



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 08:38 PM UTC

PDB ID : 7XTO / pdb_00007xto
Title : Structure of CIA2 reveal the Mechanism of soil bacterial derived chlorinase
Authors : Liu, Y.H.; Liu, Y.; Li, Y.
Deposited on : 2022-05-17
Resolution : 2.48 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

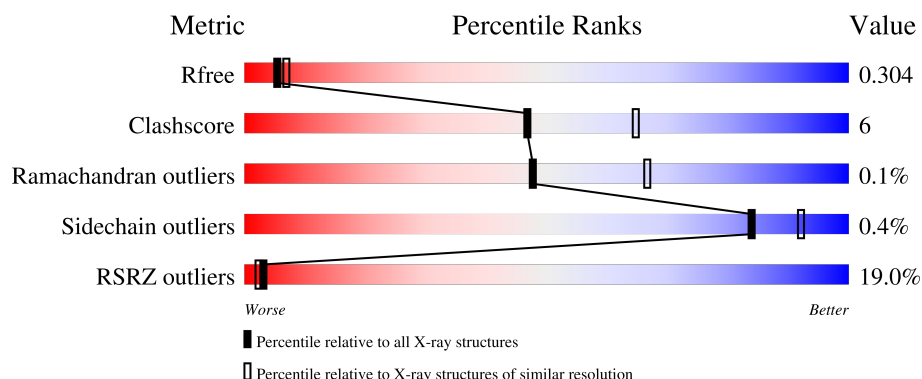
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.48 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	7589 (2.50-2.46)
Clashscore	190562	8295 (2.50-2.46)
Ramachandran outliers	187476	8164 (2.50-2.46)
Sidechain outliers	187428	8166 (2.50-2.46)
RSRZ outliers	180081	7593 (2.50-2.46)

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	276	17% 75% 14% 11%
1	B	276	11% 79% 12% 9%
1	C	276	14% 78% 12% 10%
1	D	276	19% 76% 13% 10%
1	E	276	20% 75% 14% 11%

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Mol	Chain	Length	Quality of chain
1	F	276	20% 77% 12% 12%

2 Entry composition [i](#)

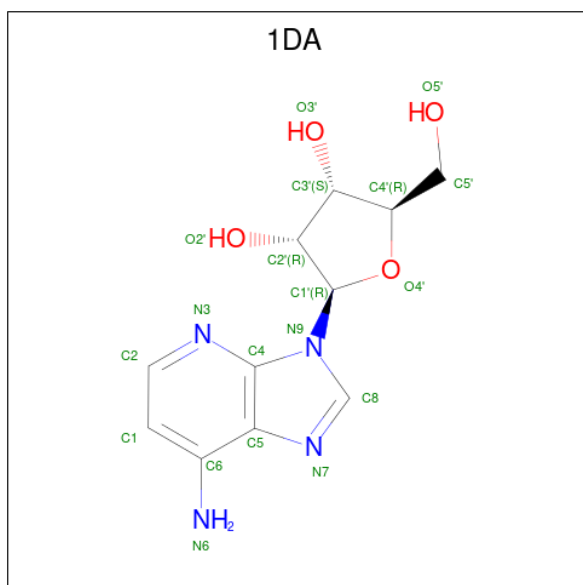
There are 3 unique types of molecules in this entry. The entry contains 10672 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 soil bacterial derived chlorinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	245	Total	C	N	O	S	0	0	0
			1706	1083	293	322	8			
1	C	248	Total	C	N	O	S	0	0	0
			1711	1084	293	326	8			
1	D	248	Total	C	N	O	S	0	0	0
			1747	1106	303	330	8			
1	B	252	Total	C	N	O	S	0	0	0
			1752	1113	299	332	8			
1	E	247	Total	C	N	O	S	0	0	0
			1705	1076	298	323	8			
1	F	244	Total	C	N	O	S	0	0	0
			1698	1075	293	322	8			

- Molecule 2 is 1-DEAZA-ADENOSINE (CCD ID: 1DA) (formula: $C_{11}H_{14}N_4O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			19	11	4	4		
2	C	1	Total	C	N	O	0	0
			19	11	4	4		
2	D	1	Total	C	N	O	0	0
			19	11	4	4		
2	B	1	Total	C	N	O	0	0
			19	11	4	4		
2	E	1	Total	C	N	O	0	0
			19	11	4	4		
2	F	1	Total	C	N	O	0	0
			19	11	4	4		

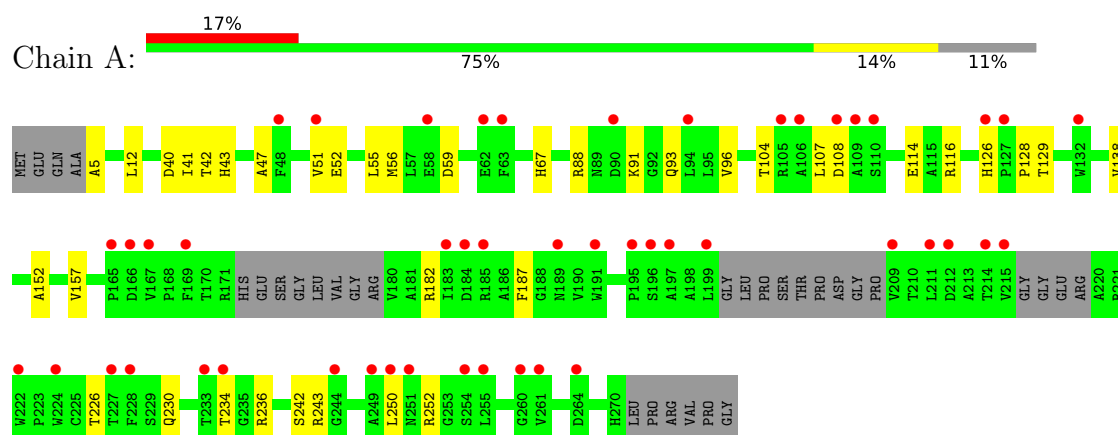
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	37	Total	O	0	0
			37	37		
3	C	39	Total	O	0	0
			39	39		
3	D	56	Total	O	0	0
			56	56		
3	B	28	Total	O	0	0
			28	28		
3	E	31	Total	O	0	0
			31	31		
3	F	48	Total	O	0	0
			48	48		

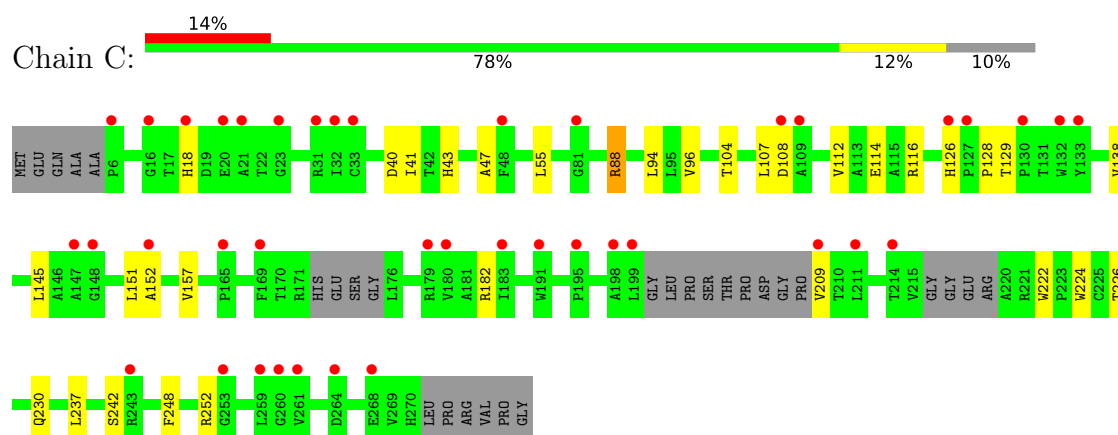
3 Residue-property plots [i](#)

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.

