



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 28, 2025 – 10:14 AM EDT

PDB ID : 9EK6 / pdb_00009ek6
Title : Crystal structure of MAIT TCR in complex with MR1-5FU
Authors : Awad, W.; Rossjohn, J.
Deposited on : 2024-12-01
Resolution : 2.22 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 Phenix2.0rc1
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

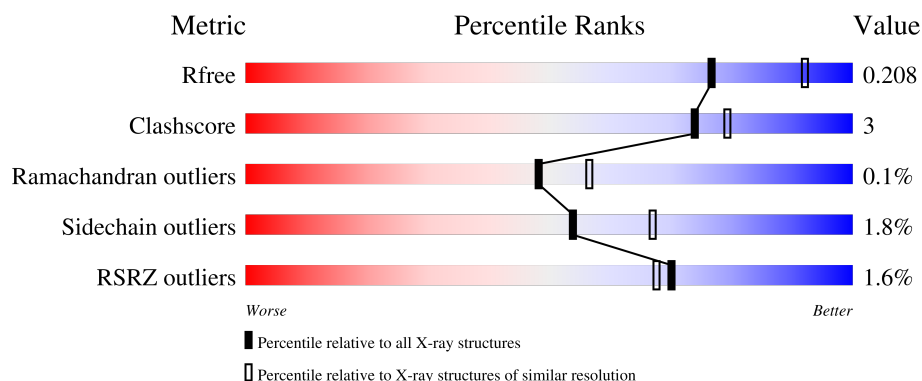
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.22 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}	164625	7167 (2.24-2.20)
Clashscore	180529	8096 (2.24-2.20)
Ramachandran outliers	177936	8010 (2.24-2.20)
Sidechain outliers	177891	8011 (2.24-2.20)
RSRZ outliers	164620	7166 (2.24-2.20)

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	271	<div> <div>89%</div> <div>8%</div> <div>.</div> </div>
1	C	271	<div> <div>88%</div> <div>9%</div> <div>..</div> </div>
2	B	100	<div> <div>95%</div> <div>..</div> </div>
2	F	100	<div> <div>95%</div> <div>5%</div> </div>
3	D	204	<div> <div>85%</div> <div>8%</div> <div>6%</div> </div>

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Mol	Chain	Length	Quality of chain
3	G	204	<div><div></div><div>88%</div><div>11%</div><div></div></div>
4	E	246	<div><div>3%</div><div></div><div>91%</div><div>7%</div><div></div></div>
4	H	246	<div><div>%</div><div></div><div>92%</div><div>7%</div><div></div></div>

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 14308 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 Major histocompatibility complex class I-related gene protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	265	Total	C	N	O	S	0	9	0
			2198	1410	379	396	13			
1	C	266	Total	C	N	O	S	0	10	0
			2242	1443	381	406	12			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP Q95460
A	261	SER	CYS	conflict	UNP Q95460
C	0	MET	-	initiating methionine	UNP Q95460
C	261	SER	CYS	conflict	UNP Q95460

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	98	Total	C	N	O	S	0	0	0
			796	509	136	148	3			
2	F	100	Total	C	N	O	S	0	0	0
			809	517	138	150	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP P61769
F	0	MET	-	initiating methionine	UNP P61769

- Molecule 3 is a protein called TCR alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	192	Total	C	N	O	S	0	6	0
			1497	957	237	293	10			

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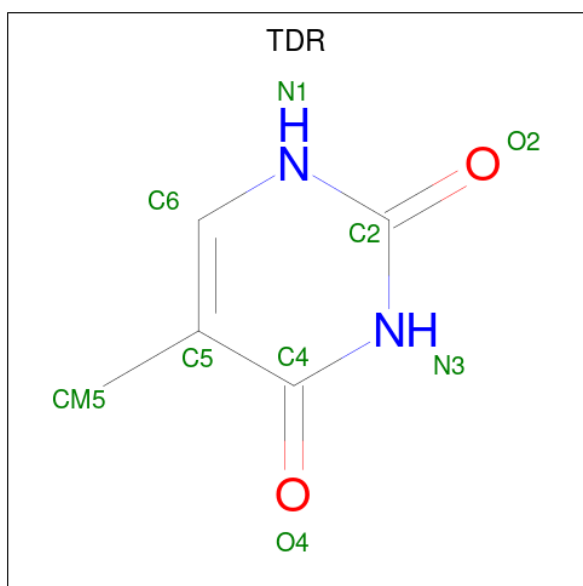
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	201	Total	C	N	O	S	0	12	0
			1619	1028	257	323	11			

