



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:31 PM UTC

PDB ID : 3O0G / pdb_00003o0g
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 ⓘ 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 Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

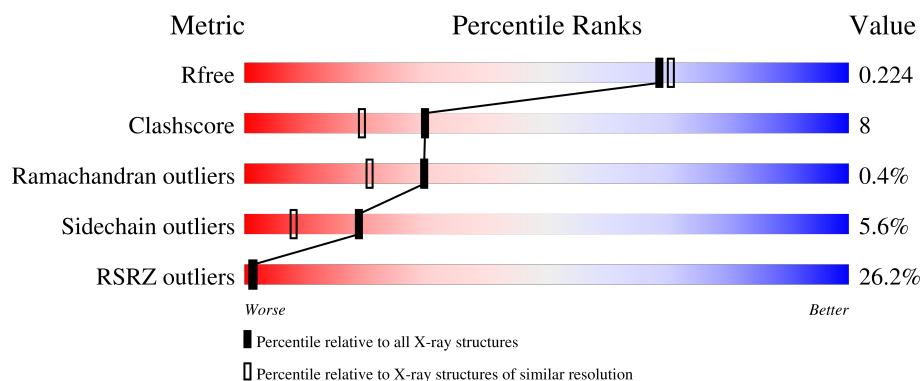
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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}	180053	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (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 $\leq 5\%$. 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	292	13% 75% 20% .
1	B	292	18% 73% 15% 10%
2	D	149	7% 85% 15%
2	E	149	81% 88% 11% .

2 Entry composition

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			

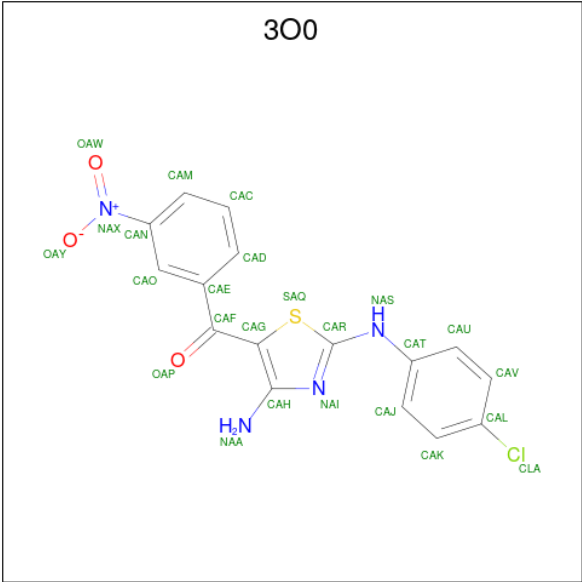
There are 2 discrepancies between the modelled and reference sequences:

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 (CCD ID: 3O0) (formula: C₁₆H₁₁ClN₄O₃S).



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

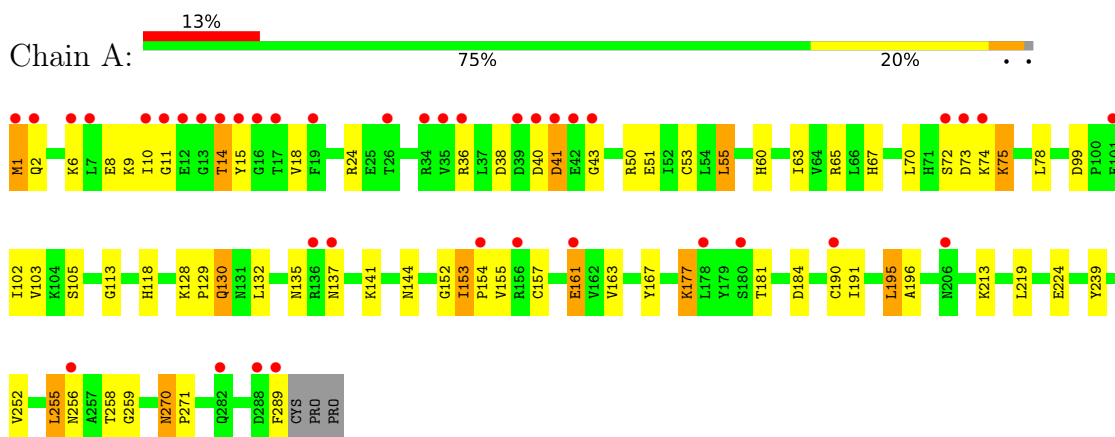
- Molecule 4 is water.

