Full wwPDB X-ray Structure Validation Report (i)

Dec 2, 2024 – 06:05 PM EST

PDB ID	:	9D79
Title	:	OXA-58-NA-1-157 1.5 min complex
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Deposited on	:	2024-08-16
Resolution	:	1.90 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:

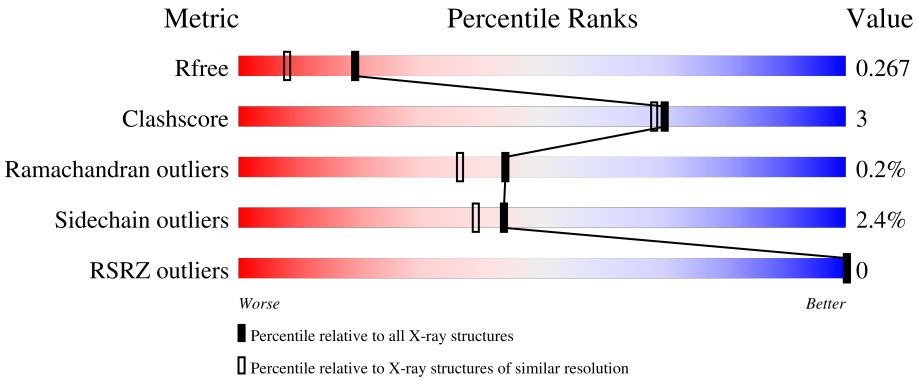
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

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 1.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	7293 (1.90-1.90)
Clashscore	180529	8090 (1.90-1.90)
Ramachandran outliers	177936	8022 (1.90-1.90)
Sidechain outliers	177891	8022 (1.90-1.90)
RSRZ outliers	164620	7292 (1.90-1.90)

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	280	77% 9% • 13%
1	B	280	80% 6% 13%
1	C	280	79% 8% 13%
1	D	280	74% 12% • 12%

2 Entry composition

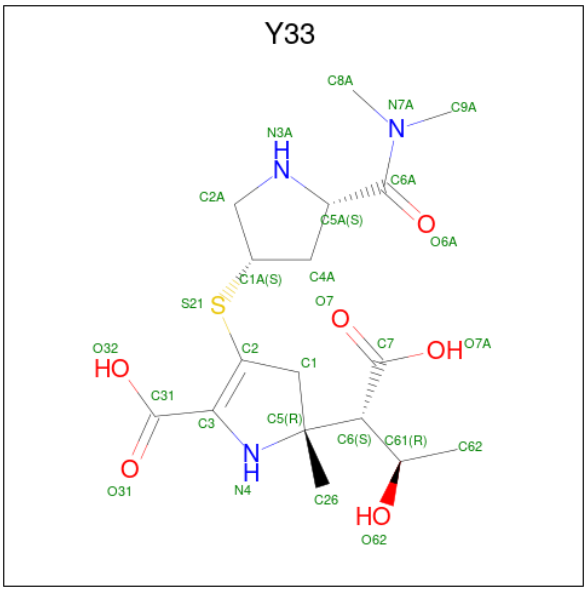
There are 4 unique types of molecules in this entry. The entry contains 8080 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Beta-lactamase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	243	Total	C	N	O	S	0	2	0
			1951	1257	325	362	7			
1	B	243	Total	C	N	O	S	0	1	0
			1946	1254	325	360	7			
1	C	243	Total	C	N	O	S	0	0	0
			1940	1250	325	358	7			
1	D	245	Total	C	N	O	S	0	0	0
			1956	1258	329	362	7			

- Molecule 2 is (5R)-3-{[(3S,5S)-5-(dimethylcarbamoyl)pyrrolidin-3-yl]sulfanyl}-5-[(2S,3R)-3-hydroxy-1-oxobutan-2-yl]-5-methyl-4,5-dihydro-1H-pyrrole-2-carboxylic acid (three-letter code: Y33) (formula: $C_{17}H_{27}N_3O_6S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			26	17	3	5	1		

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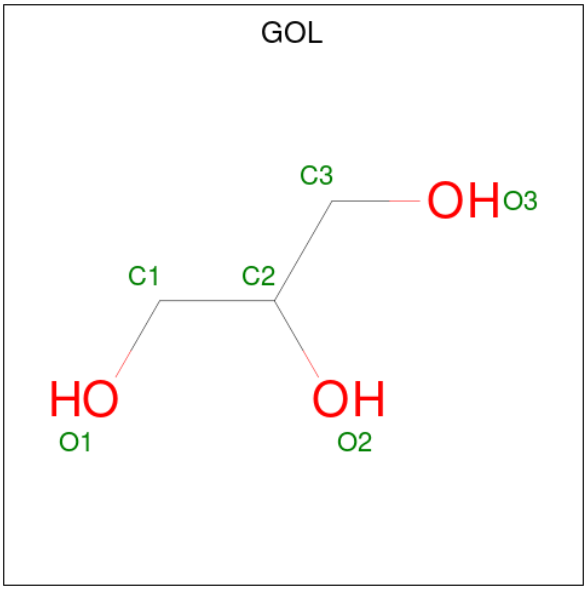
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	S	0	0
			26	17	3	5	1		
2	C	1	Total	C	N	O	S	0	0
			26	17	3	5	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 4 is water.

