Full wwPDB X-ray Structure Validation Report (i)

Aug 29, 2023 – 01:46 AM EDT

PDB ID	:	3O0G
Title	:	Crystal Structure of Cdk5:p25 in complex with an ATP analogue
Authors	:	Mapelli, M.
Deposited on	:	2010-07-19
Resolution	:	1.95 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 (i) 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 (i)) were used in the production of this report:

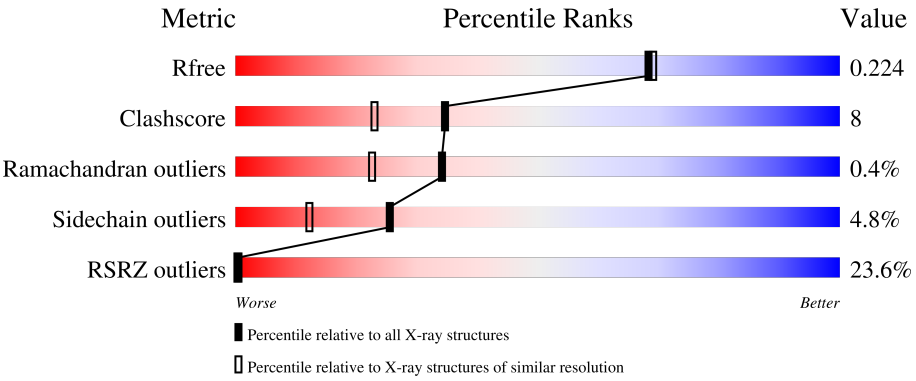
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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 <=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	292	15% 73% 23%
1	B	292	15% 70% 18% 10%
2	D	149	7% 83% 17%
2	E	149	68% 89% 10%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 7105 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 Cell division protein kinase 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	289	Total	C	N	O	S	0	0	0
			2325	1492	400	422	11			
1	B	264	Total	C	N	O	S	0	0	0
			2117	1366	366	375	10			

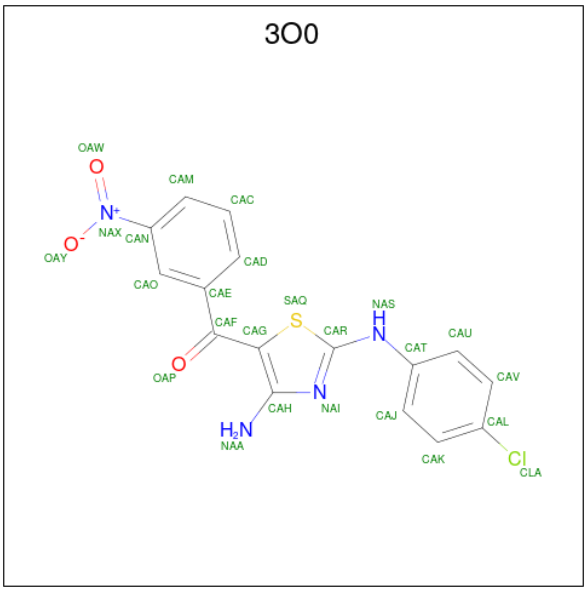
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	144	ASN	ASP	engineered mutation	UNP Q00535
B	144	ASN	ASP	engineered mutation	UNP Q00535

- Molecule 2 is a protein called Cyclin-dependent kinase 5 activator 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	149	Total	C	N	O	S	0	0	0
			1202	771	198	222	11			
2	E	149	Total	C	N	O	S	0	0	0
			1202	771	198	222	11			

- Molecule 3 is {4-amino-2-[(4-chlorophenyl)amino]-1,3-thiazol-5-yl}(3-nitrophenyl)methanone (three-letter code: 3O0) (formula: $C_{16}H_{11}ClN_4O_3S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	B	1	Total	C	Cl	N	O	S	0	0
			25	16	1	4	3	1		

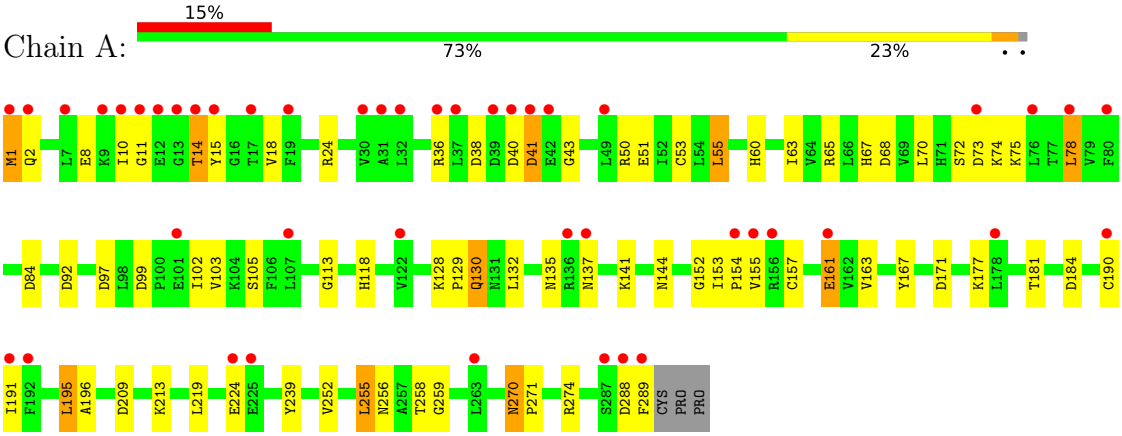
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	124	Total	O	0	0
			124	124		
4	D	37	Total	O	0	0
			37	37		
4	B	63	Total	O	0	0
			63	63		
4	E	10	Total	O	0	0
			10	10		