- Molecule 4 is a protein called TCR beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	241	Total	C	N	O	S	0	1	0
			1867	1177	320	360	10			
4	H	244	Total	C	N	O	S	0	11	0
			1951	1231	335	371	14			

- Molecule 5 is THYMINE (CCD ID: TDR) (formula: $C_5H_6N_2O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			9	5	2	2		
5	C	1	Total	C	N	O	0	0
			9	5	2	2		

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 7 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 8 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	E	1	Total	Na	0	0
			1	1		

- Molecule 9 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	H	1	Total	Ca	0	0
			1	1		

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	233	Total	O	0	0
			233	233		
10	B	69	Total	O	0	0
			69	69		
10	C	218	Total	O	0	0
			218	218		
10	D	111	Total	O	0	0
			111	111		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	E	108	Total 108	O 108	0	0
10	F	91	Total 91	O 91	0	0
10	G	205	Total 205	O 205	0	0
10	H	228	Total 228	O 228	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.

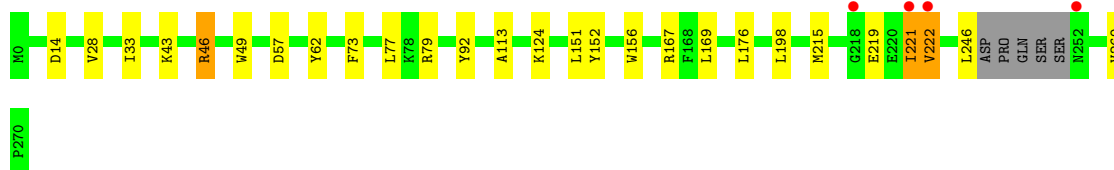
- Molecule 1: Major histocompatibility complex class I-related gene protein

Chain A: 



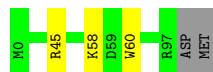
- Molecule 1: Major histocompatibility complex class I-related gene protein

Chain C: 



- Molecule 2: Beta-2-microglobulin

Chain B: 




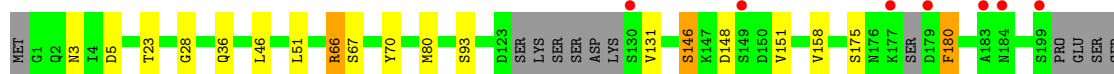
- Molecule 2: Beta-2-microglobulin

Chain F: 




- Molecule 3: TCR alpha

Chain D: 




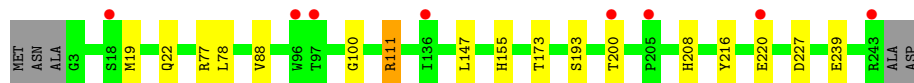
- Molecule 3: TCR alpha

Chain G:  88% 11%




- Molecule 4: TCR beta

Chain E:  91% 7% 3%



- Molecule 4: TCR beta

Chain H:  92% 7% 1%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	216.37Å 70.04Å 142.52Å 90.00° 104.25° 90.00°	Depositor
Resolution (Å)	46.04 – 2.22 46.04 – 2.22	Depositor EDS
% Data completeness (in resolution range)	99.7 (46.04-2.22) 99.7 (46.04-2.22)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.21 (at 2.22Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.181 , 0.210 0.181 , 0.208	Depositor DCC
R_{free} test set	5236 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	38.3	Xtriage
Anisotropy	0.220	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 50.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	14308	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.94% 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: GOL, CA, ACT, TDR, NA

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	0.08	0/2291	0.24	0/3113
1	C	0.09	0/2337	0.26	0/3176
2	B	0.08	0/819	0.26	0/1114
2	F	0.08	0/832	0.27	0/1131
3	D	0.08	0/1548	0.27	0/2103
3	G	0.09	0/1689	0.30	0/2289
4	E	0.08	0/1920	0.27	0/2617
4	H	0.09	0/2035	0.28	0/2768
All	All	0.08	0/13471	0.27	0/18311

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	2198	0	2091	14	0
1	C	2242	0	2137	17	0
2	B	796	0	745	3	0
2	F	809	0	756	3	0
3	D	1497	0	1392	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	1619	0	1561	15	0
4	E	1867	0	1726	6	0
4	H	1951	0	1854	10	0
5	A	9	0	5	1	0
5	C	9	0	5	0	0
6	A	18	0	24	0	0
6	C	18	0	24	2	0
6	F	6	0	8	0	0
7	A	4	0	3	1	0
8	E	1	0	0	0	0
9	H	1	0	0	0	0
10	A	233	0	0	2	0
10	B	69	0	0	1	0
10	C	218	0	0	2	0
10	D	111	0	0	2	0
10	E	108	0	0	0	0
10	F	91	0	0	0	0
10	G	205	0	0	1	0
10	H	228	0	0	0	0
All	All	14308	0	12331	76	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 3.