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		

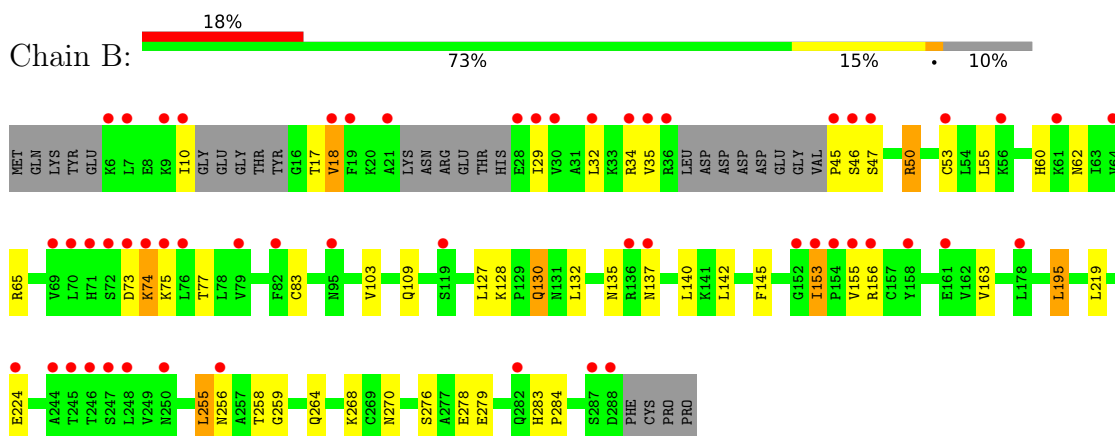
3 Residue-property plots [i](#)

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.

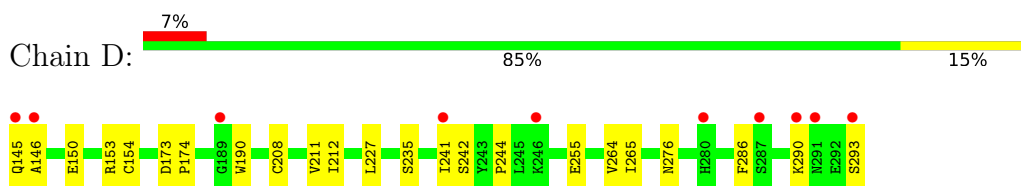
- Molecule 1: Cell division protein kinase 5



- Molecule 1: Cell division protein kinase 5

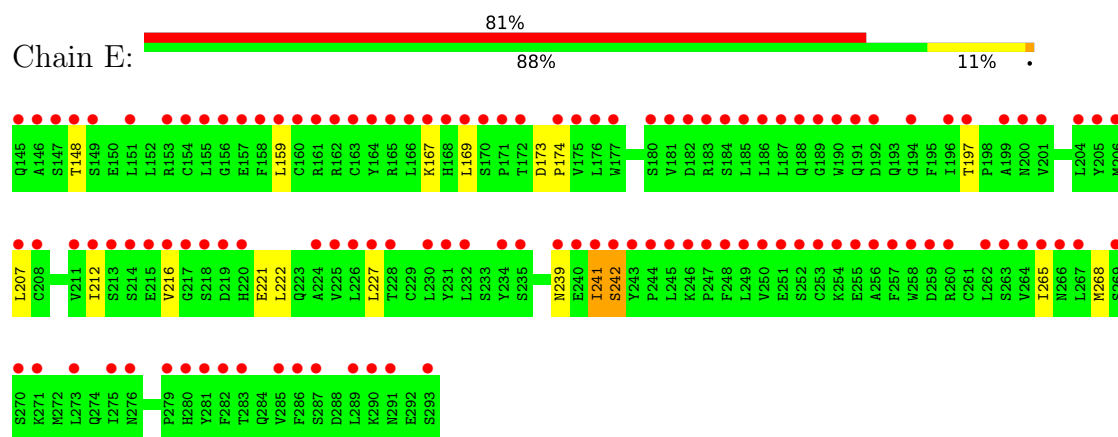


- Molecule 2: Cyclin-dependent kinase 5 activator 1



- Molecule 2: Cyclin-dependent kinase 5 activator 1

Chain E:



4 Data and refinement statistics

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 19.96 – 1.95	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.96-1.95) 97.9 (19.96-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ 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)	0.43 , 58.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	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.*

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: 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	0.68	0/2379	0.87	1/3219 (0.0%)
1	B	0.53	0/2164	0.83	0/2925
2	D	0.59	0/1230	0.79	0/1667
2	E	0.44	0/1230	0.86	0/1667
All	All	0.58	0/7003	0.84	1/9478 (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	40	ASP	N-CA-C	-6.63	104.78	114.39

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	61	0
1	B	2117	0	2162	31	0
2	D	1202	0	1187	17	0
2	E	1202	0	1187	13	0
3	B	25	0	11	3	0
4	A	124	0	0	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	117	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 (117) 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
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:73:ASP:CG	1:A:74:LYS:H	1.97	0.70
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
3:B:293:3O0:HAU	3:B:293:3O0:SAQ	2.38	0.63
2:E:207:LEU:HA	2:E:268:MET:HE2	1.82	0.62
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:A:270:ASN:HD22	1:A:270:ASN:C	2.14	0.54
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: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
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:B:270:ASN:C	1:B:270:ASN:HD22	2.22	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:73:ASP:CG	1:B:74:LYS:H	2.22	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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
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:177:LYS:HZ2	1:A:177:LYS:HA	1.85	0.41
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:E:167:LYS:C	2:E:169:LEU:H	2.29	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%)	36	28
1	B	256/292 (88%)	243 (95%)	11 (4%)	2 (1%)	16	8
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%)	30	21

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%)	235 (91%)	22 (9%)	10	2
1	B	235/260 (90%)	222 (94%)	13 (6%)	19	8
2	D	138/139 (99%)	135 (98%)	3 (2%)	45	40
2	E	138/139 (99%)	133 (96%)	5 (4%)	31	21
All	All	768/798 (96%)	725 (94%)	43 (6%)	19	8

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	6	LYS
1	A	8	GLU
1	A	9	LYS
1	A	10	ILE
1	A	14	THR
1	A	41	ASP
1	A	55	LEU
1	A	65	ARG
1	A	75	LYS
1	A	78	LEU
1	A	130	GLN
1	A	132	LEU
1	A	141	LYS
1	A	153	ILE
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	227	LEU
2	D	241	ILE
2	D	255	GLU
1	B	17	THR
1	B	18	VAL
1	B	50	ARG
1	B	65	ARG
1	B	74	LYS

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Mol	Chain	Res	Type
1	B	130	GLN
1	B	132	LEU
1	B	137	ASN
1	B	153	ILE
1	B	195	LEU
1	B	219	LEU
1	B	224	GLU
1	B	255	LEU
2	E	148	THR
2	E	212	ILE
2	E	227	LEU
2	E	241	ILE
2	E	242	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) 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	270	ASN
1	B	62	ASN
1	B	85	GLN
1	B	135	ASN
1	B	226	GLN
1	B	270	ASN
2	E	239	ASN

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 [i](#)

There are no oligosaccharides 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	-	26,27,27	2.90	6 (23%)	34,38,38	2.40	4 (11%)

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	-	-	0/14/16/16	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	293	3O0	OAW-NAX	12.02	1.43	1.22
3	B	293	3O0	CAN-NAX	-5.28	1.32	1.45
3	B	293	3O0	CAT-NAS	-3.40	1.34	1.41
3	B	293	3O0	CAR-NAI	2.57	1.35	1.31
3	B	293	3O0	CAG-CAF	2.48	1.54	1.47
3	B	293	3O0	CAG-SAQ	-2.23	1.69	1.74

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	293	3O0	CAR-SAQ-CAG	10.20	94.08	88.34
3	B	293	3O0	SAQ-CAR-NAI	-6.89	109.62	115.78
3	B	293	3O0	CAG-CAH-NAI	-3.42	114.82	117.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	293	3O0	CAM-CAN-NAX	2.83	121.81	119.34

There are no chirality outliers.