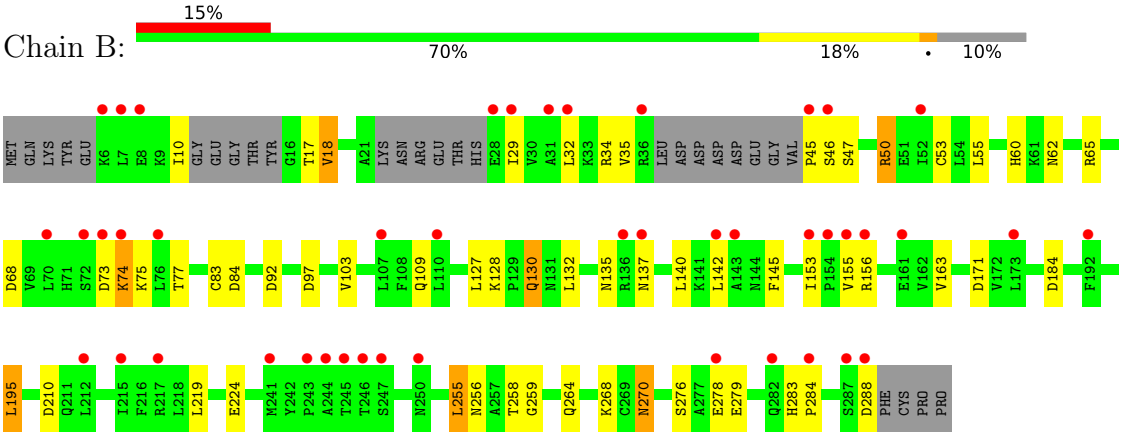
3 Residue-property plots (i)

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.

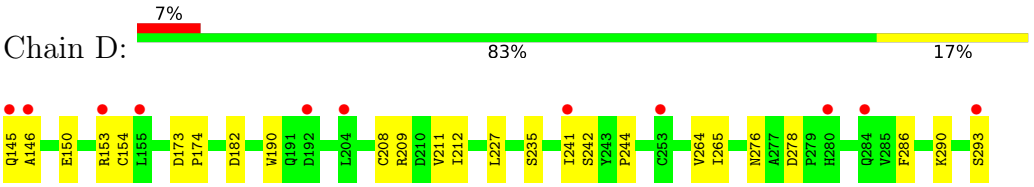
• Molecule 1: Cell division protein kinase 5



• Molecule 1: Cell division protein kinase 5

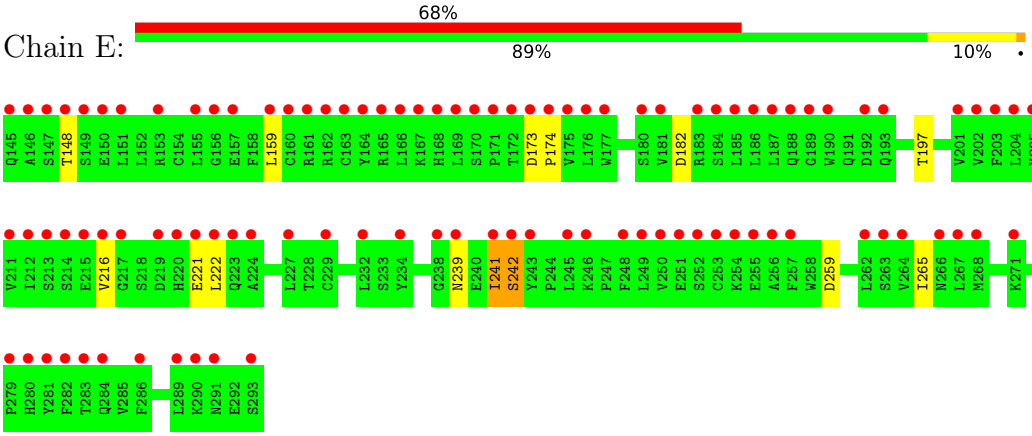


• Molecule 2: Cyclin-dependent kinase 5 activator 1



• Molecule 2: Cyclin-dependent kinase 5 activator 1

Chain E:


68%
89%
10%
Q145 A146 S147 T148 S149 E150 L151 L152 R153 C154 L155 G156 E157 F158 L159 C160 R161 R162 C163 Y164 R165 L166 K167 H168 L169 S170 P171 T172 D173 P174 V175 L176 W177 S180 V181 D182 R183 S184 L185 L186 L187 Q188 G189 W190 Q191 D192 Q193 T197 V201 V202 F203 L204 Y205 M206 L207 D210
V211 I212 S213 S214 E215 V216 G217 S218 D219 H220 E221 L222 Q223 A224 L227 T228 C229 L232 S233 Y234 G238 N239 E240 I241 S242 Y243 P244 L245 K246 P247 F248 L249 V250 E251 S252 C253 K254 E255 A256 F257 W258 D259 L262 S263 V264 I265 N266 L267 M268 K271 Q274 I275 D278
P279 H280 Y281 F282 T283 Q284 V285 F286 L289 K290 N291 E292 S293

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α, β, γ	117.12Å 117.12Å 155.60Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.96 – 1.95 19.97 – 1.95	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.96-1.95) 98.0 (19.97-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
$< I/\sigma(I) >$ [1]	1.38 (at 1.94Å)	Xtriage
Refinement program	REFMAC 5.1.24, CNS	Depositor
R, R_{free}	0.226 , 0.256 0.232 , 0.224	Depositor DCC
R_{free} test set	4427 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	31.7	Xtriage
Anisotropy	0.111	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.44 , 62.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.019 for -h,-k,l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	7105	wwPDB-VP
Average B, all atoms (Å^2)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.95% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: 3O0

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	0.58	0/2379	0.82	10/3219 (0.3%)
1	B	0.47	0/2164	0.74	8/2925 (0.3%)
2	D	0.49	0/1230	0.69	2/1667 (0.1%)
2	E	0.35	0/1230	0.62	4/1667 (0.2%)
All	All	0.50	0/7003	0.74	24/9478 (0.3%)

There are no bond length outliers.

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	288	ASP	CB-CG-OD2	7.68	125.22	118.30
1	A	68	ASP	CB-CG-OD2	6.58	124.23	118.30
2	D	182	ASP	CB-CG-OD2	6.36	124.02	118.30
1	A	84	ASP	CB-CG-OD2	6.36	124.02	118.30
1	B	210	ASP	CB-CG-OD2	6.22	123.90	118.30
2	E	278	ASP	CB-CG-OD2	6.06	123.75	118.30
2	D	278	ASP	CB-CG-OD2	5.92	123.63	118.30
2	E	210	ASP	CB-CG-OD2	5.86	123.58	118.30
1	B	97	ASP	CB-CG-OD2	5.70	123.43	118.30
1	A	78	LEU	CA-CB-CG	5.64	128.26	115.30
1	A	92	ASP	CB-CG-OD2	5.45	123.20	118.30
1	B	288	ASP	CB-CG-OD2	5.38	123.15	118.30
1	A	40	ASP	CB-CG-OD2	5.33	123.10	118.30
1	B	84	ASP	CB-CG-OD2	5.33	123.10	118.30
1	A	171	ASP	CB-CG-OD2	5.32	123.08	118.30
2	E	259	ASP	CB-CG-OD2	5.27	123.05	118.30
1	A	97	ASP	CB-CG-OD2	5.21	122.98	118.30
1	B	92	ASP	CB-CG-OD2	5.18	122.96	118.30
1	B	184	ASP	CB-CG-OD2	5.15	122.93	118.30
1	A	209	ASP	CB-CG-OD2	5.12	122.91	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	68	ASP	CB-CG-OD2	5.11	122.89	118.30
1	A	274	ARG	NE-CZ-NH2	-5.08	117.76	120.30
1	B	171	ASP	CB-CG-OD2	5.08	122.87	118.30
2	E	182	ASP	CB-CG-OD2	5.05	122.85	118.30

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	2325	0	2346	60	0
1	B	2117	0	2162	31	0
2	D	1202	0	1187	17	0
2	E	1202	0	1187	11	0
3	B	25	0	11	3	0
4	A	124	0	0	12	0
4	B	63	0	0	4	0
4	D	37	0	0	1	0
4	E	10	0	0	3	0
All	All	7105	0	6893	114	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 8.