All (76) 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:G:25:GLN:CG	3:G:25:GLN:NE2	2.42	0.82
3:G:132[B]:CYS:HB3	3:G:182:CYS:SG	2.25	0.76
3:G:25:GLN:NE2	3:G:25:GLN:OE1	2.25	0.70
3:G:25:GLN:CG	3:G:25:GLN:OE1	2.39	0.69
1:A:77:LEU:HD13	1:A:92:TYR:HB2	1.77	0.67
3:D:148:ASP:HB3	3:D:151:VAL:HG12	1.75	0.67
4:E:155:HIS:HB3	4:E:216:TYR:HB2	1.77	0.66
3:D:66[B]:ARG:NH1	10:D:301:HOH:O	2.28	0.65
7:A:305:ACT:OXT	10:A:401:HOH:O	2.14	0.64
1:C:28:VAL:HG23	1:C:33:ILE:HD13	1.79	0.62
1:A:8:PHE:CE2	1:A:95[B]:MET:HG3	2.36	0.60
3:D:23:THR:HG22	3:D:70[B]:TYR:HB2	1.83	0.60
3:G:150:ASP:HB2	3:G:177:LYS:HD2	1.86	0.58
1:C:79:ARG:NH2	10:C:409:HOH:O	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:77:LEU:HD13	1:C:92:TYR:HB2	1.86	0.56
4:E:19:MET:HB3	4:E:78:LEU:HB2	1.87	0.56
3:G:132[B]:CYS:SG	3:G:173:ALA:HB3	2.46	0.56
3:D:146:SER:HB3	3:D:151:VAL:HG13	1.88	0.55
2:F:45:ARG:NH1	2:F:47:GLU:OE1	2.39	0.55
1:A:28:VAL:HG23	1:A:33:ILE:HD13	1.87	0.54
1:A:95[B]:MET:HE1	1:A:109:PHE:CD2	2.43	0.54
1:C:221:ILE:HD12	1:C:222:VAL:N	2.23	0.53
3:D:80:MET:HE2	3:D:158:VAL:HG11	1.89	0.53
3:D:28:GLY:HA3	3:D:93[A]:SER:OG	2.09	0.53
4:H:13:LEU:HD21	4:H:19[B]:MET:HG3	1.91	0.52
1:C:198:LEU:HD13	1:C:269:VAL:HG21	1.92	0.52
1:C:124:LYS:NZ	10:C:402:HOH:O	2.43	0.52
1:C:167:ARG:HD3	6:C:304:GOL:H11	1.92	0.51
3:G:148:ASP:OD2	3:G:177:LYS:NZ	2.42	0.51
4:H:128:VAL:HG23	4:H:238:ALA:HB3	1.92	0.50
1:A:113:ALA:HB2	2:B:60:TRP:CE2	2.47	0.50
3:D:23:THR:HG22	3:D:70[A]:TYR:HB2	1.95	0.49
2:F:73:THR:OG1	2:F:76:ASP:OD1	2.21	0.49
1:A:6[A]:ARG:NH2	2:B:58:LYS:HD3	2.27	0.49
3:D:36:GLN:HB2	3:D:46:LEU:HD11	1.95	0.48
1:C:169[A]:LEU:HD23	1:C:176:LEU:HD13	1.96	0.48
1:C:152:TYR:CD1	4:E:100:GLY:HA3	2.49	0.48
3:G:3[A]:ASN:ND2	3:G:5:ASP:OD2	2.36	0.48
3:G:36:GLN:HB2	3:G:46:LEU:HD11	1.95	0.47
3:D:175:SER:HB3	3:D:180:PHE:CE1	2.50	0.47
4:H:123:PRO:HD3	4:H:231:PRO:HB3	1.97	0.47
3:D:151:VAL:HG23	3:D:175:SER:HB2	1.97	0.47
3:G:28:GLY:HA3	3:G:93:SER:OG	2.15	0.47
1:C:156:TRP:CZ2	6:C:302:GOL:H31	2.51	0.46
3:D:3[B]:ASN:HD21	3:D:5:ASP:CG	2.22	0.46
1:A:151:LEU:HD22	3:G:51:LEU:HD12	1.96	0.46
1:A:72:MET:HE2	4:H:96:TRP:CG	2.51	0.46
1:C:221:ILE:H	1:C:221:ILE:HG13	1.52	0.46
3:G:122[A]:ARG:NH2	4:H:243:ARG:HE	2.14	0.46
1:A:196:THR:HG22	1:A:246:LEU:HD12	1.97	0.45
4:H:86:THR:HG23	4:H:113:THR:HA	1.98	0.45
1:A:215:MET:HG3	1:A:257:HIS:CD2	2.52	0.45
4:E:208:HIS:NE2	4:E:239:GLU:OE1	2.46	0.45
1:A:252:ASN:HB2	1:A:254:TYR:CE2	2.51	0.45
3:G:184:ASN:ND2	10:G:305:HOH:O	2.40	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:46:ARG:HA	1:C:46:ARG:HE	1.82	0.44
1:C:43:LYS:HD2	1:C:62:TYR:HB3	1.99	0.44
4:E:88:VAL:HG22	4:E:111:ARG:HG3	2.00	0.44
1:C:151:LEU:HD22	3:D:51:LEU:HD12	2.00	0.44
3:D:67:SER:OG	4:H:220:GLU:OE1	2.35	0.43
1:C:215[A]:MET:HG3	1:C:219:GLU:O	2.18	0.43
1:C:113:ALA:HB2	2:F:60:TRP:CE2	2.53	0.42
2:B:45:ARG:NH2	10:B:102:HOH:O	2.41	0.42
1:A:214:TRP:H	1:A:225:ILE:HD13	1.84	0.42
1:A:43:LYS:HD2	1:A:66[A]:LEU:HD12	2.02	0.42
1:A:46:ARG:HD3	1:A:46:ARG:HA	1.82	0.42
5:A:301:TDR:H6	10:A:585:HOH:O	2.19	0.42
3:G:61[A]:SER:OG	3:G:74:LEU:HB3	2.20	0.42
4:H:11:GLN:HG2	4:H:19[B]:MET:SD	2.60	0.42
4:H:13:LEU:HD11	4:H:19[B]:MET:HE2	2.02	0.41
3:D:151:VAL:HA	3:D:175:SER:HB2	2.02	0.41
1:C:49:TRP:CD1	1:C:49:TRP:H	2.38	0.41
3:G:108[A]:LYS:HB3	3:G:139:SER:HB3	2.01	0.41
4:E:173:THR:HG23	4:E:193:SER:HB2	2.03	0.40
3:D:66[A]:ARG:NH1	10:D:309:HOH:O	2.52	0.40
4:H:94:SER:HB3	4:H:104:LEU:HD23	2.04	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	270/271 (100%)	267 (99%)	3 (1%)	0	100	100
1	C	272/271 (100%)	263 (97%)	8 (3%)	1 (0%)	30	33
2	B	96/100 (96%)	94 (98%)	2 (2%)	0	100	100
2	F	98/100 (98%)	98 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	D	192/204 (94%)	187 (97%)	5 (3%)	0	100	100
3	G	211/204 (103%)	208 (99%)	3 (1%)	0	100	100
4	E	240/246 (98%)	235 (98%)	5 (2%)	0	100	100
4	H	253/246 (103%)	250 (99%)	3 (1%)	0	100	100
All	All	1632/1642 (99%)	1602 (98%)	29 (2%)	1 (0%)	48	56