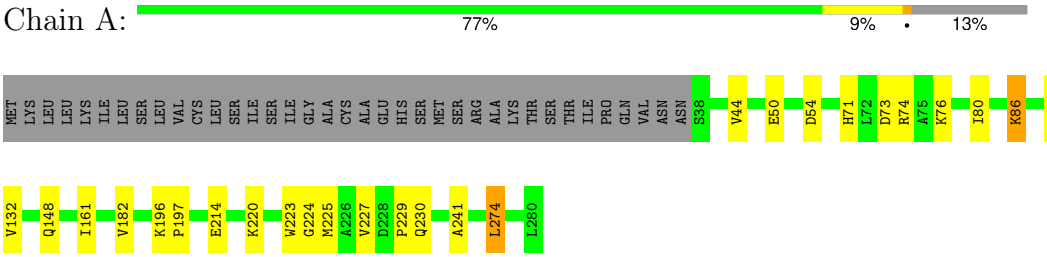
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	40	Total	O	0	1
			41	41		
4	B	57	Total	O	0	2
			59	59		
4	C	76	Total	O	0	2
			78	78		
4	D	25	Total	O	0	0
			25	25		

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.

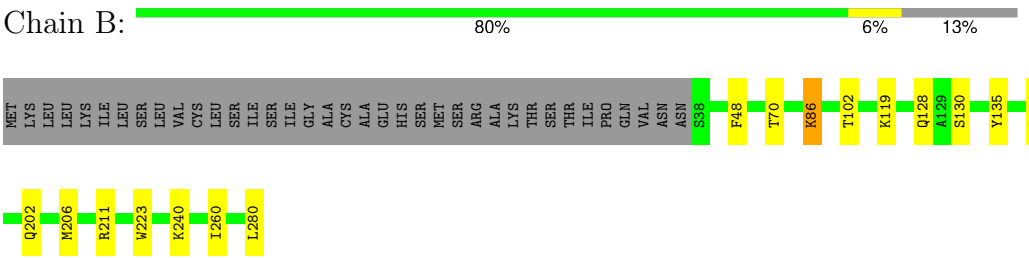
• Molecule 1: Beta-lactamase

Chain A:



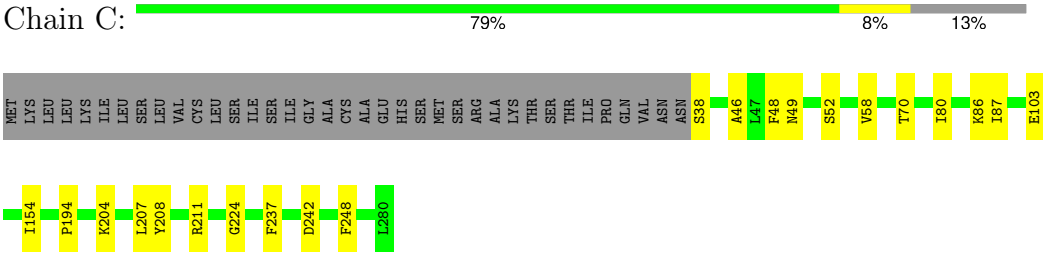
• Molecule 1: Beta-lactamase

Chain B:



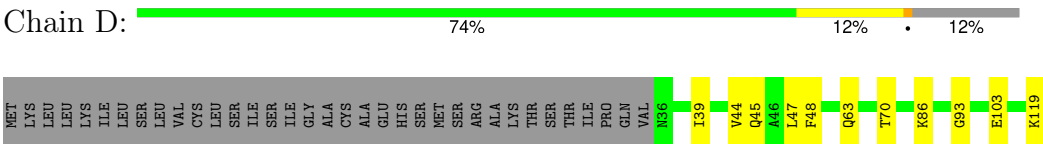
• Molecule 1: Beta-lactamase

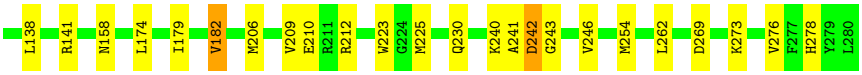
Chain C:



