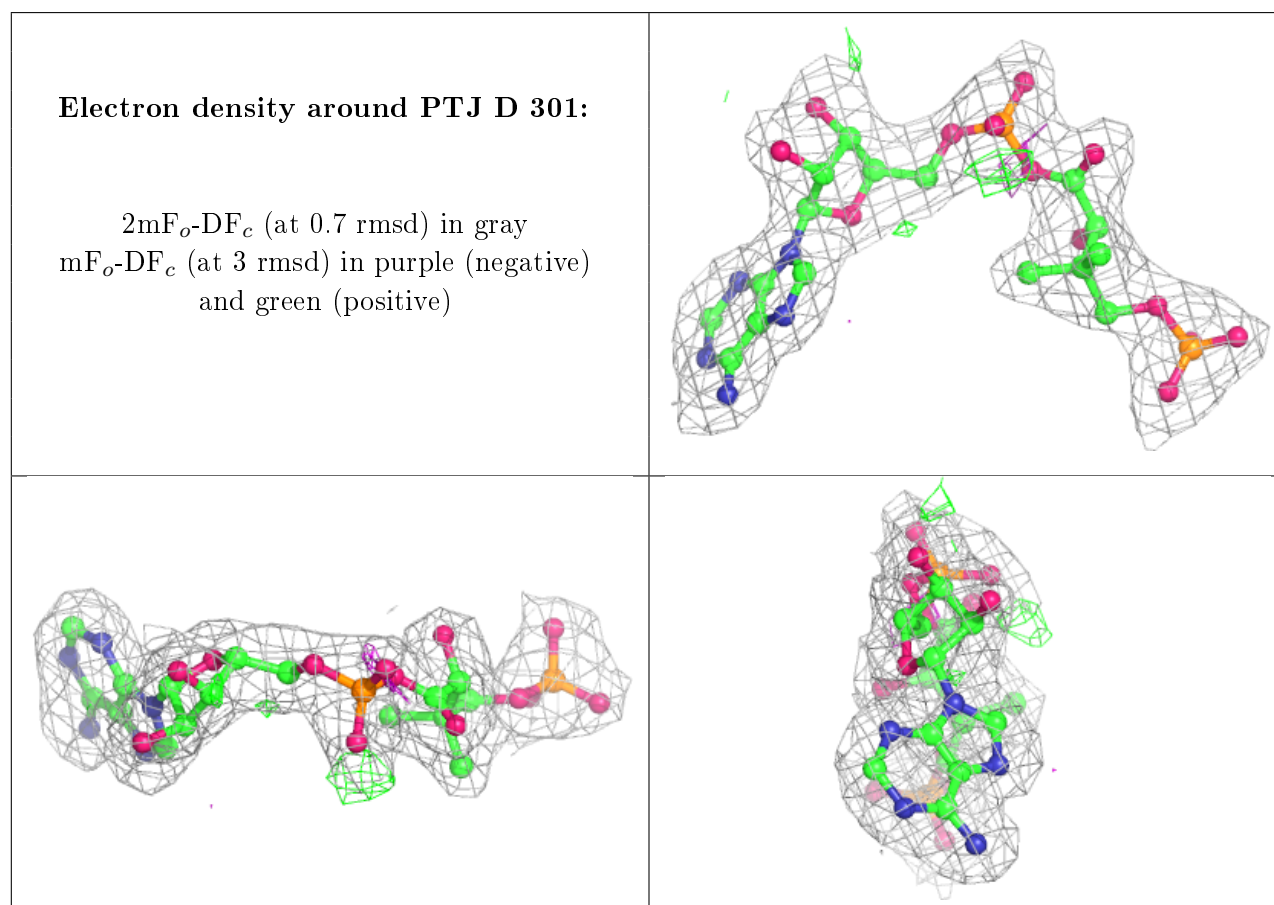
There are no carbohydrates in this entry.

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.

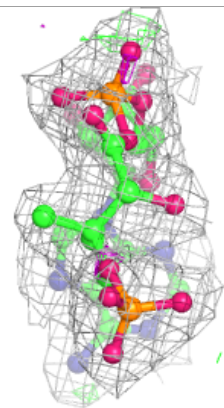
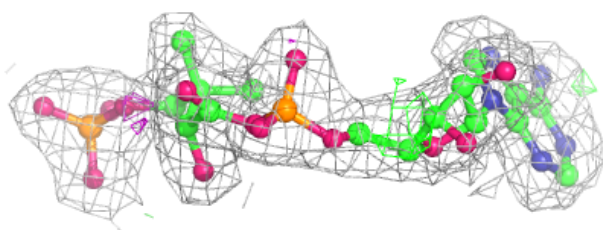
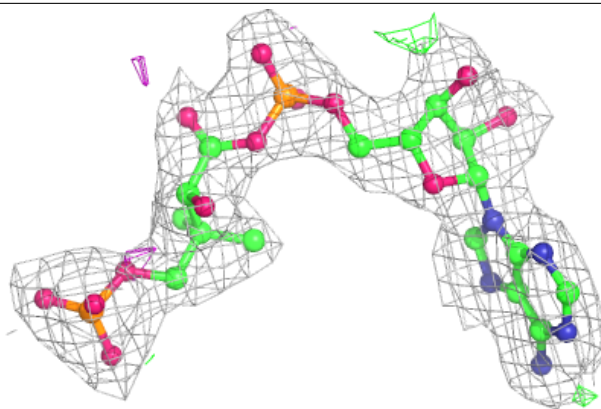
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	FLC	C	302	13/13	0.90	0.18	20,31,37,40	0
3	FLC	D	302	13/13	0.90	0.18	24,37,42,43	0
3	FLC	A	302	13/13	0.94	0.13	23,26,28,30	0
2	PTJ	D	301	36/36	0.95	0.14	13,25,31,31	0
2	PTJ	A	301	36/36	0.95	0.12	20,23,30,32	0
2	PTJ	C	301	36/36	0.95	0.12	20,25,30,33	0
2	PTJ	B	901	36/36	0.97	0.14	14,18,23,23	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.