All (114) 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:A:256:ASN:HD21	1:A:258:THR:HB	1.11	1.09
1:A:135:ASN:HB2	4:A:384:HOH:O	1.52	1.09
1:A:196:ALA:HB1	4:A:411:HOH:O	1.58	1.03
1:A:256:ASN:ND2	1:A:258:THR:HB	1.72	1.02
1:A:135:ASN:CB	4:A:384:HOH:O	2.06	0.99
1:A:60:HIS:HB3	1:A:63:ILE:HD13	1.47	0.94
1:A:1:MET:HG3	1:A:70:LEU:HD13	1.51	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:208:CYS:HA	2:D:212:ILE:HD13	1.54	0.89
1:A:190:CYS:SG	4:A:297:HOH:O	2.29	0.89
2:D:145:GLN:HA	2:D:150:GLU:HG2	1.56	0.88
1:A:11:GLY:HA3	1:A:18:VAL:HB	1.59	0.85
1:A:167:TYR:CD1	1:A:190:CYS:SG	2.71	0.82
1:B:50:ARG:HD2	4:B:346:HOH:O	1.86	0.74
2:E:239:ASN:HA	4:E:294:HOH:O	1.88	0.72
1:A:167:TYR:CE1	1:A:190:CYS:SG	2.83	0.71
1:A:99:ASP:HB3	1:A:102:ILE:HD13	1.72	0.70
1:B:10:ILE:HG13	1:B:18:VAL:HG23	1.74	0.69
1:A:1:MET:HB2	4:A:375:HOH:O	1.90	0.69
1:B:156:ARG:HD2	2:E:197:THR:HG21	1.76	0.67
1:B:34:ARG:HG3	1:B:75:LYS:HE3	1.78	0.65
1:A:73:ASP:CG	1:A:74:LYS:H	1.97	0.65
3:B:293:3O0:HAU	3:B:293:3O0:SAQ	2.38	0.63
1:A:135:ASN:HB3	4:A:384:HOH:O	1.83	0.61
1:A:129:PRO:HD3	1:A:191:ILE:HD11	1.84	0.60
2:D:153:ARG:HH12	2:D:293:SER:HB2	1.67	0.59
1:A:137:ASN:HB2	4:A:384:HOH:O	2.03	0.59
1:A:118:HIS:HD2	4:A:304:HOH:O	1.88	0.56
1:A:51:GLU:CG	1:A:55:LEU:HD22	2.36	0.56
1:B:83:CYS:HA	1:B:135:ASN:HD21	1.70	0.56
1:A:14:THR:HG21	1:A:144:ASN:HB3	1.88	0.55
1:A:256:ASN:ND2	1:A:258:THR:CB	2.60	0.55
2:E:159:LEU:HD12	2:E:174:PRO:HB3	1.89	0.53
2:E:239:ASN:HB2	4:E:297:HOH:O	2.07	0.53
1:A:43:GLY:O	2:D:242:SER:HB2	2.08	0.53
1:B:10:ILE:CG1	1:B:18:VAL:HG23	2.39	0.53
1:B:35:VAL:HG11	1:B:45:PRO:HB3	1.90	0.53
1:A:99:ASP:HB3	1:A:102:ILE:CD1	2.39	0.53
1:B:128:LYS:HG3	1:B:130:GLN:HG2	1.91	0.52
2:E:207:LEU:HD13	4:E:296:HOH:O	2.09	0.52
1:A:129:PRO:HD3	1:A:191:ILE:CD1	2.40	0.52
1:A:2:GLN:O	1:A:24:ARG:NH1	2.43	0.52
1:B:140:LEU:HB2	4:B:339:HOH:O	2.10	0.52
1:A:103:VAL:HG13	1:A:195:LEU:HB3	1.92	0.51
1:A:270:ASN:HD22	1:A:270:ASN:C	2.14	0.51
1:A:15:TYR:O	4:A:379:HOH:O	2.18	0.51
1:B:46:SER:HB3	2:E:242:SER:HA	1.93	0.51
1:A:161:GLU:HA	1:A:161:GLU:OE1	2.11	0.50
2:D:212:ILE:HD12	2:D:212:ILE:N	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:60:HIS:HE1	1:B:62:ASN:HD22	1.60	0.49
3:B:293:3O0:SAQ	3:B:293:3O0:HAD	2.52	0.49
1:B:35:VAL:CG1	1:B:45:PRO:HB3	2.42	0.49
1:B:278:GLU:HG3	4:B:336:HOH:O	2.12	0.49
1:A:118:HIS:HE1	1:A:184:ASP:OD1	1.96	0.49
2:D:173:ASP:HB2	2:D:174:PRO:HD3	1.95	0.49
1:A:73:ASP:CG	1:A:74:LYS:N	2.66	0.48
1:A:255:LEU:HG	1:A:259:GLY:HA3	1.94	0.48
1:A:50:ARG:HD3	2:D:235:SER:O	2.13	0.48
1:A:51:GLU:HG3	1:A:55:LEU:HD22	1.94	0.47
1:B:153:ILE:O	1:B:155:VAL:HG23	2.15	0.47
1:A:67:HIS:HE1	4:A:325:HOH:O	1.97	0.47
1:B:55:LEU:HD11	1:B:145:PHE:HB2	1.96	0.47
1:A:41:ASP:N	1:A:41:ASP:OD1	2.48	0.47
1:B:53:CYS:SG	2:E:265:ILE:HG12	2.55	0.47
1:A:36:ARG:NH2	1:A:38:ASP:OD2	2.48	0.46
1:B:264:GLN:O	1:B:268:LYS:HD3	2.15	0.46
2:D:208:CYS:CA	2:D:212:ILE:HD13	2.37	0.46
1:A:129:PRO:HG3	1:A:191:ILE:HD12	1.97	0.46
1:B:103:VAL:HG13	1:B:195:LEU:HB3	1.97	0.46
1:B:283:HIS:CG	1:B:284:PRO:HD2	2.51	0.46
1:A:128:LYS:HA	1:A:191:ILE:HD11	1.96	0.46
1:A:270:ASN:HD22	1:A:271:PRO:N	2.13	0.46
1:A:72:SER:O	1:A:73:ASP:HB3	2.17	0.45
1:A:105:SER:HA	1:A:289:PHE:CZ	2.52	0.45
1:B:47:SER:OG	2:E:241:ILE:O	2.33	0.45
2:E:216:VAL:HG11	2:E:222:LEU:HB2	1.99	0.45
1:A:51:GLU:HG2	1:A:55:LEU:HD22	1.98	0.44
1:A:153:ILE:O	1:A:155:VAL:HG23	2.17	0.44
1:A:60:HIS:HB3	1:A:63:ILE:CD1	2.32	0.44
2:D:146:ALA:HB1	4:D:296:HOH:O	2.18	0.44
1:A:152:GLY:HA3	2:D:276:ASN:O	2.16	0.44
1:B:73:ASP:CG	1:B:74:LYS:H	2.22	0.44
1:B:270:ASN:C	1:B:270:ASN:HD22	2.22	0.43
1:A:105:SER:HA	1:A:289:PHE:HZ	1.83	0.43
1:A:128:LYS:HG3	1:A:130:GLN:HG2	2.00	0.43
1:A:270:ASN:HD22	1:A:271:PRO:CD	2.31	0.43
1:B:109:GLN:NE2	4:B:339:HOH:O	2.50	0.43
2:D:208:CYS:HA	2:D:212:ILE:CD1	2.38	0.43
1:B:127:LEU:CD2	1:B:142:LEU:HD11	2.49	0.43
2:D:286:PHE:CZ	2:D:290:LYS:HE2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:212:ILE:N	2:D:212:ILE:CD1	2.82	0.42
1:B:10:ILE:HG13	1:B:18:VAL:CG2	2.45	0.42
2:E:216:VAL:HG13	2:E:221:GLU:HB3	2.02	0.42
1:A:270:ASN:HD22	1:A:271:PRO:HD2	1.84	0.42
1:A:63:ILE:HD11	1:A:113:GLY:HA2	2.01	0.42
1:B:256:ASN:ND2	1:B:258:THR:HB	2.35	0.42
1:A:53:CYS:SG	2:D:265:ILE:HG12	2.60	0.42
2:E:173:ASP:HB2	2:E:174:PRO:HD3	2.00	0.42
1:B:75:LYS:HE2	1:B:77:THR:OG1	2.20	0.42
2:D:211:VAL:HG21	2:D:264:VAL:HG13	2.01	0.42
3:B:293:3O0:SAQ	3:B:293:3O0:CAU	3.07	0.42
1:A:153:ILE:HG23	1:A:154:PRO:HD2	2.02	0.42
1:B:255:LEU:HG	1:B:259:GLY:HA3	2.02	0.42
1:A:252:VAL:HB	4:A:411:HOH:O	2.18	0.41
1:A:155:VAL:HG12	1:A:157:CYS:H	1.85	0.41
1:B:34:ARG:CG	1:B:75:LYS:HE3	2.50	0.41
2:D:190:TRP:CE3	2:D:244:PRO:HD3	2.56	0.40
1:B:276:SER:OG	1:B:279:GLU:HG3	2.22	0.40
1:A:118:HIS:CD2	1:A:181:THR:HB	2.56	0.40
2:D:154:CYS:SG	2:D:293:SER:HB3	2.62	0.40
1:A:36:ARG:HH11	1:A:75:LYS:CG	2.33	0.40
1:A:63:ILE:N	1:A:63:ILE:HD12	2.37	0.40
1:A:213:LYS:HG3	1:A:239:TYR:HE2	1.86	0.40
1:A:255:LEU:N	4:A:411:HOH:O	2.54	0.40
1:B:18:VAL:HA	1:B:32:LEU:O	2.21	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	287/292 (98%)	274 (96%)	12 (4%)	1 (0%)	41 30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	256/292 (88%)	243 (95%)	11 (4%)	2 (1%)	19 9
2	D	147/149 (99%)	146 (99%)	1 (1%)	0	100 100
2	E	147/149 (99%)	144 (98%)	3 (2%)	0	100 100
All	All	837/882 (95%)	807 (96%)	27 (3%)	3 (0%)	34 22