• Molecule 1: Beta-lactamase

Chain D:




L138
R141
N158
L174
I179
V182
M206
V209
E210
R211
R212
W223
G224
M225
Q230
K240
A241
D242
G243
V246
M254
L262
D269
K273
V276
F277
H278
Y279
L280

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	37.08Å 66.58Å 193.16Å 90.00° 91.13° 90.00°	Depositor
Resolution (Å)	39.09 – 1.90 39.09 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.8 (39.09-1.90) 98.9 (39.09-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.43 (at 1.89Å)	Xtriage
Refinement program	PHENIX (1.21.1_5286: ???)	Depositor
R, R_{free}	0.221 , 0.267 0.221 , 0.267	Depositor DCC
R_{free} test set	3659 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	26.0	Xtriage
Anisotropy	0.557	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 26.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.076 for h,-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	8080	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.33% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: KCX, Y33, GOL

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	0.41	0/1988	0.58	1/2687 (0.0%)
1	B	0.44	0/1980	0.59	0/2676
1	C	0.50	0/1971	0.64	1/2664 (0.0%)
1	D	0.37	0/1987	0.61	1/2686 (0.0%)
All	All	0.43	0/7926	0.60	3/10713 (0.0%)

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

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	242	ASP	CB-CA-C	7.06	124.52	110.40
1	C	109	GLY	C-N-CA	-5.81	107.18	121.70
1	A	274	LEU	CA-CB-CG	5.06	126.94	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	211	ARG	Sidechain

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	1951	0	1933	17	0
1	B	1946	0	1929	7	0
1	C	1940	0	1923	11	0
1	D	1956	0	1936	18	0
2	A	26	0	0	1	0
2	B	26	0	0	0	0
2	C	26	0	0	0	0
3	B	6	0	8	0	0
4	A	41	0	0	0	0
4	B	59	0	0	1	0
4	C	78	0	0	1	0
4	D	25	0	0	1	0
All	All	8080	0	7729	52	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (52) 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:44:VAL:HG21	1:A:274:LEU:HD12	1.72	0.71
1:D:209:VAL:HG12	1:D:210:GLU:HG2	1.83	0.60
1:A:54[B]:ASP:CG	1:A:74:ARG:HD2	2.23	0.59
1:C:137:GLU:HG3	4:C:469:HOH:O	2.04	0.56
1:D:39:ILE:HD11	4:D:315:HOH:O	2.05	0.55
1:A:54[B]:ASP:OD1	1:A:71:HIS:HB3	2.05	0.55
1:A:54[B]:ASP:OD1	1:A:74:ARG:HD2	2.08	0.54
1:C:87:ILE:CD1	1:C:207:LEU:HD21	2.39	0.53
1:A:214:GLU:HB3	1:A:241:ALA:HB2	1.89	0.53
1:A:225:MET:HA	1:A:230:GLN:HG2	1.91	0.53
1:D:103:GLU:CD	1:D:141:ARG:HH12	2.12	0.52
1:A:196:LYS:HE3	1:A:197:PRO:HD2	1.93	0.50
1:D:223:TRP:HE1	1:D:230:GLN:NE2	2.10	0.50
1:B:154:ILE:HG22	1:B:194:PRO:HG2	1.93	0.49
1:D:93:GLY:HA3	1:D:138:LEU:HD11	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:269:ASP:O	1:D:273:LYS:HG2	2.13	0.48
1:D:48:PHE:HB3	1:D:70:THR:HG23	1.95	0.48
1:D:212:ARG:NH1	1:D:278:HIS:O	2.46	0.48
1:A:73:ASP:O	1:A:76:LYS:HG2	2.14	0.48
1:C:87:ILE:HD11	1:C:207:LEU:HD21	1.95	0.48
1:D:124:GLY:HA2	1:D:206:MET:HG2	1.95	0.47
1:B:128:GLN:NE2	4:B:401:HOH:O	2.29	0.46
1:C:154:ILE:HG22	1:C:194:PRO:HG2	1.98	0.46
1:D:44:VAL:HG22	1:D:273:LYS:HB2	1.97	0.46
1:C:46:ALA:HA	1:C:49:ASN:ND2	2.31	0.46
1:C:204:LYS:HG3	1:C:237:PHE:HZ	1.81	0.45
1:D:47:LEU:HD21	1:D:273:LYS:HE2	1.98	0.45
1:D:230:GLN:HG3	1:D:254:MET:HB2	1.97	0.45
1:A:223:TRP:O	2:A:301:Y33:O62	2.35	0.45
1:B:86:KCX:HG3	1:B:135:TYR:CD2	2.52	0.45
1:D:179:ILE:O	1:D:182:VAL:HG12	2.17	0.45
1:A:86:KCX:CX	1:A:132:VAL:HG22	2.47	0.44
1:A:44:VAL:HG21	1:A:274:LEU:CD1	2.46	0.44
1:B:48:PHE:HB3	1:B:70:THR:HG23	2.00	0.43
1:D:47:LEU:HD11	1:D:273:LYS:HG3	2.00	0.43
1:C:208:TYR:OH	1:C:211:ARG:HB2	2.17	0.43
1:C:48:PHE:HB3	1:C:70:THR:HG23	2.01	0.43
1:D:246:VAL:HG11	1:D:276:VAL:HG21	2.00	0.43
1:D:45:GLN:HA	1:D:45:GLN:OE1	2.19	0.43
1:A:227:VAL:HG23	1:A:229:PRO:O	2.20	0.42
1:A:119:LYS:HE3	1:A:119:LYS:HB2	1.68	0.42
1:B:280:LEU:HD22	1:B:280:LEU:H	1.84	0.42
1:B:223:TRP:HZ3	1:B:260:ILE:HD13	1.85	0.42
1:C:87:ILE:N	1:C:87:ILE:HD13	2.35	0.41
1:A:80:ILE:HD11	1:A:224:GLY:HA3	2.01	0.41
1:C:80:ILE:HD11	1:C:224:GLY:HA3	2.02	0.41
1:D:158:ASN:OD1	1:D:174:LEU:HD12	2.20	0.41
1:B:202:GLN:O	1:B:206:MET:HG3	2.21	0.41
1:A:123:LEU:HD23	1:A:123:LEU:HA	1.85	0.41
1:A:148:GLN:OE1	1:A:161:ILE:HG12	2.20	0.41
1:C:58:VAL:O	1:C:248:PHE:HA	2.20	0.40
1:A:76:LYS:HD2	1:D:63:GLN:HG3	2.01	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	242/280 (86%)	238 (98%)	4 (2%)	0	100 100
1	B	241/280 (86%)	234 (97%)	7 (3%)	0	100 100
1	C	240/280 (86%)	236 (98%)	4 (2%)	0	100 100
1	D	242/280 (86%)	233 (96%)	7 (3%)	2 (1%)	16 8
All	All	965/1120 (86%)	941 (98%)	22 (2%)	2 (0%)	44 36