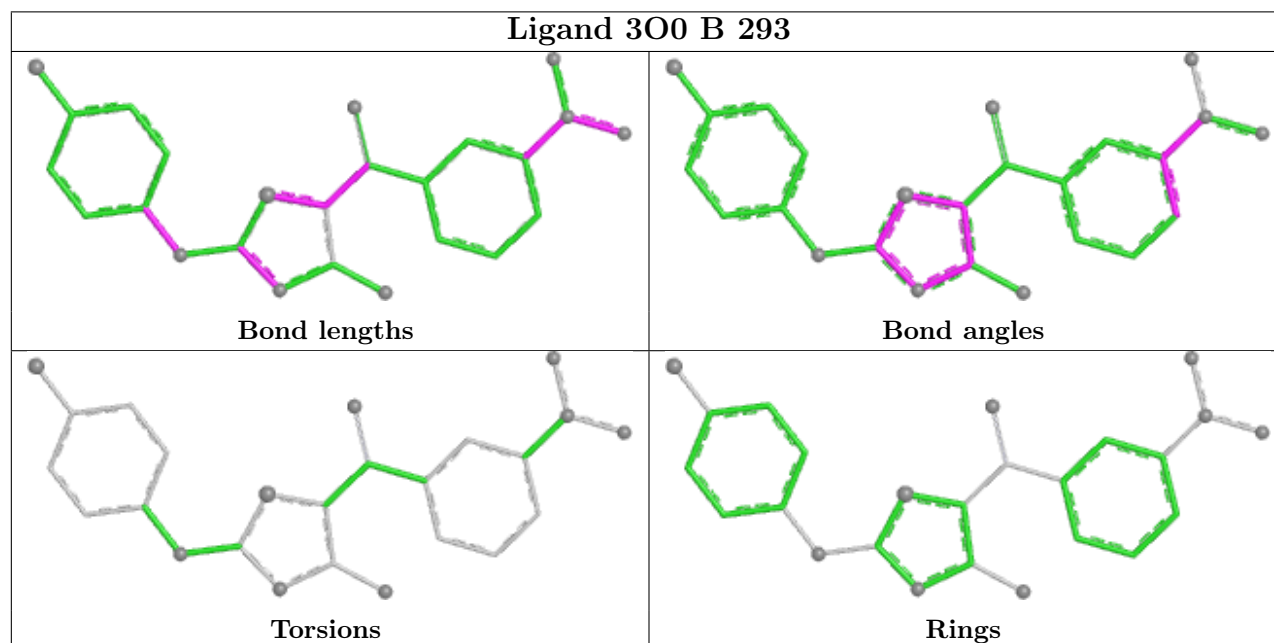
There are no torsion outliers.

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 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	289/292 (98%)	0.67	39 (13%) 7 7	23, 34, 60, 73	0
1	B	264/292 (90%)	1.14	54 (20%) 2 2	27, 45, 79, 116	0
2	D	149/149 (100%)	0.46	10 (6%) 24 27	26, 35, 53, 63	0
2	E	149/149 (100%)	3.24	120 (80%) 0 0	55, 89, 127, 140	0
All	All	851/882 (96%)	1.23	223 (26%) 1 1	23, 41, 102, 140	0

All (223) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	241	ILE	11.5
1	B	245	THR	9.8
2	E	187	LEU	9.6
2	E	242	SER	7.3
1	B	244	ALA	7.2
1	A	41	ASP	6.7
2	D	146	ALA	6.7
2	E	212	ILE	6.2
2	E	166	LEU	6.2
1	B	29	ILE	6.0
2	E	146	ALA	6.0
1	A	288	ASP	6.0
2	E	186	LEU	5.7
2	E	167	LYS	5.6
2	E	245	LEU	5.6
1	B	7	LEU	5.6
2	E	164	TYR	5.6
2	E	168	HIS	5.5
2	E	227	LEU	5.5
1	B	70	LEU	5.5
2	E	256	ALA	5.5