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	163	VAL
1	B	163	VAL
1	B	29	ILE

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	257/260 (99%)	239 (93%)	18 (7%)	15 5
1	B	235/260 (90%)	222 (94%)	13 (6%)	21 9
2	D	138/139 (99%)	135 (98%)	3 (2%)	52 44
2	E	138/139 (99%)	135 (98%)	3 (2%)	52 44
All	All	768/798 (96%)	731 (95%)	37 (5%)	25 12

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	8	GLU
1	A	10	ILE
1	A	14	THR
1	A	41	ASP
1	A	55	LEU
1	A	65	ARG
1	A	78	LEU

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Mol	Chain	Res	Type
1	A	130	GLN
1	A	132	LEU
1	A	141	LYS
1	A	161	GLU
1	A	177	LYS
1	A	195	LEU
1	A	219	LEU
1	A	224	GLU
1	A	255	LEU
1	A	270	ASN
2	D	209	ARG
2	D	227	LEU
2	D	241	ILE
1	B	17	THR
1	B	18	VAL
1	B	50	ARG
1	B	65	ARG
1	B	74	LYS
1	B	130	GLN
1	B	132	LEU
1	B	137	ASN
1	B	195	LEU
1	B	219	LEU
1	B	224	GLU
1	B	255	LEU
1	B	270	ASN
2	E	148	THR
2	E	241	ILE
2	E	242	SER