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	241	ALA
1	D	243	GLY

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	203/235 (86%)	200 (98%)	3 (2%)	60 59
1	B	202/235 (86%)	197 (98%)	5 (2%)	42 37
1	C	201/235 (86%)	197 (98%)	4 (2%)	50 47
1	D	203/235 (86%)	196 (97%)	7 (3%)	32 25
All	All	809/940 (86%)	790 (98%)	19 (2%)	44 41

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	GLU
1	A	182	VAL
1	A	220	LYS
1	B	102	THR
1	B	119	LYS
1	B	130	SER
1	B	171	LYS
1	B	240	LYS
1	C	38	SER
1	C	52	SER
1	C	103	GLU
1	C	242	ASP
1	D	119	LYS
1	D	122	THR
1	D	182	VAL
1	D	225	MET
1	D	240	LYS
1	D	242	ASP
1	D	262	LEU

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

Mol	Chain	Res	Type
1	A	202	GLN
1	B	201	GLN
1	B	265	GLN
1	C	128	GLN
1	C	152	GLN
1	C	253	GLN
1	D	63	GLN
1	D	230	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	KCX	C	86	1	10,11,12	1.63	2 (20%)	6,12,14	2.79	1 (16%)
1	KCX	A	86	1	10,11,12	1.66	2 (20%)	6,12,14	2.46	2 (33%)
1	KCX	B	86	1	10,11,12	1.76	2 (20%)	6,12,14	2.72	2 (33%)
1	KCX	D	86	1	10,11,12	1.69	2 (20%)	6,12,14	3.00	2 (33%)

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
1	KCX	C	86	1	-	1/9/10/12	-
1	KCX	A	86	1	-	1/9/10/12	-
1	KCX	B	86	1	-	1/9/10/12	-
1	KCX	D	86	1	-	2/9/10/12	-

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	86	KCX	CX-NZ	4.57	1.43	1.35
1	D	86	KCX	CX-NZ	4.46	1.43	1.35
1	C	86	KCX	CX-NZ	4.31	1.42	1.35
1	A	86	KCX	CX-NZ	4.23	1.42	1.35
1	B	86	KCX	OQ1-CX	2.68	1.26	1.21
1	A	86	KCX	OQ1-CX	2.51	1.26	1.21
1	D	86	KCX	OQ1-CX	2.31	1.25	1.21
1	C	86	KCX	OQ1-CX	2.08	1.25	1.21