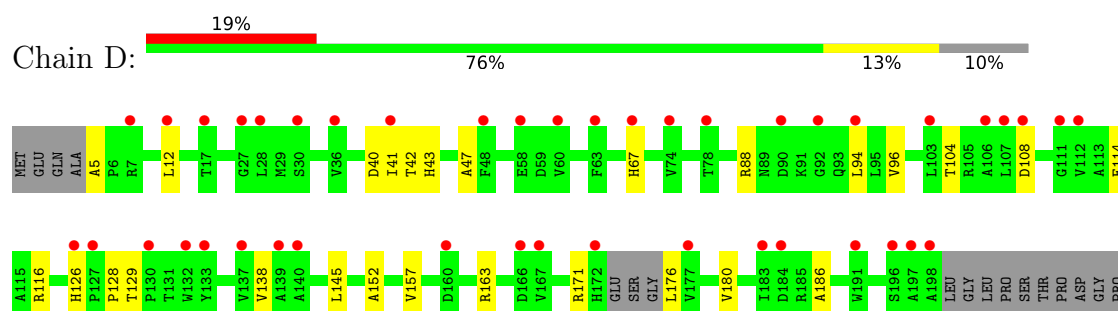
- Molecule 1: soil bacterial derived chlorinase

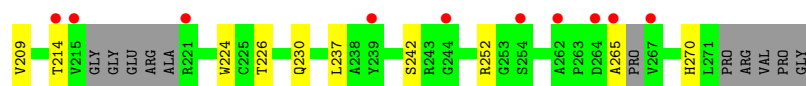


- Molecule 1: soil bacterial derived chlorinase

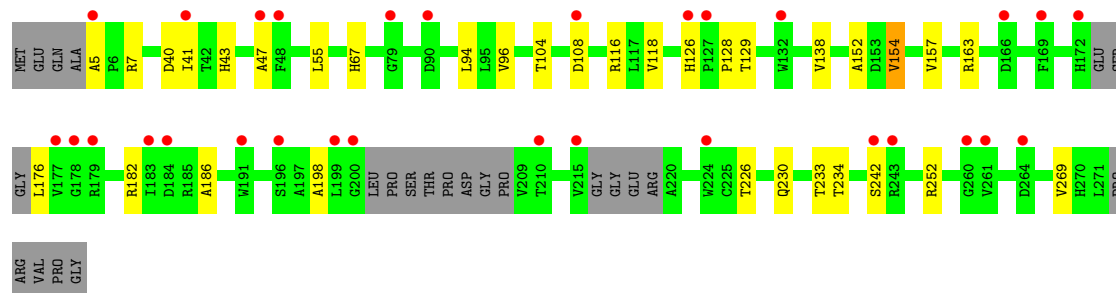
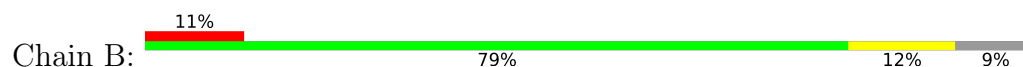


- Molecule 1: soil bacterial derived chlorinase

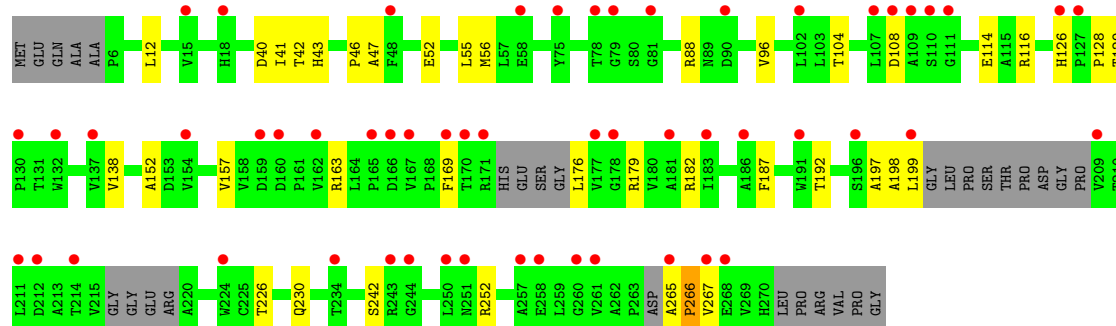




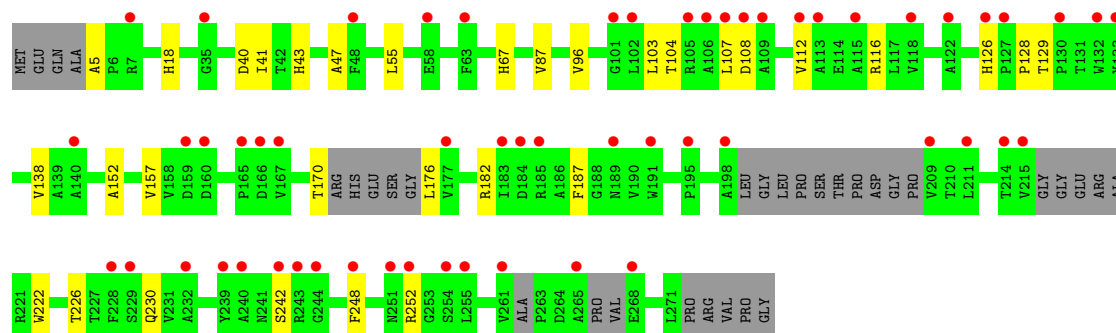
- Molecule 1: soil bacterial derived chlorinase



- Molecule 1: soil bacterial derived chlorinase



- Molecule 1: soil bacterial derived chlorinase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	181.38Å 104.42Å 124.97Å 90.00° 108.88° 90.00°	Depositor
Resolution (Å)	24.99 – 2.48 24.99 – 2.48	Depositor EDS
% Data completeness (in resolution range)	86.8 (24.99-2.48) 87.1 (24.99-2.48)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.63 (at 2.48Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.278 , 0.304 0.279 , 0.304	Depositor DCC
R_{free} test set	3353 reflections (4.27%)	wwPDB-VP
Wilson B-factor (Å ²)	36.1	Xtriage
Anisotropy	0.856	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 78.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	10672	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 56.41 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.7473e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 1DA

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	0.20	0/1745	0.51	3/2407 (0.1%)
1	B	0.21	0/1792	0.51	3/2473 (0.1%)
1	C	0.20	0/1750	0.50	3/2417 (0.1%)
1	D	0.21	0/1785	0.50	3/2460 (0.1%)
1	E	0.26	0/1744	0.59	6/2404 (0.2%)
1	F	0.21	0/1735	0.50	3/2389 (0.1%)
All	All	0.21	0/10551	0.52	21/14550 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	E	0	1
All	All	0	2

There are no bond length outliers.

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	266	PRO	N-CA-C	7.18	127.26	112.47
1	F	47	ALA	CA-C-N	6.29	134.35	123.91
1	F	47	ALA	C-N-CA	6.29	134.35	123.91
1	B	47	ALA	CA-C-N	6.29	134.35	123.91
1	B	47	ALA	C-N-CA	6.29	134.35	123.91
1	E	47	ALA	CA-C-N	6.29	134.35	123.91
1	E	47	ALA	C-N-CA	6.29	134.35	123.91
1	C	47	ALA	CA-C-N	6.29	134.34	123.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	47	ALA	C-N-CA	6.29	134.34	123.91
1	A	47	ALA	CA-C-N	6.26	134.30	123.91
1	A	47	ALA	C-N-CA	6.26	134.30	123.91
1	D	47	ALA	CA-C-N	6.25	134.29	123.91
1	D	47	ALA	C-N-CA	6.25	134.29	123.91
1	E	265	ALA	CA-C-N	5.73	127.00	119.84
1	E	265	ALA	C-N-CA	5.73	127.00	119.84
1	C	41	ILE	N-CA-C	-5.10	106.10	110.74
1	A	41	ILE	N-CA-C	-5.07	106.12	110.74
1	D	41	ILE	N-CA-C	-5.07	106.12	110.74
1	B	41	ILE	N-CA-C	-5.07	106.13	110.74
1	E	41	ILE	N-CA-C	-5.06	106.13	110.74
1	F	41	ILE	N-CA-C	-5.06	106.14	110.74

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	198	ALA	Mainchain
1	E	198	ALA	Mainchain

5.2 Too-close contacts

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	1706	0	1578	22	0
1	B	1752	0	1625	19	0
1	C	1711	0	1570	20	0
1	D	1747	0	1639	20	0
1	E	1705	0	1554	20	0
1	F	1698	0	1552	23	0
2	A	19	0	14	1	0
2	B	19	0	14	2	0
2	C	19	0	14	1	0
2	D	19	0	14	2	0
2	E	19	0	14	2	0
2	F	19	0	14	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	37	0	0	0	0
3	B	28	0	0	0	0
3	C	39	0	0	1	0
3	D	56	0	0	0	0
3	E	31	0	0	0	1
3	F	48	0	0	0	1
All	All	10672	0	9602	115	1

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 6.