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	222	VAL

5.3.2 Protein sidechains ⓘ

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	234/241 (97%)	233 (100%)	1 (0%)	89	94
1	C	239/241 (99%)	233 (98%)	6 (2%)	42	54
2	B	87/95 (92%)	87 (100%)	0	100	100
2	F	88/95 (93%)	88 (100%)	0	100	100
3	D	160/181 (88%)	155 (97%)	5 (3%)	35	45
3	G	185/181 (102%)	183 (99%)	2 (1%)	70	81
4	E	197/212 (93%)	190 (96%)	7 (4%)	30	38
4	H	213/212 (100%)	206 (97%)	7 (3%)	33	42
All	All	1403/1458 (96%)	1375 (98%)	28 (2%)	54	63

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	HIS
1	C	14	ASP
1	C	46	ARG

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Mol	Chain	Res	Type
1	C	57	ASP
1	C	73	PHE
1	C	221	ILE
1	C	246	LEU
3	D	66[A]	ARG
3	D	66[B]	ARG
3	D	131	VAL
3	D	146	SER
3	D	180	PHE
4	E	22	GLN
4	E	77	ARG
4	E	111	ARG
4	E	147	LEU
4	E	200	THR
4	E	220	GLU
4	E	227	ASP
3	G	164	MET
3	G	201	GLU
4	H	65[A]	ASN
4	H	65[B]	ASN
4	H	108	GLU
4	H	112	LEU
4	H	206[A]	ARG
4	H	206[B]	ARG
4	H	220	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	239	GLN
1	C	70	GLN
1	C	93	GLN
1	C	111	GLN
1	C	177	GLN
3	D	25	GLN
4	E	168	HIS
2	F	13	HIS
2	F	17	ASN
3	G	21	ASN
4	H	30	ASN
4	H	168	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 for Mogul analysis.