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	86	KCX	OQ1-CX-NZ	-6.52	115.01	124.92
1	D	86	KCX	OQ1-CX-NZ	-6.29	115.36	124.92
1	B	86	KCX	OQ1-CX-NZ	-5.79	116.13	124.92
1	A	86	KCX	OQ1-CX-NZ	-5.16	117.08	124.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	86	KCX	CE-NZ-CX	3.36	127.69	121.98
1	A	86	KCX	CE-NZ-CX	2.79	126.71	121.98
1	B	86	KCX	CE-NZ-CX	2.67	126.51	121.98

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	86	KCX	C-CA-CB-CG
1	B	86	KCX	C-CA-CB-CG
1	C	86	KCX	O-C-CA-CB
1	D	86	KCX	OQ1-CX-NZ-CE
1	D	86	KCX	OQ2-CX-NZ-CE

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	86	KCX	1	0
1	B	86	KCX	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

4 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	Y33	B	301	1	20,27,28	1.61	5 (25%)	20,40,42	1.99	5 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
2	Y33	A	301	1	20,27,28	1.38	2 (10%)	20,40,42	1.55	5 (25%)
3	GOL	B	302	-	5,5,5	0.25	0	5,5,5	0.47	0
2	Y33	C	301	1	20,27,28	1.29	2 (10%)	20,40,42	1.11	2 (10%)

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	Y33	B	301	1	-	8/23/51/53	0/2/2/2
2	Y33	A	301	1	-	9/23/51/53	0/2/2/2
3	GOL	B	302	-	-	0/4/4/4	-
2	Y33	C	301	1	-	8/23/51/53	0/2/2/2

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	Y33	C1A-S21	-3.69	1.77	1.82
2	A	301	Y33	C1A-S21	-3.62	1.77	1.82
2	A	301	Y33	C2-S21	-3.60	1.67	1.74
2	B	301	Y33	C2-S21	-3.58	1.67	1.74
2	C	301	Y33	C1A-S21	-3.57	1.77	1.82
2	C	301	Y33	C2-S21	-3.33	1.68	1.74
2	B	301	Y33	C6-C7	2.66	1.56	1.50
2	B	301	Y33	C3-C31	-2.42	1.44	1.48
2	B	301	Y33	O32-C31	-2.19	1.24	1.30

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	301	Y33	O7-C7-C6	-5.76	109.72	124.67
2	B	301	Y33	C3-C2-S21	4.38	130.41	124.37
2	A	301	Y33	O7-C7-C6	-3.73	114.99	124.67
2	A	301	Y33	C1-C5-N4	3.30	104.81	101.44
2	B	301	Y33	C5A-C6A-N7A	-3.16	114.95	118.53
2	A	301	Y33	C61-C6-C7	2.82	115.81	109.70
2	C	301	Y33	O7-C7-C6	-2.78	117.46	124.67
2	C	301	Y33	O32-C31-C3	2.66	120.95	116.73
2	B	301	Y33	O31-C31-C3	-2.48	115.89	120.20
2	B	301	Y33	O6A-C6A-C5A	2.13	123.51	119.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	301	Y33	O32-C31-C3	2.11	120.07	116.73
2	A	301	Y33	O31-C31-C3	-2.01	116.70	120.20

There are no chirality outliers.

All (25) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	Y33	C2-C3-C31-O31
2	A	301	Y33	C2-C3-C31-O32
2	A	301	Y33	N4-C3-C31-O31
2	A	301	Y33	N4-C3-C31-O32
2	A	301	Y33	C7-C6-C61-C62
2	A	301	Y33	C2A-C1A-S21-C2
2	B	301	Y33	C5-C6-C61-C62
2	B	301	Y33	C5-C6-C61-O62
2	B	301	Y33	C7-C6-C61-C62
2	B	301	Y33	C2A-C1A-S21-C2
2	B	301	Y33	C4A-C1A-S21-C2
2	C	301	Y33	C1-C5-C6-C7
2	C	301	Y33	C5-C6-C61-C62
2	C	301	Y33	C2A-C1A-S21-C2
2	A	301	Y33	C7-C6-C61-O62
2	B	301	Y33	C7-C6-C61-O62
2	C	301	Y33	N4-C3-C31-O32
2	C	301	Y33	C2-C3-C31-O31
2	C	301	Y33	N4-C3-C31-O31
2	C	301	Y33	C2-C3-C31-O32
2	A	301	Y33	C4A-C1A-S21-C2
2	C	301	Y33	C4A-C1A-S21-C2
2	A	301	Y33	O6A-C6A-N7A-C8A
2	B	301	Y33	C4A-C5A-C6A-N7A
2	B	301	Y33	C4A-C5A-C6A-O6A

There are no ring outliers.