All (115) 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:F:103:LEU:HB3	1:F:107:LEU:HD23	1.52	0.91
1:E:88:ARG:NH2	1:E:114:GLU:OE1	2.07	0.86
1:E:129:THR:HG21	1:F:242:SER:HA	1.58	0.84
1:C:252:ARG:NH1	3:C:401:HOH:O	2.12	0.83
1:A:129:THR:HG21	1:C:242:SER:HA	1.60	0.82
1:A:59:ASP:OD2	1:A:243:ARG:NE	2.12	0.81
1:D:209:VAL:HG23	1:D:224:TRP:HB3	1.63	0.80
1:C:94:LEU:HD23	1:C:145:LEU:HD13	1.67	0.77
1:A:242:SER:HA	1:D:129:THR:HG21	1.66	0.76
1:B:242:SER:HA	1:F:129:THR:HG21	1.67	0.76
1:D:88:ARG:NH2	1:D:114:GLU:OE1	2.19	0.76
2:A:301:1DA:H1	1:C:252:ARG:H	1.49	0.75
1:B:129:THR:HG21	1:E:242:SER:HA	1.68	0.73
2:E:301:1DA:H1	1:F:252:ARG:H	1.54	0.72
1:C:129:THR:HG21	1:D:242:SER:HA	1.70	0.72
1:D:108:ASP:OD1	1:D:163:ARG:NH1	2.22	0.72
1:E:108:ASP:OD1	1:E:163:ARG:NH2	2.25	0.69
1:B:252:ARG:H	2:F:301:1DA:H1	1.58	0.68
1:A:88:ARG:NH2	1:A:114:GLU:OE1	2.29	0.66
1:E:52:GLU:HG3	1:E:56:MET:HE3	1.77	0.66
1:A:252:ARG:H	2:D:301:1DA:H1	1.60	0.66
1:C:209:VAL:HG23	1:C:224:TRP:HB3	1.78	0.66
1:E:226:THR:N	1:E:230:GLN:OE1	2.30	0.65
1:F:226:THR:N	1:F:230:GLN:OE1	2.30	0.65
1:B:226:THR:N	1:B:230:GLN:OE1	2.30	0.65
1:A:52:GLU:HG3	1:A:56:MET:HE3	1.79	0.64
1:D:126:HIS:O	1:D:128:PRO:HD3	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:126:HIS:O	1:F:128:PRO:HD3	1.98	0.63
1:A:126:HIS:O	1:A:128:PRO:HD3	1.98	0.63
1:B:126:HIS:O	1:B:128:PRO:HD3	1.98	0.63
1:A:226:THR:N	1:A:230:GLN:OE1	2.30	0.63
1:C:126:HIS:O	1:C:128:PRO:HD3	1.98	0.63
1:C:226:THR:N	1:C:230:GLN:OE1	2.30	0.62
2:C:301:1DA:H1	1:D:252:ARG:H	1.65	0.62
1:E:126:HIS:O	1:E:128:PRO:HD3	1.98	0.62
2:B:301:1DA:H1	1:E:252:ARG:H	1.64	0.62
1:D:226:THR:N	1:D:230:GLN:OE1	2.30	0.62
1:B:186:ALA:HB2	1:F:18:HIS:CE1	2.34	0.61
1:F:103:LEU:HB3	1:F:107:LEU:CD2	2.29	0.60
1:B:96:VAL:HG12	1:B:138:VAL:HG13	1.83	0.60
1:A:96:VAL:HG12	1:A:138:VAL:HG13	1.83	0.60
1:C:96:VAL:HG12	1:C:138:VAL:HG13	1.83	0.59
1:D:171:ARG:HA	1:D:176:LEU:HD12	1.83	0.59
1:E:96:VAL:HG12	1:E:138:VAL:HG13	1.83	0.59
1:F:96:VAL:HG12	1:F:138:VAL:HG13	1.83	0.59
1:D:96:VAL:HG12	1:D:138:VAL:HG13	1.83	0.59
1:E:197:ALA:C	1:E:199:LEU:H	2.11	0.59
1:B:7:ARG:NH1	1:B:94:LEU:HD13	2.18	0.58
1:F:103:LEU:O	1:F:107:LEU:HD23	2.04	0.57
1:C:88:ARG:HH21	1:C:151:LEU:HD23	1.69	0.57
1:D:94:LEU:HD23	1:D:145:LEU:HB3	1.86	0.57
1:A:40:ASP:OD1	1:A:43:HIS:NE2	2.37	0.54
1:F:87:VAL:HG11	1:F:107:LEU:HD11	1.90	0.54
1:C:107:LEU:HD13	1:C:112:VAL:HG22	1.91	0.52
1:F:55:LEU:HB3	1:F:182:ARG:HD2	1.92	0.52
1:A:91:LYS:HE2	1:A:93:GLN:NE2	2.25	0.51
1:F:107:LEU:HD12	1:F:112:VAL:HG22	1.92	0.51
1:D:180:VAL:CG1	1:D:265:ALA:H	2.24	0.51
1:B:176:LEU:HB2	1:B:269:VAL:HB	1.92	0.50
1:E:40:ASP:OD1	1:E:43:HIS:NE2	2.37	0.50
1:C:40:ASP:OD1	1:C:43:HIS:NE2	2.38	0.49
1:B:5:ALA:O	1:B:67:HIS:NE2	2.43	0.49
1:F:40:ASP:OD1	1:F:43:HIS:NE2	2.37	0.49
1:B:118:VAL:HA	1:B:154:VAL:HG13	1.95	0.49
1:C:55:LEU:HB3	1:C:182:ARG:HD2	1.95	0.49
1:C:222:TRP:CD2	1:C:248:PHE:HD2	2.31	0.49
1:B:55:LEU:HB3	1:B:182:ARG:HD2	1.95	0.49
1:E:55:LEU:HB3	1:E:182:ARG:HD2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:108:ASP:OD1	1:B:163:ARG:NH1	2.46	0.48
1:B:186:ALA:HB2	1:F:18:HIS:HE1	1.76	0.48
1:C:88:ARG:NH2	1:C:114:GLU:OE1	2.47	0.48
1:B:40:ASP:OD1	1:B:43:HIS:NE2	2.38	0.48
1:C:18:HIS:HE1	1:D:186:ALA:HB2	1.78	0.48
1:D:40:ASP:OD1	1:D:43:HIS:NE2	2.38	0.46
1:A:55:LEU:HB3	1:A:182:ARG:HD2	1.98	0.46
1:F:170:THR:O	1:F:176:LEU:HA	2.16	0.46
1:B:116:ARG:NE	1:B:152:ALA:HA	2.31	0.46
1:A:107:LEU:HD23	1:A:107:LEU:HA	1.72	0.45
1:F:5:ALA:O	1:F:67:HIS:NE2	2.44	0.45
1:D:5:ALA:O	1:D:67:HIS:NE2	2.45	0.45
1:C:116:ARG:NE	1:C:152:ALA:HA	2.31	0.45
1:A:116:ARG:NE	1:A:152:ALA:HA	2.31	0.45
1:D:116:ARG:NE	1:D:152:ALA:HA	2.31	0.45
1:F:116:ARG:NE	1:F:152:ALA:HA	2.31	0.45
1:A:116:ARG:NH1	1:A:157:VAL:HG23	2.32	0.45
1:E:116:ARG:NE	1:E:152:ALA:HA	2.31	0.45
1:B:116:ARG:NH1	1:B:157:VAL:HG23	2.32	0.44
1:A:187:PHE:CZ	2:D:301:1DA:H2'	2.53	0.44
1:E:116:ARG:NH1	1:E:157:VAL:HG23	2.32	0.44
1:C:116:ARG:NH1	1:C:157:VAL:HG23	2.32	0.44
2:E:301:1DA:H2'	1:F:187:PHE:CZ	2.52	0.44
1:F:116:ARG:NH1	1:F:157:VAL:HG23	2.32	0.44
1:D:116:ARG:NH1	1:D:157:VAL:HG23	2.32	0.44
1:F:107:LEU:HD13	1:F:107:LEU:HA	1.80	0.44
2:B:301:1DA:H2'	1:E:187:PHE:CZ	2.52	0.44
1:E:169:PHE:CE2	1:E:176:LEU:HD22	2.53	0.43
1:D:214:THR:HG23	1:D:270:HIS:NE2	2.33	0.43
1:B:104:THR:O	1:B:108:ASP:OD2	2.37	0.43
1:A:104:THR:O	1:A:108:ASP:OD2	2.37	0.43
1:D:104:THR:O	1:D:108:ASP:OD2	2.37	0.43
1:F:104:THR:O	1:F:108:ASP:OD2	2.37	0.42
1:E:104:THR:O	1:E:108:ASP:OD2	2.37	0.42
1:C:104:THR:O	1:C:108:ASP:OD2	2.37	0.42
1:A:51:VAL:O	1:A:55:LEU:HG	2.20	0.42
1:E:46:PRO:HD2	1:E:52:GLU:HG2	2.01	0.42
1:A:236:ARG:HA	1:A:250:LEU:HD23	2.02	0.42
1:C:222:TRP:CE3	1:C:248:PHE:HD2	2.38	0.42
1:B:233:THR:HG22	1:B:234:THR:HG23	2.02	0.41
1:A:5:ALA:O	1:A:67:HIS:NE2	2.48	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:THR:O	1:A:250:LEU:HD22	2.20	0.40
1:A:12:LEU:HA	1:A:42:THR:O	2.22	0.40
1:D:12:LEU:HA	1:D:42:THR:O	2.22	0.40
1:E:12:LEU:HA	1:E:42:THR:O	2.22	0.40
1:E:179:ARG:O	1:E:192:THR:HA	2.21	0.40
1:F:222:TRP:CD2	1:F:248:PHE:HD2	2.39	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:421:HOH:O	3:F:440:HOH:O[4_555]	2.17	0.03

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	237/276 (86%)	230 (97%)	7 (3%)	0	100	100
1	B	244/276 (88%)	237 (97%)	7 (3%)	0	100	100
1	C	240/276 (87%)	232 (97%)	8 (3%)	0	100	100
1	D	238/276 (86%)	231 (97%)	7 (3%)	0	100	100
1	E	237/276 (86%)	227 (96%)	8 (3%)	2 (1%)	16	28
1	F	232/276 (84%)	225 (97%)	7 (3%)	0	100	100
All	All	1428/1656 (86%)	1382 (97%)	44 (3%)	2 (0%)	48	66

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	266	PRO
1	E	267	VAL

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	161/217 (74%)	161 (100%)	0	100	100
1	B	166/217 (76%)	165 (99%)	1 (1%)	78	90
1	C	161/217 (74%)	159 (99%)	2 (1%)	63	81
1	D	170/217 (78%)	169 (99%)	1 (1%)	78	90
1	E	158/217 (73%)	158 (100%)	0	100	100
1	F	159/217 (73%)	159 (100%)	0	100	100
All	All	975/1302 (75%)	971 (100%)	4 (0%)	84	92

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	88	ARG
1	C	237	LEU
1	D	237	LEU
1	B	154	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 oligosaccharides in this entry.