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Mol	Chain	Res	Type	RSRZ
2	E	249	LEU	5.4
1	B	288	ASP	5.4
2	E	169	LEU	5.3
2	E	156	GLY	5.3
1	A	154	PRO	5.3
1	A	14	THR	5.2
1	B	246	THR	5.2
2	E	171	PRO	5.2
1	A	10	ILE	5.0
2	E	190	TRP	5.0
1	A	40	ASP	5.0
1	B	155	VAL	5.0
1	A	190	CYS	4.9
1	B	36	ARG	4.9
1	A	12	GLU	4.9
1	A	42	GLU	4.9
1	B	73	ASP	4.8
2	E	176	LEU	4.8
2	E	217	GLY	4.8
2	E	201	VAL	4.8
1	B	74	LYS	4.8
2	E	239	ASN	4.8
2	E	262	LEU	4.7
1	B	76	LEU	4.7
2	E	185	LEU	4.7
1	B	154	PRO	4.6
2	E	246	LYS	4.6
1	A	39	ASP	4.5
1	B	28	GLU	4.5
1	A	13	GLY	4.5
2	E	250	VAL	4.5
1	B	287	SER	4.5
2	E	145	GLN	4.4
2	E	230	LEU	4.3
2	E	205	TYR	4.3
2	D	145	GLN	4.2
2	E	216	VAL	4.1
2	E	267	LEU	4.1
2	E	177	TRP	4.0
1	A	73	ASP	4.0
2	E	254	LYS	4.0
1	A	1	MET	4.0

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Mol	Chain	Res	Type	RSRZ
1	B	156	ARG	4.0
2	E	247	PRO	4.0
2	E	224	ALA	4.0
2	E	180	SER	4.0
1	A	74	LYS	3.9
2	E	226	LEU	3.9
2	E	148	THR	3.9
1	A	2	GLN	3.9
2	E	181	VAL	3.9
2	E	290	LYS	3.9
1	B	153	ILE	3.9
2	D	241	ILE	3.9
2	E	265	ILE	3.9
2	E	258	TRP	3.8
2	E	172	THR	3.8
2	E	188	GLN	3.8
2	E	275	ILE	3.7
2	E	208	CYS	3.7
2	E	253	CYS	3.7
2	E	257	PHE	3.7
1	A	17	THR	3.7
2	E	243	TYR	3.6
1	A	11	GLY	3.6
1	A	136	ARG	3.6
2	E	244	PRO	3.6
1	A	289	PHE	3.6
1	B	6	LYS	3.6
1	B	224	GLU	3.6
2	E	232	LEU	3.6
1	B	250	ASN	3.5
1	B	47	SER	3.5
1	B	75	LYS	3.5
2	E	147	SER	3.5
1	B	10	ILE	3.5
2	E	285	VAL	3.4
2	E	248	PHE	3.4
2	E	282	PHE	3.4
1	A	156	ARG	3.4
2	E	211	VAL	3.3
1	A	36	ARG	3.3
2	E	220	HIS	3.3
1	B	45	PRO	3.3