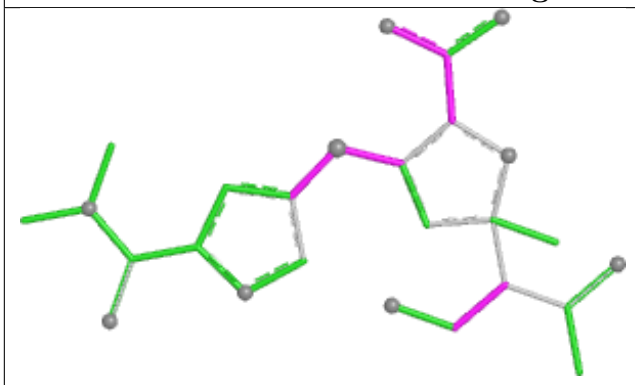
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	Y33	1	0

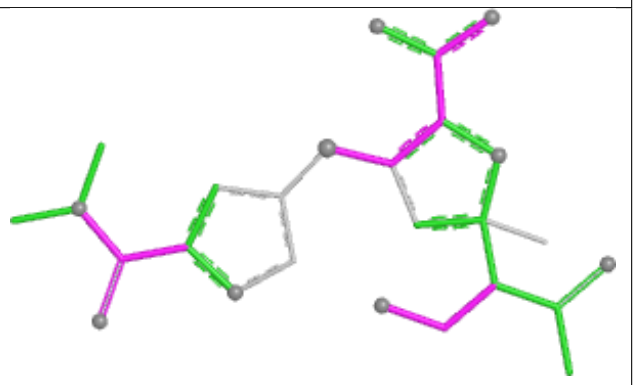
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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.