5.6 Ligand geometry

6 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
2	1DA	A	301	-	20,21,21	1.35	3 (15%)	29,31,31	2.01	11 (37%)
2	1DA	D	301	-	20,21,21	1.35	3 (15%)	29,31,31	2.01	11 (37%)
2	1DA	F	301	-	20,21,21	1.35	3 (15%)	29,31,31	2.01	11 (37%)
2	1DA	E	301	-	20,21,21	1.35	3 (15%)	29,31,31	2.01	11 (37%)
2	1DA	C	301	-	20,21,21	1.35	3 (15%)	29,31,31	2.01	11 (37%)
2	1DA	B	301	-	20,21,21	1.35	3 (15%)	29,31,31	2.01	11 (37%)

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
2	1DA	A	301	-	-	2/6/22/22	0/3/3/3
2	1DA	D	301	-	-	2/6/22/22	0/3/3/3
2	1DA	F	301	-	-	2/6/22/22	0/3/3/3
2	1DA	E	301	-	-	2/6/22/22	0/3/3/3
2	1DA	C	301	-	-	2/6/22/22	0/3/3/3
2	1DA	B	301	-	-	2/6/22/22	0/3/3/3

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	1DA	C5-N7	-2.83	1.33	1.39
2	B	301	1DA	C5-N7	-2.82	1.33	1.39
2	F	301	1DA	C5-N7	-2.82	1.33	1.39
2	E	301	1DA	C5-N7	-2.82	1.33	1.39
2	D	301	1DA	C5-N7	-2.82	1.33	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	301	1DA	C5-N7	-2.82	1.33	1.39
2	A	301	1DA	C6-N6	2.29	1.45	1.38
2	D	301	1DA	C6-N6	2.29	1.45	1.38
2	B	301	1DA	C6-N6	2.29	1.45	1.38
2	F	301	1DA	C6-N6	2.29	1.45	1.38
2	C	301	1DA	C6-N6	2.28	1.45	1.38
2	E	301	1DA	C6-N6	2.28	1.45	1.38
2	D	301	1DA	C1-C6	-2.26	1.35	1.40
2	B	301	1DA	C1-C6	-2.26	1.35	1.40
2	E	301	1DA	C1-C6	-2.26	1.35	1.40
2	C	301	1DA	C1-C6	-2.26	1.35	1.40
2	A	301	1DA	C1-C6	-2.26	1.35	1.40
2	F	301	1DA	C1-C6	-2.26	1.35	1.40

All (66) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	301	1DA	C5-C4-N3	-4.65	120.31	126.72
2	B	301	1DA	C5-C4-N3	-4.65	120.31	126.72
2	E	301	1DA	C5-C4-N3	-4.65	120.31	126.72
2	C	301	1DA	C5-C4-N3	-4.65	120.31	126.72
2	A	301	1DA	C5-C4-N3	-4.65	120.31	126.72
2	F	301	1DA	C5-C4-N3	-4.65	120.31	126.72
2	A	301	1DA	N9-C8-N7	-4.47	107.59	113.94
2	F	301	1DA	N9-C8-N7	-4.47	107.59	113.94
2	B	301	1DA	N9-C8-N7	-4.47	107.60	113.94
2	E	301	1DA	N9-C8-N7	-4.47	107.60	113.94
2	C	301	1DA	N9-C8-N7	-4.47	107.60	113.94
2	D	301	1DA	N9-C8-N7	-4.46	107.60	113.94
2	B	301	1DA	C1-C2-N3	-3.40	119.80	123.97
2	C	301	1DA	C1-C2-N3	-3.40	119.80	123.97
2	F	301	1DA	C1-C2-N3	-3.40	119.80	123.97
2	D	301	1DA	C1-C2-N3	-3.40	119.81	123.97
2	E	301	1DA	C1-C2-N3	-3.40	119.81	123.97
2	A	301	1DA	C1-C2-N3	-3.40	119.81	123.97
2	A	301	1DA	C5-N7-C8	3.10	108.32	103.45
2	C	301	1DA	C5-N7-C8	3.10	108.31	103.45
2	B	301	1DA	C5-N7-C8	3.10	108.31	103.45
2	E	301	1DA	C5-N7-C8	3.10	108.31	103.45
2	F	301	1DA	C5-N7-C8	3.09	108.31	103.45
2	D	301	1DA	C5-N7-C8	3.09	108.31	103.45
2	A	301	1DA	C6-C5-N7	2.71	132.66	130.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	301	1DA	C6-C5-N7	2.71	132.66	130.14
2	E	301	1DA	C6-C5-N7	2.71	132.66	130.14
2	B	301	1DA	C6-C5-N7	2.71	132.66	130.14
2	F	301	1DA	C6-C5-N7	2.71	132.65	130.14
2	D	301	1DA	C6-C5-N7	2.70	132.65	130.14
2	C	301	1DA	C4-C5-N7	-2.56	107.66	110.58
2	E	301	1DA	C4-C5-N7	-2.56	107.66	110.58
2	B	301	1DA	C4-C5-N7	-2.56	107.66	110.58
2	A	301	1DA	C4-C5-N7	-2.56	107.66	110.58
2	D	301	1DA	C4-C5-N7	-2.55	107.66	110.58
2	F	301	1DA	C4-C5-N7	-2.55	107.66	110.58
2	E	301	1DA	N3-C4-N9	2.54	131.48	127.17
2	F	301	1DA	N3-C4-N9	2.53	131.48	127.17
2	B	301	1DA	N3-C4-N9	2.53	131.48	127.17
2	A	301	1DA	N3-C4-N9	2.53	131.48	127.17
2	D	301	1DA	N3-C4-N9	2.53	131.48	127.17
2	C	301	1DA	N3-C4-N9	2.53	131.47	127.17
2	E	301	1DA	C1-C6-N6	-2.48	115.26	120.11
2	A	301	1DA	C1-C6-N6	-2.48	115.26	120.11
2	F	301	1DA	C1-C6-N6	-2.48	115.26	120.11
2	B	301	1DA	C1-C6-N6	-2.47	115.27	120.11
2	C	301	1DA	C1-C6-N6	-2.47	115.27	120.11
2	D	301	1DA	C1-C6-N6	-2.47	115.27	120.11
2	F	301	1DA	C4-N9-C8	2.36	108.22	105.74
2	E	301	1DA	C4-N9-C8	2.36	108.22	105.74
2	A	301	1DA	C4-N9-C8	2.36	108.22	105.74
2	B	301	1DA	C4-N9-C8	2.36	108.21	105.74
2	C	301	1DA	C4-N9-C8	2.36	108.21	105.74
2	D	301	1DA	C4-N9-C8	2.36	108.21	105.74
2	B	301	1DA	C2-N3-C4	2.24	120.12	115.05
2	E	301	1DA	C2-N3-C4	2.24	120.12	115.05
2	C	301	1DA	C2-N3-C4	2.24	120.12	115.05
2	D	301	1DA	C2-N3-C4	2.24	120.12	115.05
2	F	301	1DA	C2-N3-C4	2.24	120.12	115.05
2	A	301	1DA	C2-N3-C4	2.24	120.11	115.05
2	C	301	1DA	C5-C4-N9	2.20	108.21	105.81
2	D	301	1DA	C5-C4-N9	2.20	108.21	105.81
2	B	301	1DA	C5-C4-N9	2.20	108.21	105.81
2	A	301	1DA	C5-C4-N9	2.20	108.21	105.81
2	E	301	1DA	C5-C4-N9	2.20	108.21	105.81
2	F	301	1DA	C5-C4-N9	2.20	108.21	105.81