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	$\# Z > 2$
5	TDR	A	301	1	9,9,9	1.03	1 (11%)	12,12,12	2.31	2 (16%)
6	GOL	A	302	-	5,5,5	0.93	0	5,5,5	1.09	0
6	GOL	C	302	-	5,5,5	0.89	0	5,5,5	1.14	1 (20%)
7	ACT	A	305	-	3,3,3	1.40	1 (33%)	3,3,3	1.36	0
6	GOL	C	304	-	5,5,5	0.87	0	5,5,5	1.15	1 (20%)
5	TDR	C	301	1	9,9,9	0.98	1 (11%)	12,12,12	1.11	1 (8%)
6	GOL	F	101	-	5,5,5	0.96	0	5,5,5	1.03	0
6	GOL	A	303	-	5,5,5	0.82	0	5,5,5	1.17	1 (20%)
6	GOL	C	303	-	5,5,5	0.93	0	5,5,5	1.06	0
6	GOL	A	304	-	5,5,5	0.97	0	5,5,5	1.01	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. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	TDR	A	301	1	-	-	0/1/1/1
6	GOL	A	302	-	-	2/4/4/4	-
6	GOL	C	302	-	-	2/4/4/4	-
6	GOL	C	304	-	-	4/4/4/4	-
6	GOL	F	101	-	-	0/4/4/4	-
5	TDR	C	301	1	-	-	0/1/1/1
6	GOL	A	303	-	-	1/4/4/4	-
6	GOL	C	303	-	-	0/4/4/4	-
6	GOL	A	304	-	-	2/4/4/4	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	301	TDR	CM5-C5	-2.19	1.45	1.50
5	C	301	TDR	C6-C5	2.18	1.37	1.34
7	A	305	ACT	CH3-C	2.01	1.57	1.49

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	301	TDR	CM5-C5-C6	-6.82	116.21	123.23
5	A	301	TDR	CM5-C5-C4	3.86	122.90	118.78
5	C	301	TDR	CM5-C5-C6	-3.36	119.77	123.23
6	A	303	GOL	C3-C2-C1	-2.15	103.93	111.80
6	C	304	GOL	C3-C2-C1	-2.04	104.33	111.80
6	C	302	GOL	C3-C2-C1	-2.03	104.34	111.80

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	302	GOL	C1-C2-C3-O3
6	A	304	GOL	O1-C1-C2-O2
6	A	304	GOL	O1-C1-C2-C3
6	C	302	GOL	C1-C2-C3-O3
6	C	302	GOL	O2-C2-C3-O3
6	C	304	GOL	C1-C2-C3-O3
6	C	304	GOL	O1-C1-C2-C3
6	C	304	GOL	O2-C2-C3-O3
6	A	302	GOL	O2-C2-C3-O3
6	A	303	GOL	C1-C2-C3-O3