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	62	ASN
1	A	67	HIS
1	A	118	HIS
1	A	135	ASN
1	A	206	ASN
1	A	226	GLN
1	A	256	ASN
1	A	270	ASN
1	B	62	ASN

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Mol	Chain	Res	Type
1	B	135	ASN
1	B	226	GLN
1	B	270	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

1 ligand is 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	3O0	B	293	-	21,27,27	3.08	4 (19%)	26,38,38	0.95	1 (3%)

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	3O0	B	293	-	-	0/8/16/16	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	293	3O0	OAW-NAX	12.22	1.43	1.22
3	B	293	3O0	CAN-NAX	-5.21	1.32	1.45
3	B	293	3O0	CAT-NAS	-2.70	1.34	1.40
3	B	293	3O0	CAE-CAF	2.07	1.53	1.49

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	293	3O0	CAM-CAN-NAX	3.23	121.81	119.38

There are no chirality outliers.

There are no torsion outliers.

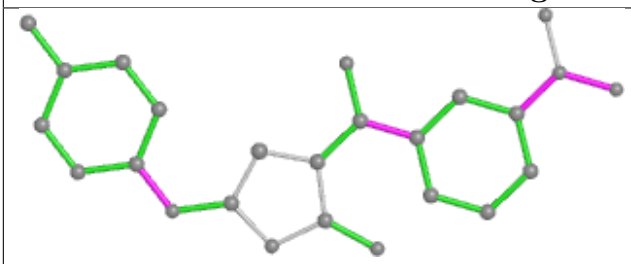
There are no ring outliers.

1 monomer is involved in 3 short contacts:

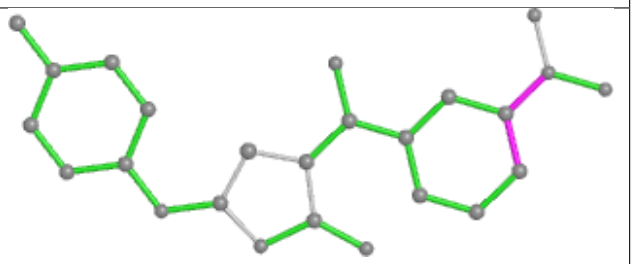
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	293	3O0	3	0

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 then 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.

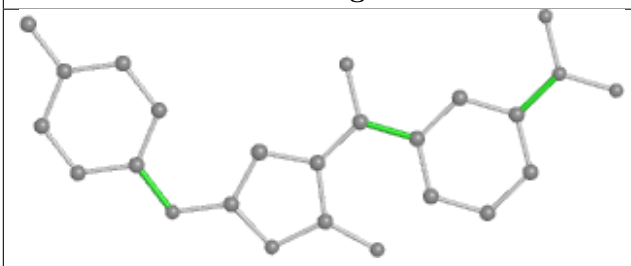
Ligand 3O0 B 293



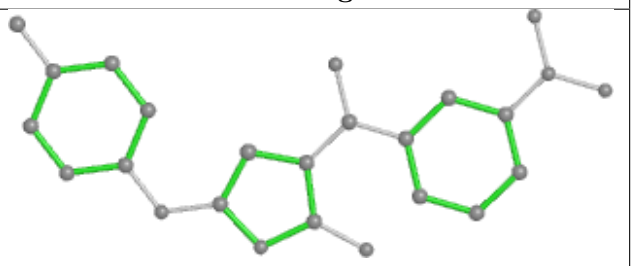
Bond lengths



Bond angles



Torsions



Rings

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, 95^{th} 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	289/292 (98%)	0.91	45 (15%)	2	3	23, 34, 60, 73	0
1	B	264/292 (90%)	1.07	44 (16%)	1	2	27, 45, 79, 116	0
2	D	149/149 (100%)	0.52	11 (7%)	14	22	26, 35, 53, 63	0
2	E	149/149 (100%)	3.36	101 (67%)	0	0	55, 89, 127, 140	0
All	All	851/882 (96%)	1.32	201 (23%)	0	0	23, 41, 102, 140	0

All (201) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	245	THR	15.6
2	E	187	LEU	14.2
2	E	241	ILE	11.3
2	E	168	HIS	11.0
2	E	290	LYS	10.9
2	E	212	ILE	10.8
1	B	288	ASP	9.5
1	B	73	ASP	8.6
1	A	41	ASP	8.2
2	E	146	ALA	8.2
2	E	217	GLY	8.1
1	B	244	ALA	7.9
2	E	166	LEU	7.8
2	E	249	LEU	7.7
2	E	176	LEU	7.5
1	A	288	ASP	7.3
2	E	220	HIS	7.3
2	E	215	GLU	7.2
1	B	28	GLU	7.1
2	E	180	SER	6.8
1	B	154	PRO	6.7