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	1DA	O4'-C4'-C5'-O5'
2	C	301	1DA	O4'-C4'-C5'-O5'
2	D	301	1DA	O4'-C4'-C5'-O5'
2	B	301	1DA	O4'-C4'-C5'-O5'
2	E	301	1DA	O4'-C4'-C5'-O5'
2	F	301	1DA	O4'-C4'-C5'-O5'
2	A	301	1DA	C3'-C4'-C5'-O5'
2	C	301	1DA	C3'-C4'-C5'-O5'
2	D	301	1DA	C3'-C4'-C5'-O5'
2	B	301	1DA	C3'-C4'-C5'-O5'
2	E	301	1DA	C3'-C4'-C5'-O5'
2	F	301	1DA	C3'-C4'-C5'-O5'

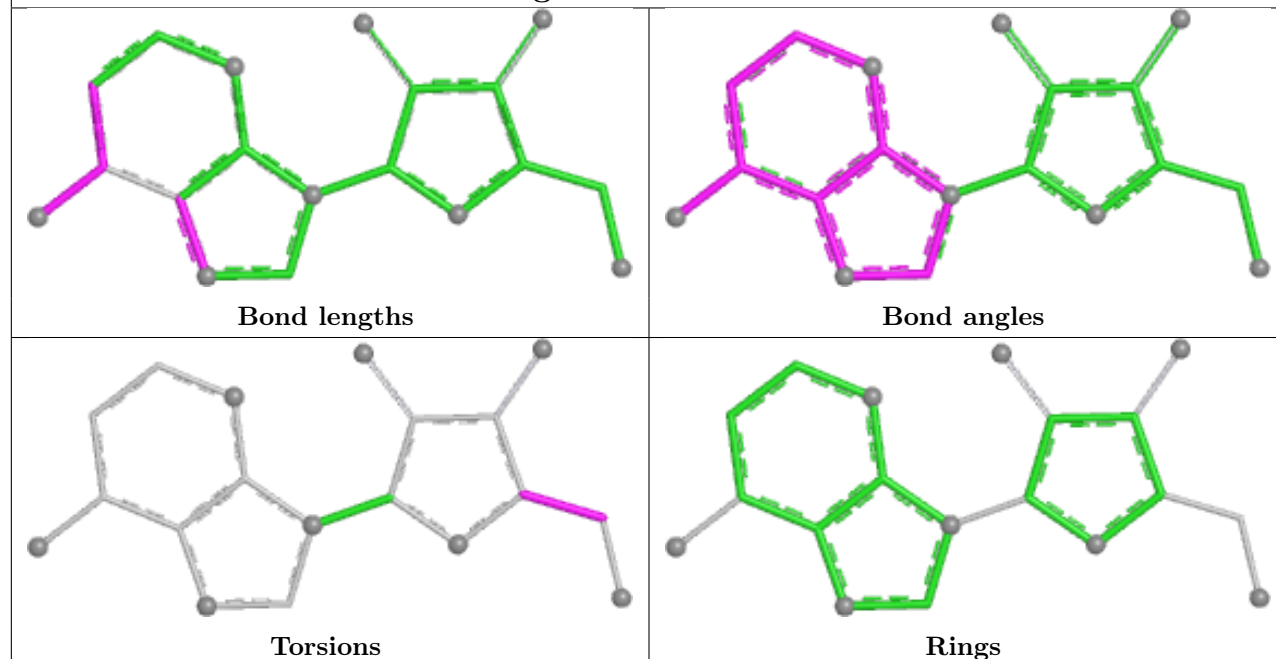
There are no ring outliers.

6 monomers are involved in 9 short contacts:

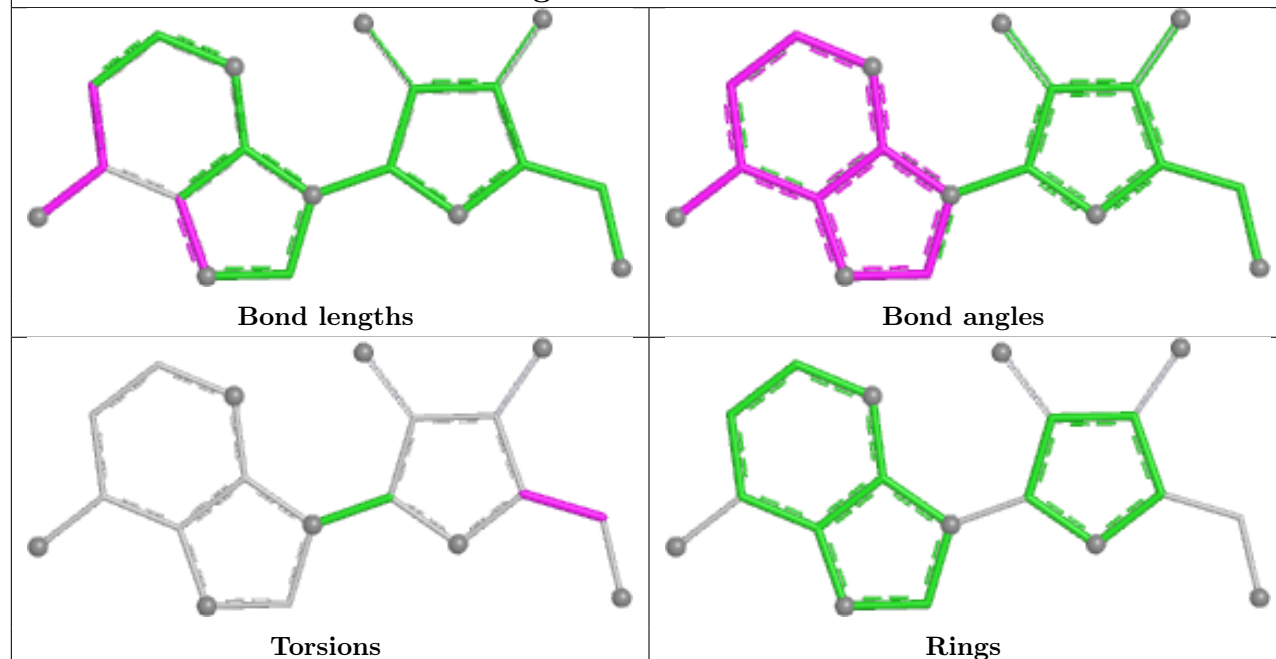
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	1DA	1	0
2	D	301	1DA	2	0
2	F	301	1DA	1	0
2	E	301	1DA	2	0
2	C	301	1DA	1	0
2	B	301	1DA	2	0

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.