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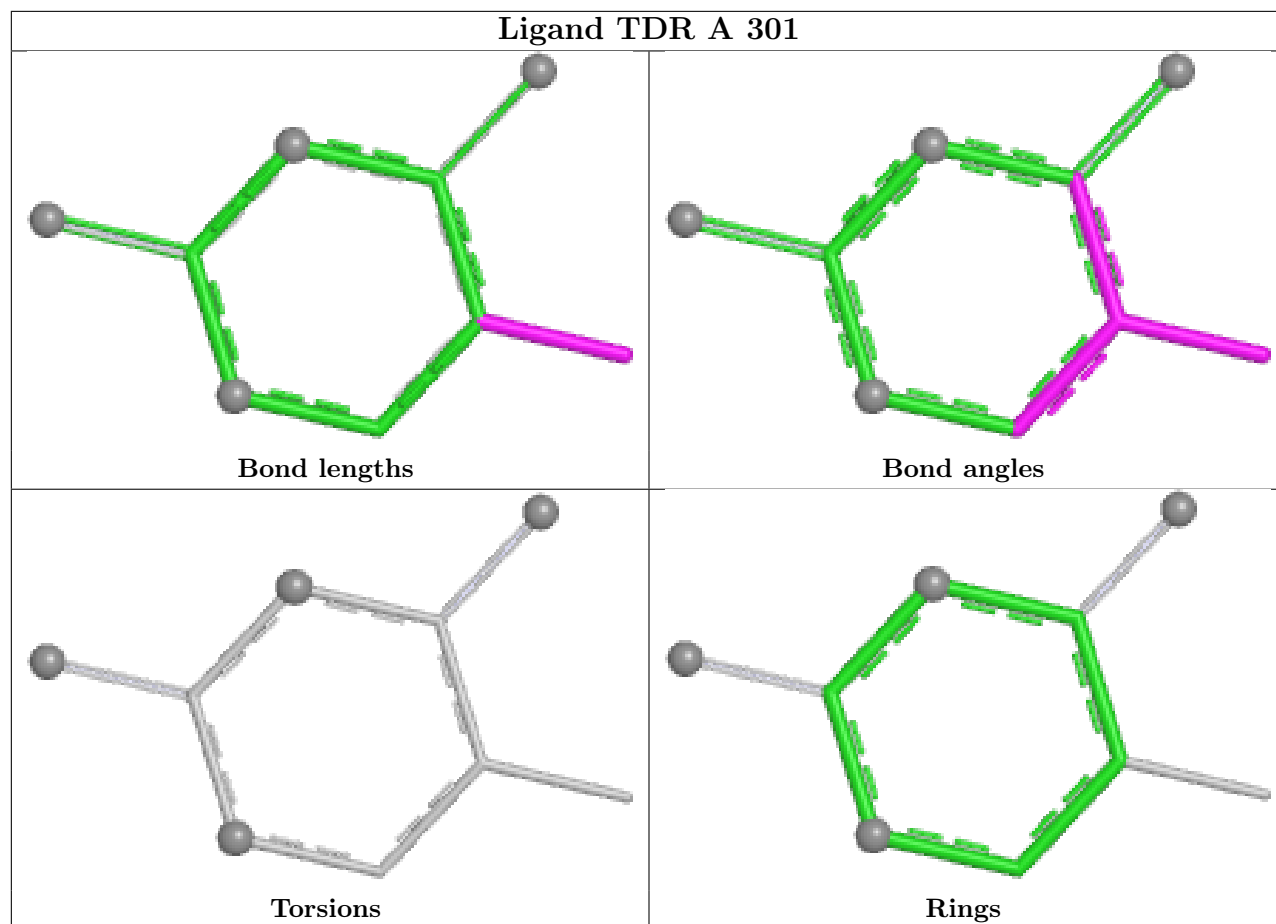
Mol	Chain	Res	Type	Atoms
6	C	304	GOL	O1-C1-C2-O2