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Mol	Chain	Res	Type	RSRZ
2	E	163	CYS	3.3
2	E	204	LEU	3.2
2	E	283	THR	3.2
1	A	16	GLY	3.2
2	E	218	SER	3.2
2	E	271	LYS	3.2
1	B	34	ARG	3.2
2	E	159	LEU	3.2
2	E	165	ARG	3.2
2	E	191	GLN	3.1
1	B	35	VAL	3.1
2	E	184	SER	3.1
1	A	137	ASN	3.1
2	E	252	SER	3.1
1	A	7	LEU	3.1
2	E	215	GLU	3.0
2	E	240	GLU	3.0
2	E	214	SER	3.0
2	E	255	GLU	3.0
1	B	256	ASN	2.9
1	B	21	ALA	2.9
2	E	235	SER	2.9
2	E	189	GLY	2.9
2	E	279	PRO	2.9
2	E	153	ARG	2.9
2	D	287	SER	2.9
2	E	192	ASP	2.9
1	B	32	LEU	2.9
1	A	15	TYR	2.9
1	A	19	PHE	2.9
2	E	286	PHE	2.9
1	B	72	SER	2.9
2	E	291	ASN	2.8
2	E	280	HIS	2.8
1	B	64	VAL	2.8
2	E	175	VAL	2.8
2	E	225	VAL	2.8
2	E	263	SER	2.8
1	B	178	LEU	2.8
2	E	234	TYR	2.8
2	D	189	GLY	2.8
1	B	69	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
2	E	149	SER	2.7
2	E	266	ASN	2.7
1	B	61	LYS	2.7
2	E	158	PHE	2.7
1	B	30	VAL	2.7
1	B	137	ASN	2.7
1	B	19	PHE	2.7
2	E	151	LEU	2.7
1	B	56	LYS	2.7
2	E	160	CYS	2.7
1	B	9	LYS	2.7
1	B	161	GLU	2.6
1	B	248	LEU	2.6
2	E	161	ARG	2.6
2	E	228	THR	2.6
1	B	46	SER	2.6
2	E	293	SER	2.6
1	B	95	ASN	2.6
2	E	174	PRO	2.6
2	E	155	LEU	2.6
1	B	282	GLN	2.6
2	E	219	ASP	2.6
2	E	213	SER	2.6
2	E	287	SER	2.6
2	E	206	MET	2.6
2	E	182	ASP	2.6
2	D	291	ASN	2.6
1	A	282	GLN	2.5
1	A	161	GLU	2.5
1	A	6	LYS	2.5
2	E	199	ALA	2.5
2	E	270	SER	2.5
2	E	264	VAL	2.5
2	E	251	GLU	2.5
1	A	178	LEU	2.5
2	E	207	LEU	2.5
1	A	180	SER	2.5
1	B	18	VAL	2.5
2	E	281	TYR	2.5
2	E	196	ILE	2.5
1	A	43	GLY	2.4
2	E	194	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	256	ASN	2.4
2	D	280	HIS	2.4
1	B	158	TYR	2.4
2	D	293	SER	2.4
1	B	119	SER	2.4
2	E	154	CYS	2.4
2	E	170	SER	2.4
2	E	231	TYR	2.4
2	D	290	LYS	2.4
2	E	269	SER	2.3
2	E	197	THR	2.3
1	B	82	PHE	2.3
1	B	79	VAL	2.3
1	B	136	ARG	2.3
2	E	260	ARG	2.2
1	B	152	GLY	2.2
2	E	157	GLU	2.2
1	B	247	SER	2.2
2	E	259	ASP	2.2
1	A	26	THR	2.2
1	A	72	SER	2.2
1	A	34	ARG	2.2
2	E	289	LEU	2.2
2	E	200	ASN	2.2
1	A	35	VAL	2.1
1	B	53	CYS	2.1
1	A	206	ASN	2.1
2	E	183	ARG	2.1
1	A	101	GLU	2.1
1	B	71	HIS	2.1
2	E	273	LEU	2.1
2	E	276	ASN	2.1
2	D	246	LYS	2.0
2	E	162	ARG	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

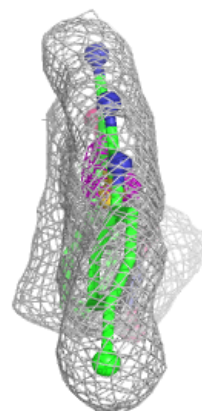
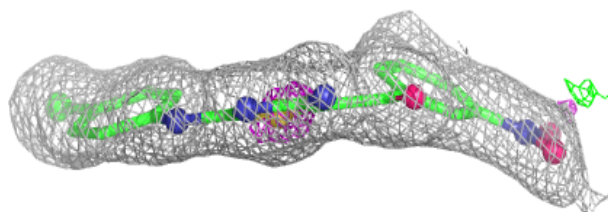
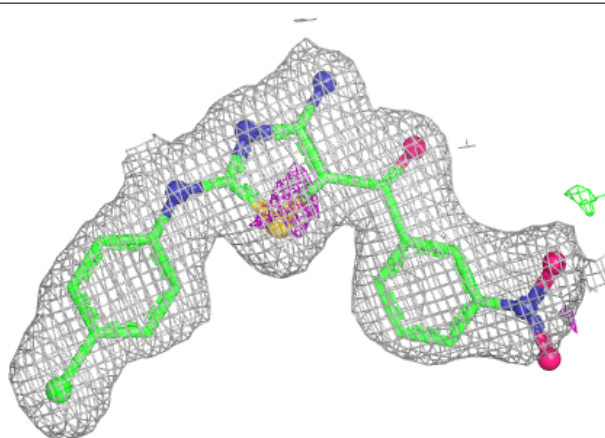
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	3O0	B	293	25/25	0.92	0.10	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.