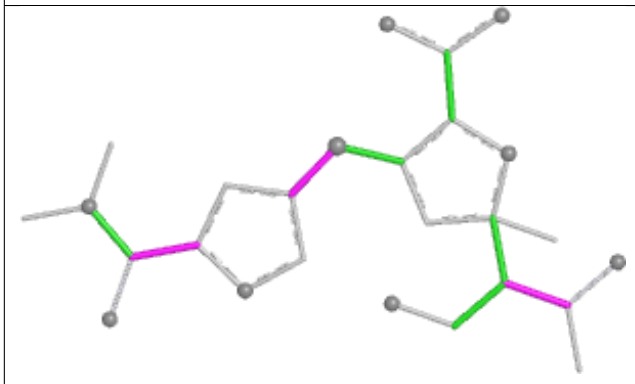
Ligand Y33 B 301



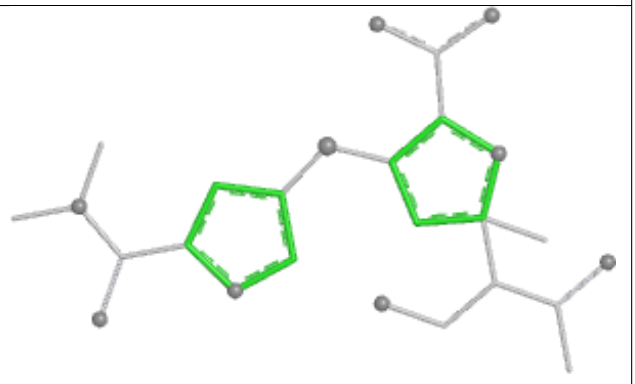
Bond lengths



Bond angles

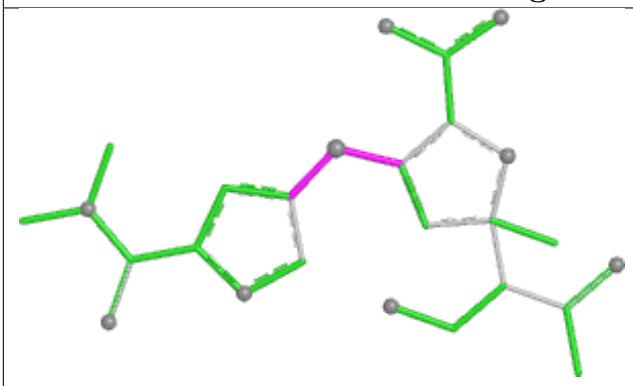


Torsions

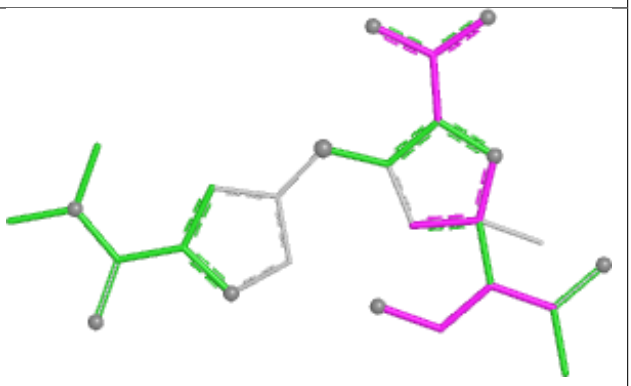


Rings

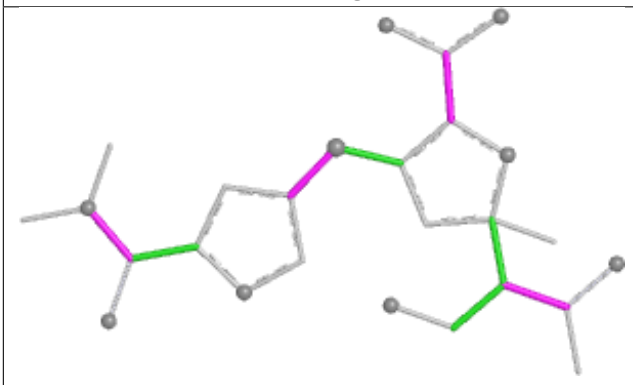
Ligand Y33 A 301



Bond lengths



Bond angles



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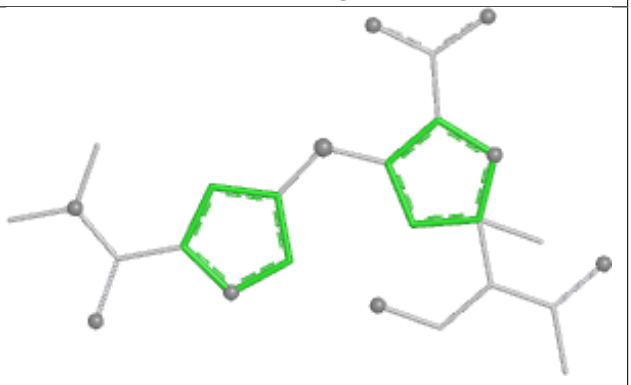
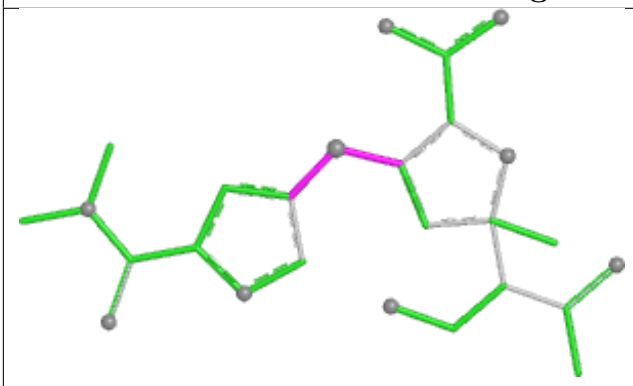
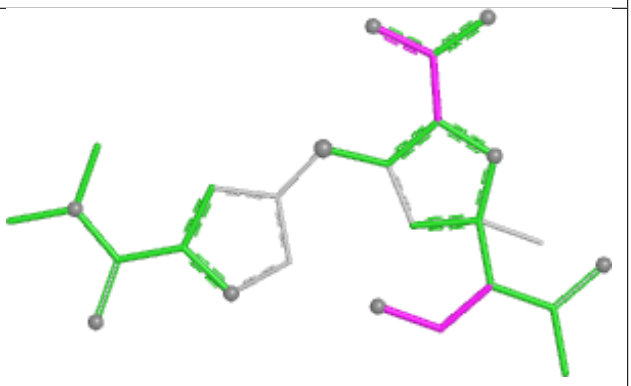