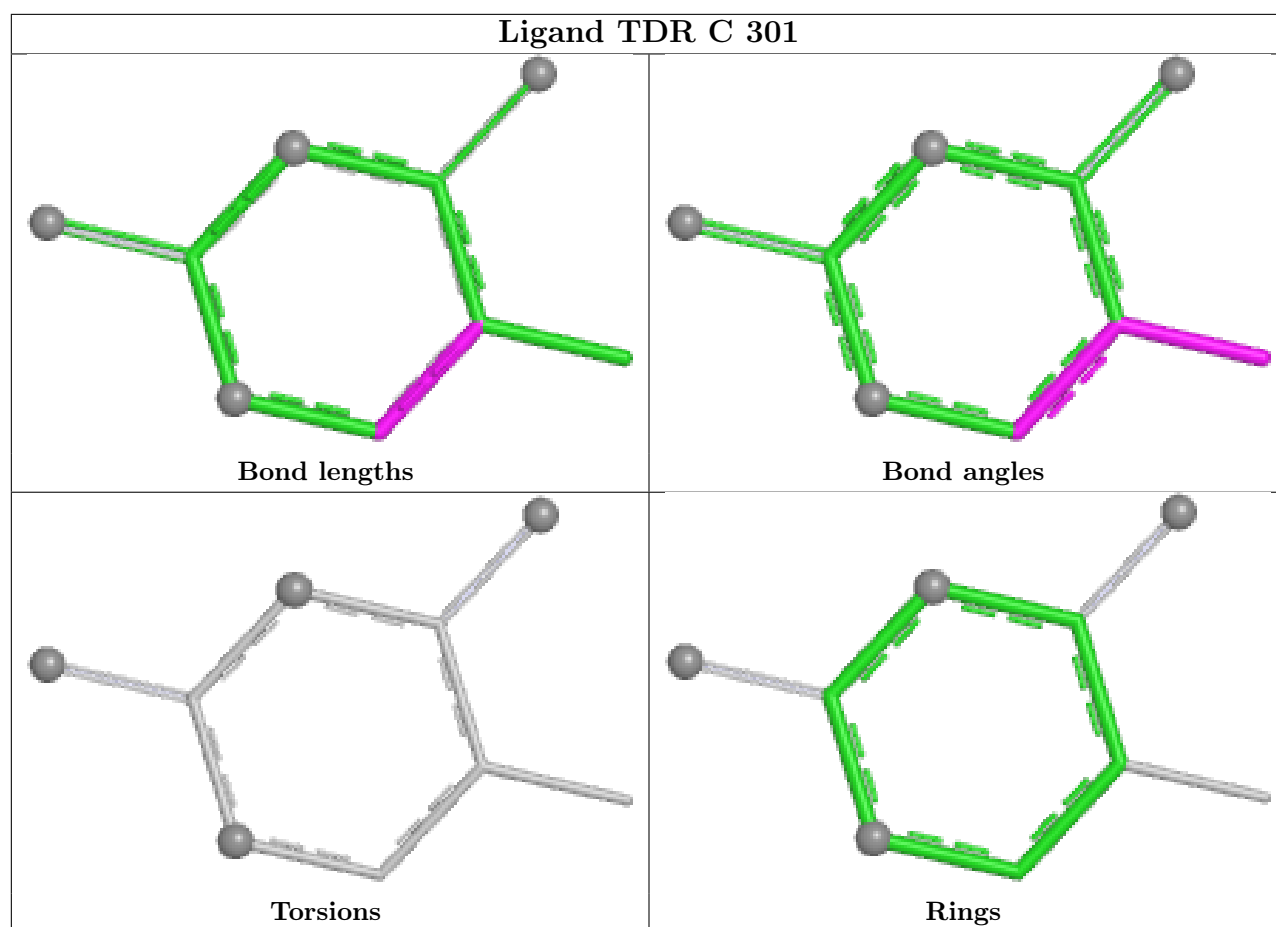
There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	301	TDR	1	0
6	C	302	GOL	1	0
7	A	305	ACT	1	0
6	C	304	GOL	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

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	265/271 (97%)	-0.24	3 (1%) 77 76	19, 39, 73, 90	16 (6%)
1	C	266/271 (98%)	-0.20	4 (1%) 71 69	17, 37, 60, 77	23 (8%)
2	B	98/100 (98%)	0.11	0 100 100	33, 57, 84, 90	2 (2%)
2	F	100/100 (100%)	-0.35	1 (1%) 79 77	30, 40, 61, 67	4 (4%)
3	D	192/204 (94%)	0.27	7 (3%) 46 43	21, 50, 86, 103	15 (7%)
3	G	201/204 (98%)	-0.34	1 (0%) 87 86	20, 35, 57, 86	21 (10%)
4	E	241/246 (97%)	0.16	8 (3%) 49 46	34, 50, 81, 96	12 (4%)
4	H	244/246 (99%)	-0.35	2 (0%) 82 81	23, 36, 54, 79	23 (9%)
All	All	1607/1642 (97%)	-0.13	26 (1%) 70 68	17, 40, 76, 103	116 (7%)

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	E	96	TRP	4.3
3	D	199	SER	3.4
1	C	222	VAL	3.0
4	E	200	THR	3.0
1	C	252	ASN	2.9
1	A	222	VAL	2.8
3	D	130	SER	2.8
3	D	179	ASP	2.6
4	E	243	ARG	2.6
1	C	218	GLY	2.6
1	A	221	ILE	2.5
3	D	149	SER	2.5
4	E	136	ILE	2.4
1	C	221	ILE	2.4
4	E	220	GLU	2.3
4	E	205	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	223	GLN	2.3
3	D	183	ALA	2.2
4	H	244	ALA	2.2
4	E	97	THR	2.1
4	H	100	GLY	2.1
4	E	18	SER	2.1
3	G	70[A]	TYR	2.0
2	F	99	MET	2.0
3	D	177	LYS	2.0
3	D	184	ASN	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