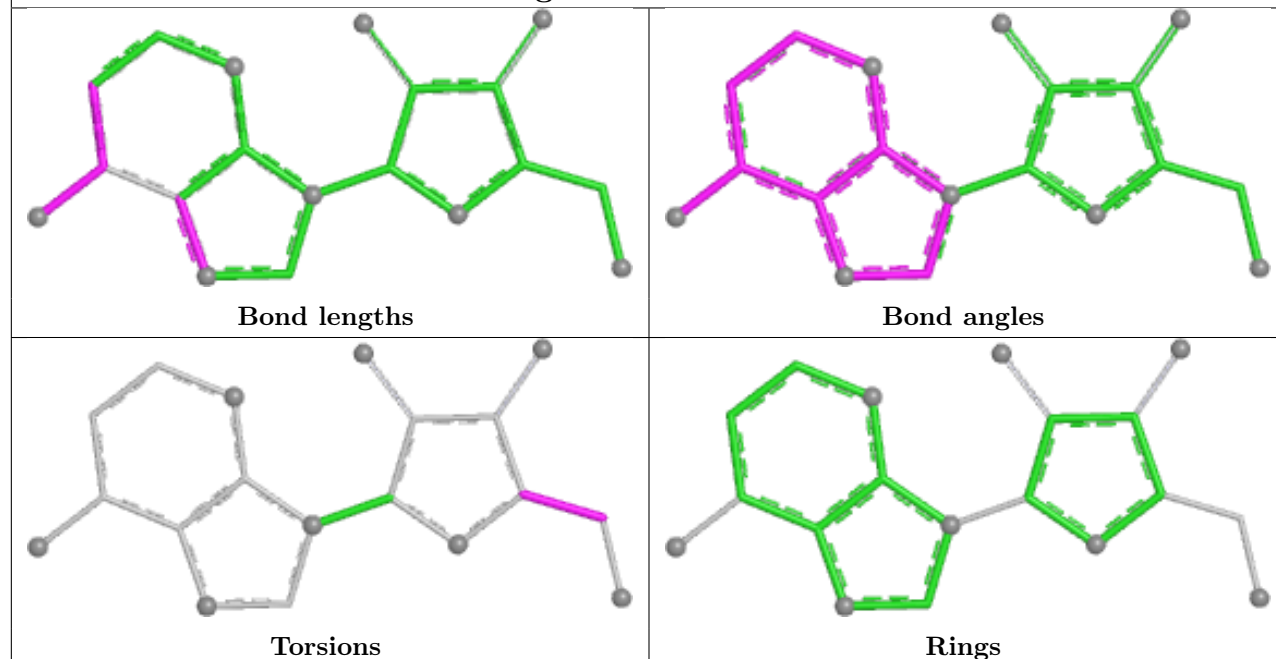
Ligand 1DA A 301



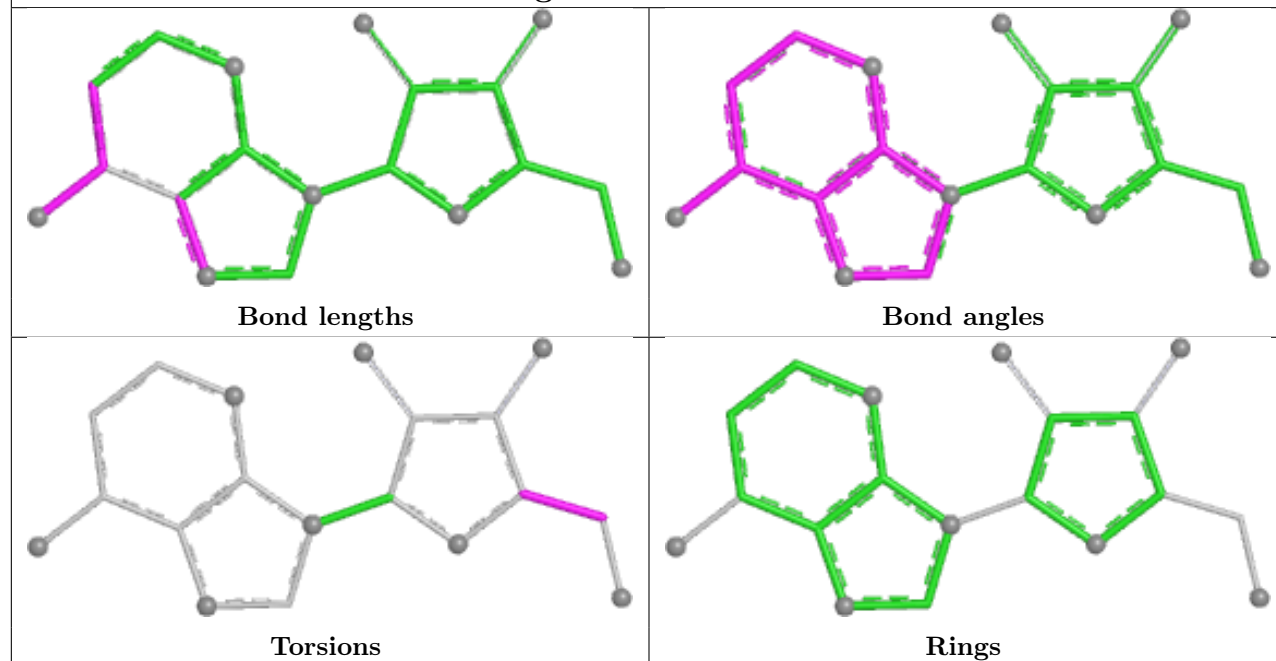
Ligand 1DA D 301

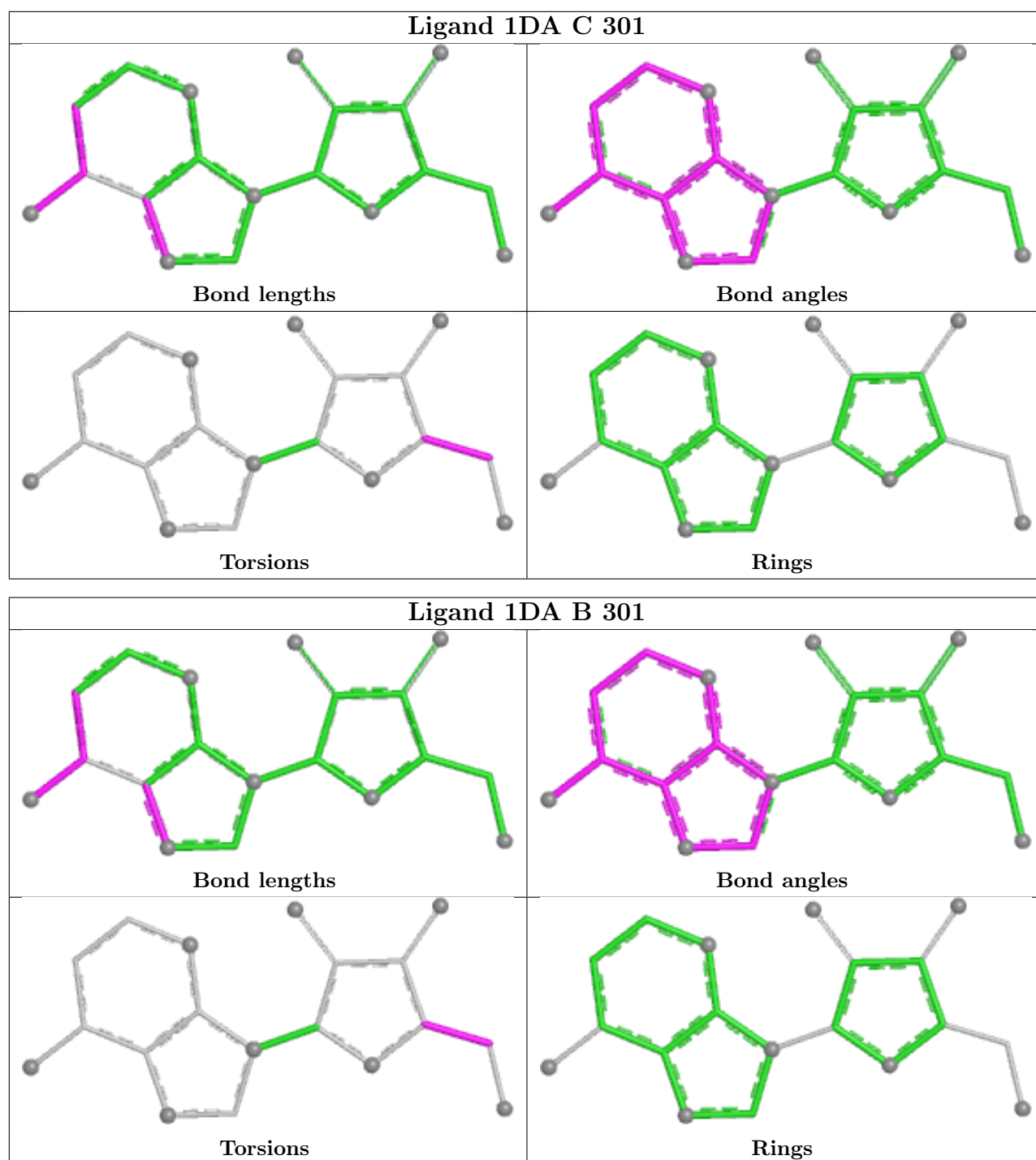


Ligand 1DA F 301



Ligand 1DA E 301





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	245/276 (88%)	1.12	48 (19%) 3 2	24, 40, 71, 100	0
1	B	252/276 (91%)	0.80	30 (11%) 9 7	24, 40, 75, 93	0
1	C	248/276 (89%)	1.03	40 (16%) 4 3	24, 40, 75, 112	0
1	D	248/276 (89%)	1.29	53 (21%) 2 2	24, 40, 74, 94	0
1	E	247/276 (89%)	1.31	55 (22%) 2 2	24, 40, 73, 94	0
1	F	244/276 (88%)	1.42	56 (22%) 2 1	24, 40, 73, 112	0
All	All	1484/1656 (89%)	1.16	282 (19%) 3 2	24, 40, 74, 112	0

All (282) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	127	PRO	6.8
1	D	127	PRO	6.0
1	E	166	ASP	5.9
1	F	126	HIS	5.9
1	B	264	ASP	5.8
1	C	127	PRO	5.6
1	E	90	ASP	5.1
1	F	239	TYR	5.0
1	E	108	ASP	4.7
1	C	23	GLY	4.7
1	C	126	HIS	4.6
1	F	191	TRP	4.6
1	C	199	LEU	4.5
1	B	127	PRO	4.4
1	F	183	ILE	4.3
1	D	126	HIS	4.3
1	B	166	ASP	4.2
1	F	261	VAL	4.1
1	F	265	ALA	4.1