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Mol	Chain	Res	Type	RSRZ
2	E	186	LEU	6.5
1	A	40	ASP	6.4
1	A	12	GLU	6.4
1	A	2	GLN	6.3
2	D	146	ALA	6.3
1	A	1	MET	6.2
1	A	136	ARG	6.2
1	B	287	SER	6.1
2	E	167	LYS	6.1
2	E	267	LEU	5.9
2	E	189	GLY	5.9
1	A	14	THR	5.8
2	E	262	LEU	5.8
2	E	156	GLY	5.7
2	E	181	VAL	5.6
1	B	72	SER	5.5
2	E	159	LEU	5.4
2	E	164	TYR	5.4
2	E	242	SER	5.3
1	A	156	ARG	5.3
1	B	29	ILE	5.3
2	E	172	THR	5.3
1	A	13	GLY	5.3
2	E	161	ARG	5.3
2	E	183	ARG	5.3
2	E	246	LYS	5.3
1	A	39	ASP	5.2
2	E	216	VAL	5.2
2	E	153	ARG	5.1
2	E	252	SER	5.1
2	E	291	ASN	5.1
2	E	280	HIS	5.0
1	A	73	ASP	4.9
2	E	193	GLN	4.9
2	E	190	TRP	4.9
1	B	136	ARG	4.9
1	B	156	ARG	4.9
2	E	177	TRP	4.8
2	E	245	LEU	4.7
2	E	279	PRO	4.7
1	B	250	ASN	4.7
2	E	211	VAL	4.6

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Mol	Chain	Res	Type	RSRZ
1	A	11	GLY	4.6
1	B	246	THR	4.5
2	E	239	ASN	4.5
1	B	247	SER	4.5
2	E	253	CYS	4.5
2	E	169	LEU	4.5
1	A	154	PRO	4.5
2	D	241	ILE	4.5
2	E	219	ASP	4.4
2	E	192	ASP	4.4
2	E	255	GLU	4.3
1	B	36	ARG	4.3
1	B	107	LEU	4.3
1	A	7	LEU	4.3
2	E	171	PRO	4.2
1	B	155	VAL	4.2
2	E	283	THR	4.1
2	D	145	GLN	4.0
2	E	293	SER	4.0
2	E	188	GLN	4.0
2	E	170	SER	3.9
2	E	250	VAL	3.9
1	A	42	GLU	3.8
2	E	243	TYR	3.8
2	E	202	VAL	3.7
2	E	286	PHE	3.7
2	E	213	SER	3.7
2	E	256	ALA	3.7
2	E	224	ALA	3.7
2	E	147	SER	3.6
2	E	227	LEU	3.6
2	E	205	TYR	3.6
1	A	224	GLU	3.5
1	A	36	ARG	3.4
1	A	190	CYS	3.4
1	B	282	GLN	3.4
2	E	163	CYS	3.3
2	E	145	GLN	3.3
2	E	248	PHE	3.3
2	E	160	CYS	3.3
2	E	275	ILE	3.2
1	B	161	GLU	3.2

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Mol	Chain	Res	Type	RSRZ
2	E	271	LYS	3.2
1	B	153	ILE	3.2
1	A	225	GLU	3.2
2	E	148	THR	3.2
1	B	74	LYS	3.2
2	E	282	PHE	3.2
1	B	7	LEU	3.1
1	B	137	ASN	3.1
2	D	293	SER	3.1
2	E	266	ASN	3.1
1	A	19	PHE	3.0
2	E	263	SER	3.0
2	E	149	SER	3.0
2	D	280	HIS	3.0
1	B	45	PRO	3.0
1	A	137	ASN	3.0
2	E	201	VAL	3.0
1	A	32	LEU	2.9
1	B	212	LEU	2.9
2	E	150	GLU	2.9
2	E	203	PHE	2.9
1	A	37	LEU	2.9
2	E	229	CYS	2.9
1	A	15	TYR	2.9
1	A	289	PHE	2.9
2	E	165	ARG	2.9
1	B	8	GLU	2.8
1	A	10	ILE	2.8
1	A	17	THR	2.8
2	E	221	GLU	2.8
1	A	9	LYS	2.8
1	B	284	PRO	2.8
1	B	173	LEU	2.7
1	A	31	ALA	2.7
2	E	234	TYR	2.7
2	E	254	LYS	2.6
1	B	6	LYS	2.6
2	E	204	LEU	2.5
2	E	289	LEU	2.5
1	B	278	GLU	2.5
2	D	192	ASP	2.5
2	E	175	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	192	PHE	2.5
1	A	76	LEU	2.5
2	E	257	PHE	2.5
2	D	155	LEU	2.5
2	D	204	LEU	2.5
2	E	281	TYR	2.5
1	A	178	LEU	2.5
1	B	143	ALA	2.4
1	A	287	SER	2.4
1	A	49	LEU	2.4
2	E	274	GLN	2.4
1	B	31	ALA	2.4
1	B	243	PRO	2.4
1	A	161	GLU	2.3
1	A	191	ILE	2.3
1	A	78	LEU	2.3
2	E	238	GLY	2.3
2	E	268	MET	2.3
2	E	162	ARG	2.3
1	B	70	LEU	2.3
1	B	110	LEU	2.3
2	D	253	CYS	2.3
1	A	155	VAL	2.2
1	B	215	ILE	2.2
1	B	32	LEU	2.2
1	A	80	PHE	2.2
1	B	241	MET	2.2
2	E	214	SER	2.2
1	A	122	VAL	2.2
2	E	173	ASP	2.2
1	B	76	LEU	2.2
2	E	232	LEU	2.2
1	A	101	GLU	2.2
2	E	222	LEU	2.2
1	B	217	ARG	2.2
1	A	30	VAL	2.2
2	E	264	VAL	2.2
2	E	184	SER	2.1
2	E	157	GLU	2.1
2	E	174	PRO	2.1
2	D	284	GLN	2.1
1	A	192	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
2	E	223	GLN	2.1
2	E	284	GLN	2.1
2	E	251	GLU	2.1
1	A	263	LEU	2.1
1	B	142	LEU	2.1
2	D	153	ARG	2.1
1	B	52	ILE	2.1
1	B	46	SER	2.0
1	A	107	LEU	2.0
2	E	155	LEU	2.0
2	E	151	LEU	2.0
2	E	185	LEU	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)