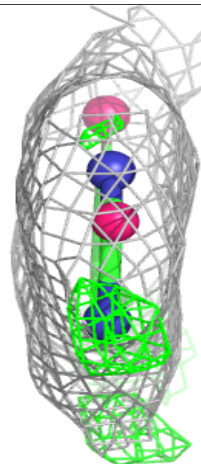
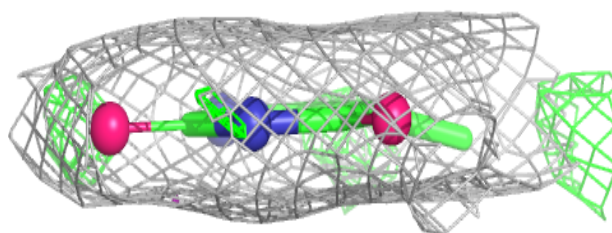
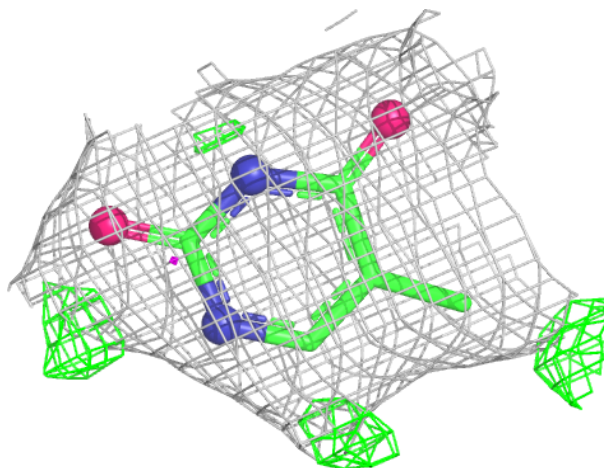
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	GOL	A	304	6/6	0.82	0.16	34,39,43,45	6
6	GOL	C	304	6/6	0.85	0.14	39,43,52,52	6
6	GOL	C	303	6/6	0.86	0.18	34,47,50,55	6
6	GOL	C	302	6/6	0.86	0.14	51,54,56,56	0
6	GOL	A	302	6/6	0.89	0.15	40,47,50,52	0
6	GOL	A	303	6/6	0.90	0.14	48,52,54,56	0
5	TDR	A	301	9/9	0.91	0.10	28,35,41,43	0
7	ACT	A	305	4/4	0.91	0.09	35,38,45,46	0
5	TDR	C	301	9/9	0.92	0.09	36,43,47,49	0
6	GOL	F	101	6/6	0.94	0.10	32,35,38,39	0
8	NA	E	301	1/1	0.98	0.04	48,48,48,48	1
9	CA	H	301	1/1	0.99	0.03	37,37,37,37	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.

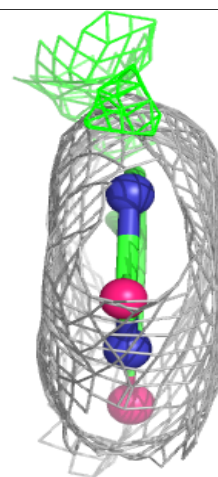
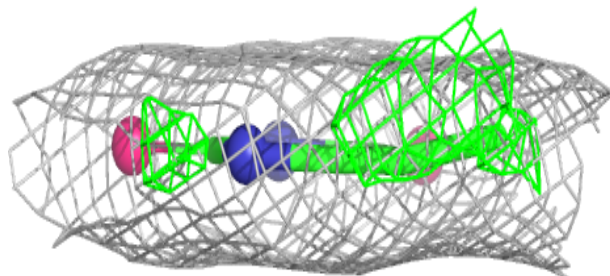
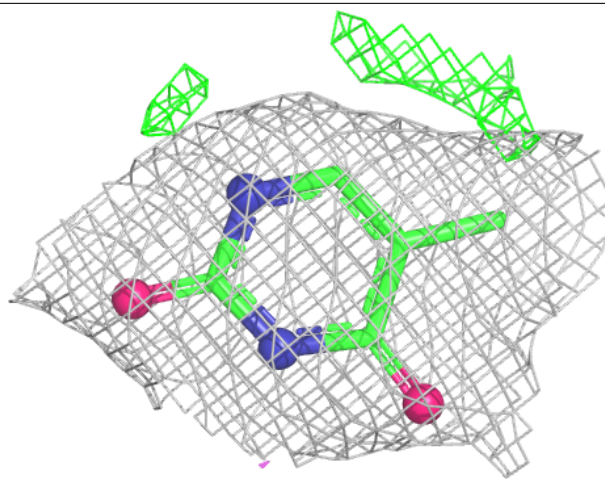
Electron density around TDR A 301:

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



Electron density around TDR 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.