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Mol	Chain	Res	Type	RSRZ
1	B	200	GLY	4.1
1	A	199	LEU	4.0
1	E	127	PRO	4.0
1	B	177	VAL	4.0
1	F	108	ASP	3.9
1	F	130	PRO	3.9
1	C	183	ILE	3.9
1	A	254	SER	3.9
1	D	166	ASP	3.9
1	F	184	ASP	3.9
1	A	126	HIS	3.8
1	B	178	GLY	3.8
1	A	108	ASP	3.8
1	E	261	VAL	3.8
1	B	199	LEU	3.8
1	E	167	VAL	3.8
1	D	264	ASP	3.8
1	D	221	ARG	3.7
1	F	101	GLY	3.7
1	D	191	TRP	3.7
1	F	132	TRP	3.7
1	D	133	TYR	3.7
1	C	130	PRO	3.7
1	D	184	ASP	3.6
1	F	242	SER	3.6
1	C	21	ALA	3.6
1	F	115	ALA	3.6
1	A	127	PRO	3.6
1	E	126	HIS	3.6
1	C	147	ALA	3.6
1	E	165	PRO	3.6
1	F	215	VAL	3.6
1	B	215	VAL	3.5
1	E	109	ALA	3.5
1	D	172	HIS	3.5
1	D	78	THR	3.5
1	D	177	VAL	3.5
1	C	108	ASP	3.5
1	B	172	HIS	3.4
1	E	81	GLY	3.4
1	F	268	GLU	3.3
1	A	255	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	261	VAL	3.3
1	F	112	VAL	3.3
1	C	198	ALA	3.3
1	F	198	ALA	3.3
1	E	191	TRP	3.3
1	D	265	ALA	3.3
1	F	254	SER	3.2
1	C	243	ARG	3.2
1	A	214	THR	3.2
1	E	212	ASP	3.2
1	A	244	GLY	3.2
1	E	209	VAL	3.2
1	A	264	ASP	3.2
1	E	130	PRO	3.2
1	E	183	ILE	3.1
1	A	166	ASP	3.1
1	D	108	ASP	3.1
1	E	178	GLY	3.1
1	A	191	TRP	3.1
1	C	180	VAL	3.1
1	E	186	ALA	3.0
1	F	185	ARG	3.0
1	A	234	THR	3.0
1	F	165	PRO	3.0
1	F	105	ARG	3.0
1	C	48	PHE	3.0
1	F	133	TYR	3.0
1	E	243	ARG	3.0
1	F	243	ARG	3.0
1	A	228	PHE	3.0
1	F	109	ALA	2.9
1	A	184	ASP	2.9
1	E	159	ASP	2.9
1	A	109	ALA	2.9
1	D	198	ALA	2.9
1	C	191	TRP	2.9
1	F	229	SER	2.9
1	D	60	VAL	2.9
1	F	167	VAL	2.9
1	E	234	THR	2.9
1	F	195	PRO	2.9
1	B	191	TRP	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	48	PHE	2.9
1	B	196	SER	2.9
1	D	48	PHE	2.9
1	B	183	ILE	2.8
1	E	251	ASN	2.8
1	A	215	VAL	2.8
1	A	58	GLU	2.8
1	E	162	VAL	2.8
1	B	48	PHE	2.8
1	A	51	VAL	2.8
1	D	90	ASP	2.8
1	D	130	PRO	2.7
1	F	102	LEU	2.7
1	B	169	PHE	2.7
1	D	183	ILE	2.7
1	A	224	TRP	2.7
1	A	94	LEU	2.7
1	F	214	THR	2.7
1	E	211	LEU	2.7
1	E	171	ARG	2.7
1	D	7	ARG	2.7
1	A	63	PHE	2.6
1	F	189	ASN	2.6
1	F	177	VAL	2.6
1	C	20	GLU	2.6
1	A	260	GLY	2.6
1	D	111	GLY	2.6
1	F	166	ASP	2.6
1	E	258	GLU	2.6
1	C	109	ALA	2.6
1	A	90	ASP	2.6
1	C	253	GLY	2.6
1	F	159	ASP	2.6
1	D	112	VAL	2.6
1	A	197	ALA	2.6
1	A	249	ALA	2.6
1	E	78	THR	2.6
1	F	140	ALA	2.6
1	A	105	ARG	2.6
1	C	195	PRO	2.6
1	D	28	LEU	2.6
1	D	215	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	261	VAL	2.6
1	B	184	ASP	2.5
1	C	33	CYS	2.5
1	E	257	ALA	2.5
1	E	265	ALA	2.5
1	E	111	GLY	2.5
1	F	35	GLY	2.5
1	A	222	TRP	2.5
1	E	132	TRP	2.5
1	D	67	HIS	2.5
1	B	126	HIS	2.5
1	E	267	VAL	2.5
1	B	5	ALA	2.5
1	B	243	ARG	2.5
1	A	189	ASN	2.5
1	A	209	VAL	2.5
1	A	185	ARG	2.5
1	C	179	ARG	2.5
1	F	7	ARG	2.5
1	F	106	ALA	2.5
1	C	214	THR	2.5
1	D	196	SER	2.5
1	C	133	TYR	2.5
1	E	58	GLU	2.5
1	E	75	TYR	2.5
1	A	167	VAL	2.5
1	D	36	VAL	2.5
1	A	110	SER	2.5
1	D	214	THR	2.5
1	E	268	GLU	2.4
1	F	58	GLU	2.4
1	C	132	TRP	2.4
1	E	15	VAL	2.4
1	B	242	SER	2.4
1	F	63	PHE	2.4
1	D	137	VAL	2.4
1	F	251	ASN	2.4
1	D	139	ALA	2.4
1	E	181	ALA	2.4
1	C	268	GLU	2.4
1	E	260	GLY	2.4
1	A	183	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	E	102	LEU	2.4
1	F	228	PHE	2.4
1	D	106	ALA	2.4
1	A	165	PRO	2.4
1	D	94	LEU	2.4
1	F	211	LEU	2.4
1	E	137	VAL	2.4
1	A	227	THR	2.3
1	D	132	TRP	2.4
1	C	81	GLY	2.3
1	F	244	GLY	2.3
1	C	32	ILE	2.3
1	A	212	ASP	2.3
1	F	107	LEU	2.3
1	C	209	VAL	2.3
1	E	154	VAL	2.3
1	F	118	VAL	2.3
1	F	209	VAL	2.3
1	C	152	ALA	2.3
1	C	31	ARG	2.3
1	D	107	LEU	2.3
1	A	106	ALA	2.3
1	A	233	THR	2.3
1	A	196	SER	2.3
1	C	211	LEU	2.3
1	C	264	ASP	2.3
1	C	261	VAL	2.3
1	D	167	VAL	2.3
1	C	6	PRO	2.3
1	D	197	ALA	2.3
1	D	254	SER	2.3
1	B	108	ASP	2.3
1	F	160	ASP	2.3
1	D	63	PHE	2.3
1	F	48	PHE	2.3
1	A	251	ASN	2.2
1	C	259	LEU	2.2
1	D	41	ILE	2.2
1	D	103	LEU	2.2
1	E	250	LEU	2.2
1	E	160	ASP	2.2
1	E	224	TRP	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	74	VAL	2.2
1	B	179	ARG	2.2
1	F	232	ALA	2.2
1	D	30	SER	2.2
1	A	211	LEU	2.2
1	E	199	LEU	2.2
1	F	252	ARG	2.2
1	E	18	HIS	2.2
1	F	240	ALA	2.2
1	C	148	GLY	2.2
1	E	110	SER	2.2
1	D	160	ASP	2.2
1	C	165	PRO	2.2
1	A	169	PHE	2.2
1	E	48	PHE	2.2
1	E	169	PHE	2.2
1	E	177	VAL	2.1
1	A	250	LEU	2.1
1	D	27	GLY	2.1
1	B	260	GLY	2.1
1	F	255	LEU	2.1
1	B	41	ILE	2.1
1	E	196	SER	2.1
1	F	248	PHE	2.1
1	C	18	HIS	2.1
1	B	47	ALA	2.1
1	F	113	ALA	2.1
1	D	17	THR	2.1
1	E	79	GLY	2.1
1	E	244	GLY	2.1
1	D	12	LEU	2.1
1	E	170	THR	2.1
1	D	239	TYR	2.1
1	A	195	PRO	2.1
1	D	140	ALA	2.1
1	B	224	TRP	2.1
1	D	92	GLY	2.1
1	D	58	GLU	2.1
1	E	214	THR	2.1
1	C	169	PHE	2.0
1	D	262	ALA	2.0
1	E	107	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	62	GLU	2.0
1	A	132	TRP	2.0
1	C	16	GLY	2.0
1	C	260	GLY	2.0
1	B	79	GLY	2.0
1	D	267	VAL	2.0
1	F	122	ALA	2.0
1	D	244	GLY	2.0
1	B	210	THR	2.0
1	B	132	TRP	2.0
1	B	90	ASP	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

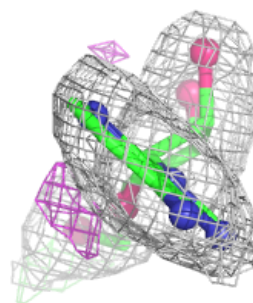
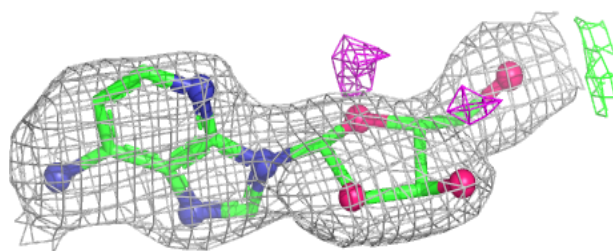
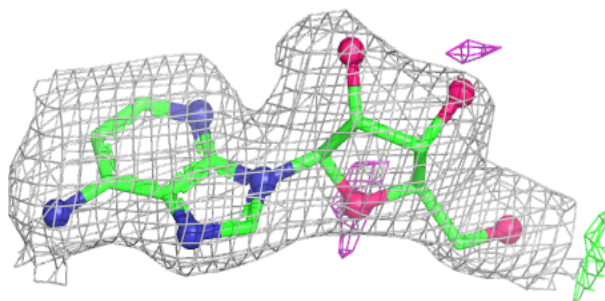
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	1DA	C	301	19/19	0.90	0.12	20,35,53,69	0
2	1DA	D	301	19/19	0.90	0.12	20,35,53,69	0
2	1DA	B	301	19/19	0.90	0.12	20,35,53,69	0
2	1DA	E	301	19/19	0.90	0.12	20,35,53,69	0
2	1DA	F	301	19/19	0.91	0.12	20,35,53,69	0
2	1DA	A	301	19/19	0.92	0.12	20,35,53,69	0