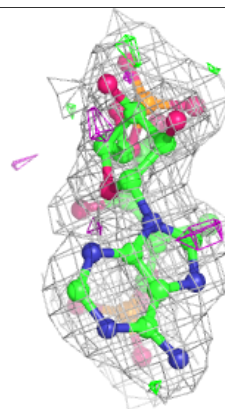
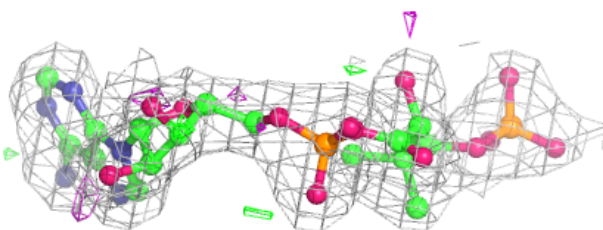
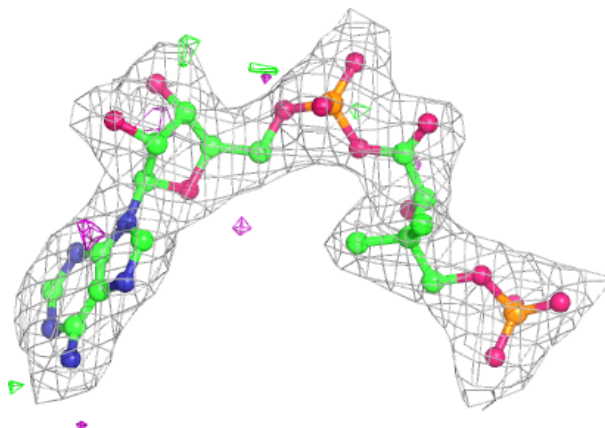


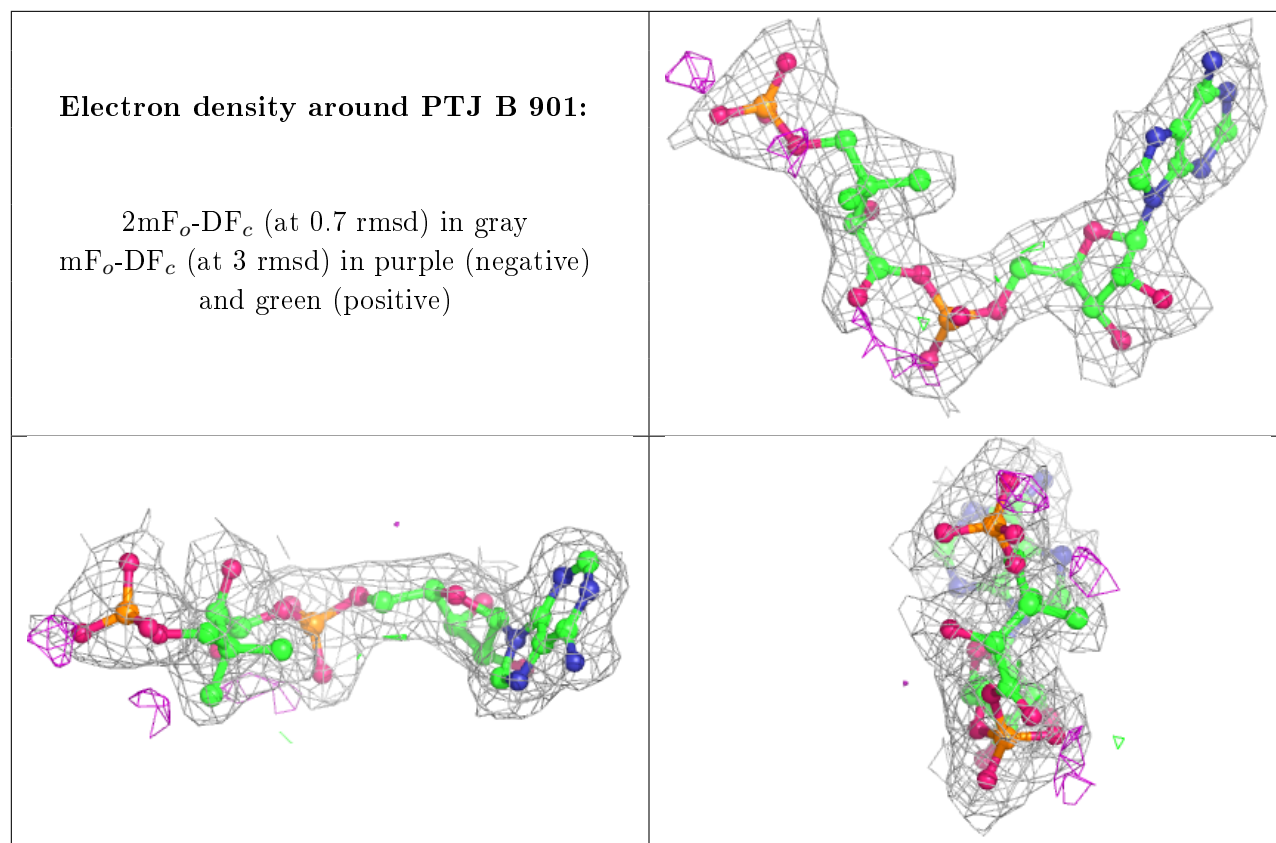
Electron density around PTJ A 301:

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

**Electron density around PTJ C 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 [i](#)

There are no such residues in this entry.