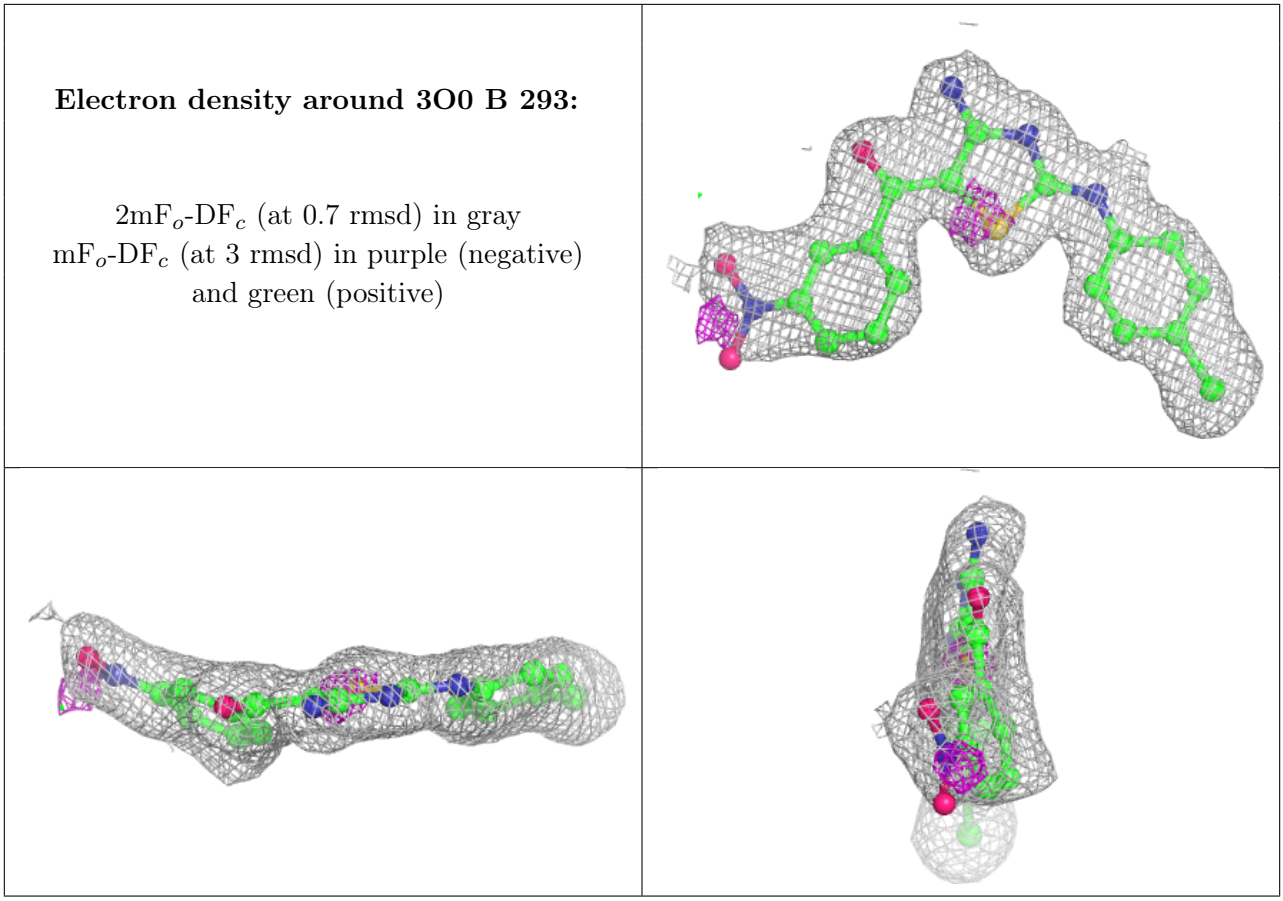
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	3O0	B	293	25/25	0.87	0.14	43,47,62,69	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 3O0 B 293:

$2mF_o$-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.