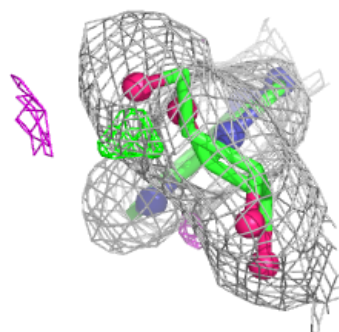
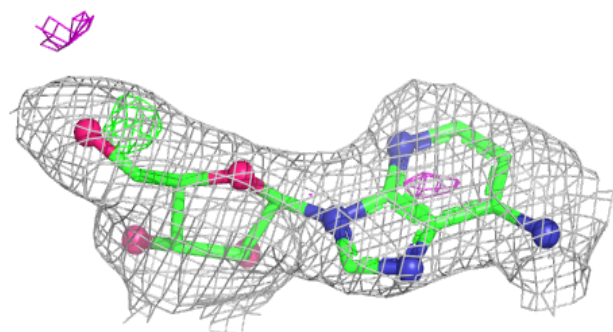
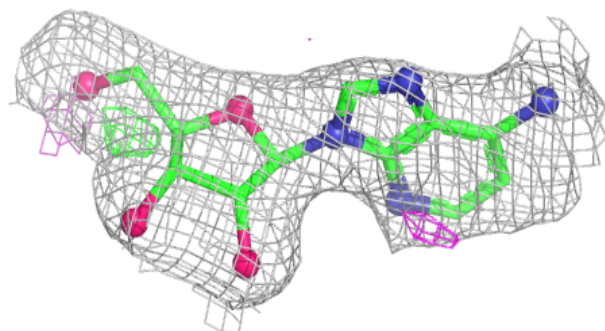
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around 1DA 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)

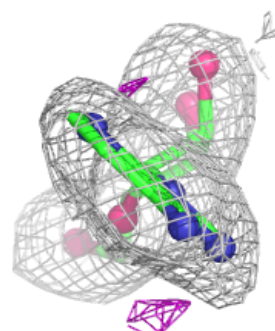
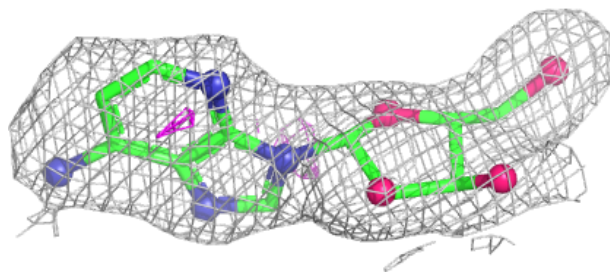
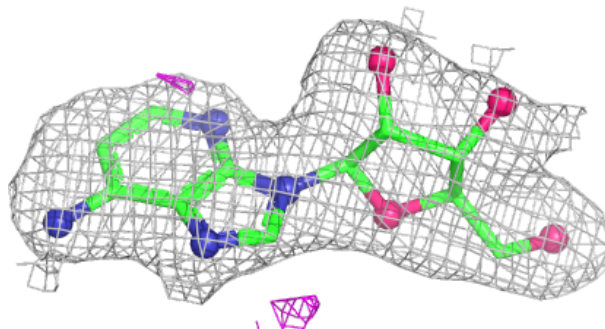
**Electron density around 1DA D 301:**

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

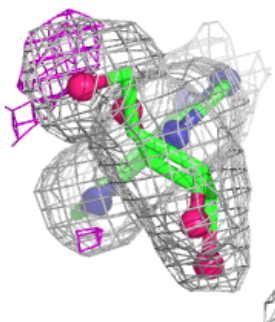
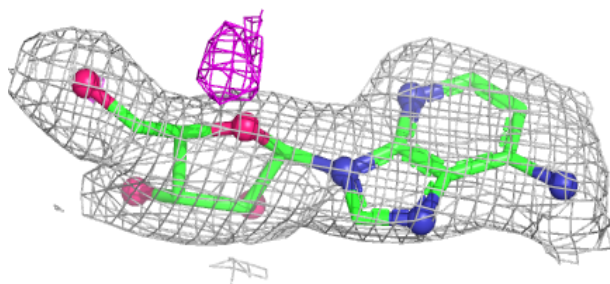
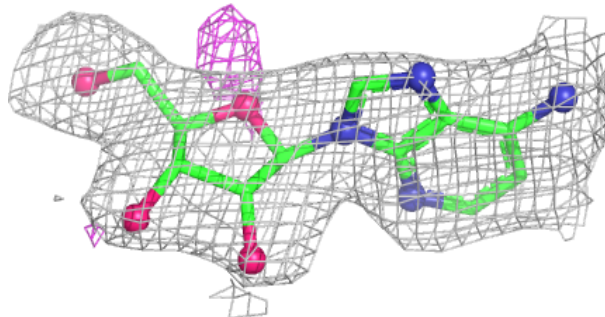


Electron density around 1DA B 301:

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

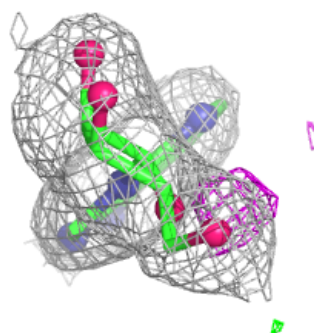
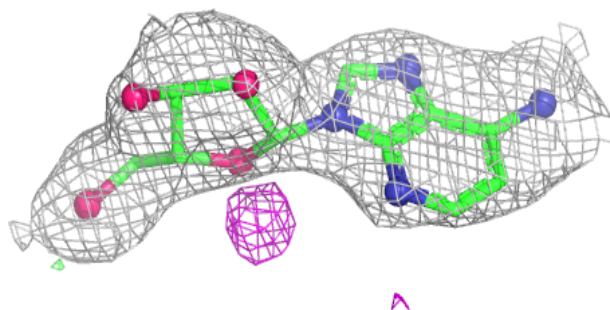
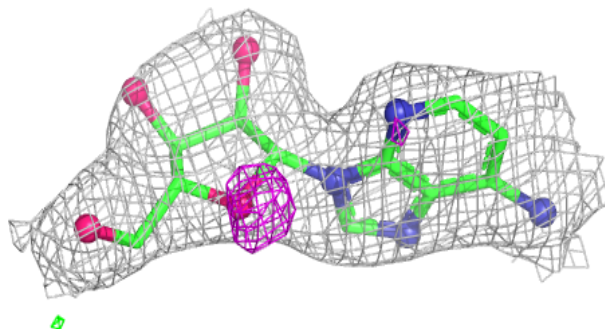
**Electron density around 1DA E 301:**

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

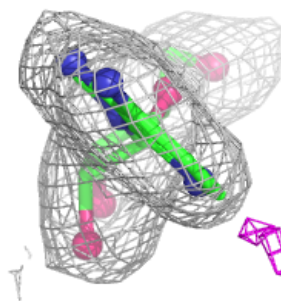
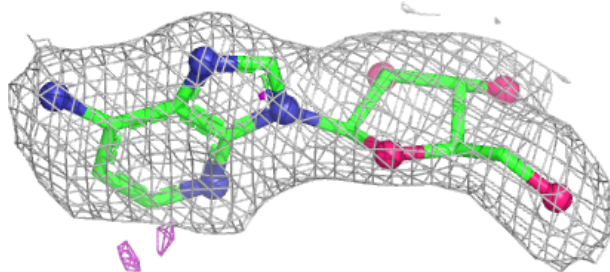
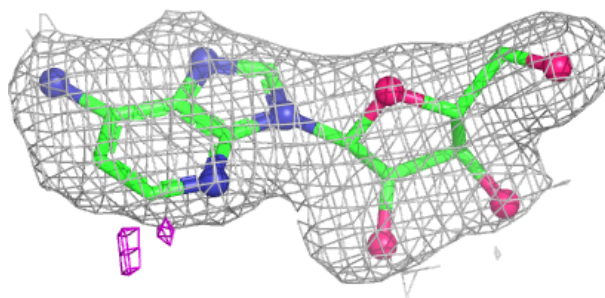


Electron density around 1DA F 301:

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

**Electron density around 1DA 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.