Rings

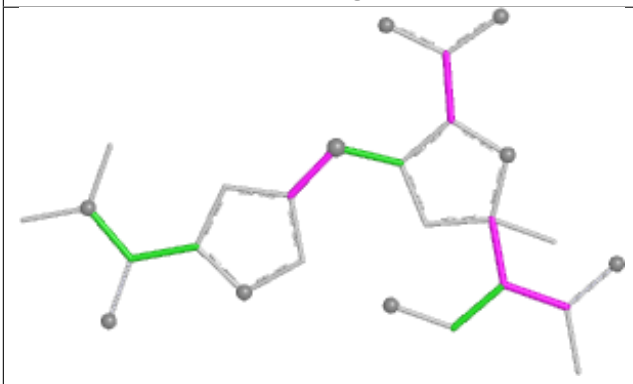
Ligand Y33 C 301



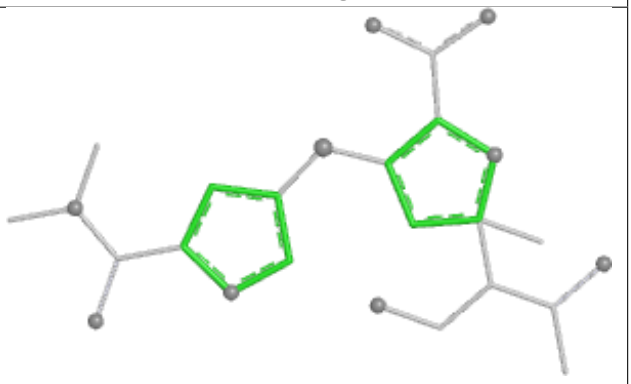
Bond lengths



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	242/280 (86%)	-1.24	0	100	100	20, 30, 50, 80	2 (0%)
1	B	242/280 (86%)	-1.38	0	100	100	15, 25, 40, 69	1 (0%)
1	C	242/280 (86%)	-1.37	0	100	100	17, 26, 42, 59	0
1	D	244/280 (87%)	-1.05	0	100	100	28, 39, 67, 100	0
All	All	970/1120 (86%)	-1.26	0	100	100	15, 30, 52, 100	3 (0%)

There are no RSRZ outliers to report.

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

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
1	KCX	A	86	12/13	0.98	0.04	20,22,25,27	2
1	KCX	C	86	12/13	0.98	0.04	19,22,26,28	2
1	KCX	D	86	12/13	0.98	0.05	28,31,37,39	2
1	KCX	B	86	12/13	0.99	0.04	17,20,24,25	2

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands (i)

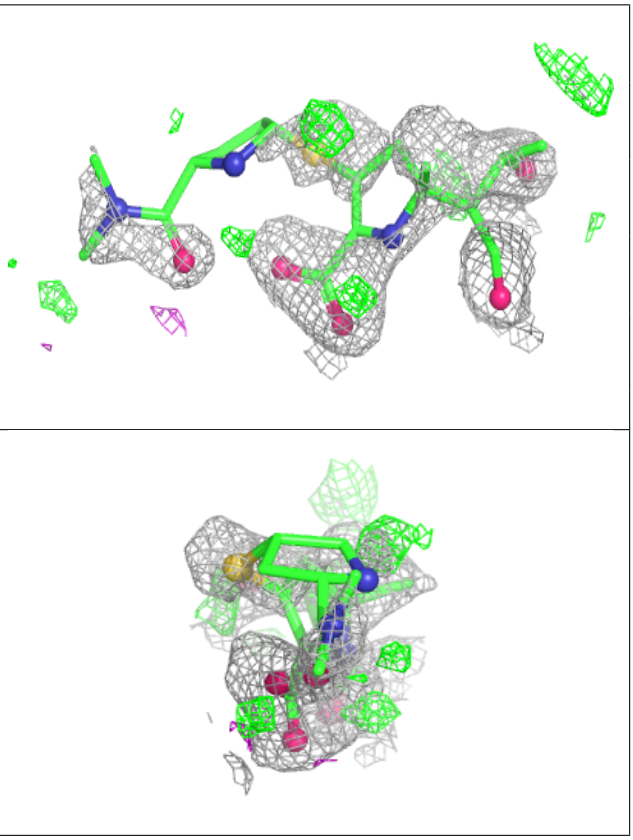
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
2	Y33	A	301	26/27	0.96	0.07	26,35,45,45	26
2	Y33	B	301	26/27	0.96	0.07	20,29,39,41	26
2	Y33	C	301	26/27	0.97	0.08	24,32,37,38	26
3	GOL	B	302	6/6	0.97	0.05	31,36,40,43	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 Y33 A 301:

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



Electron density around Y33 B 301:

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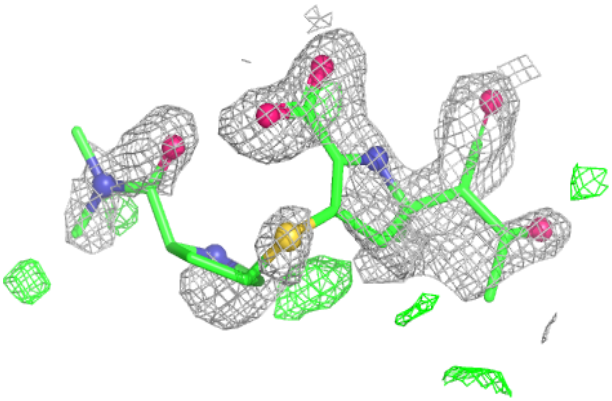
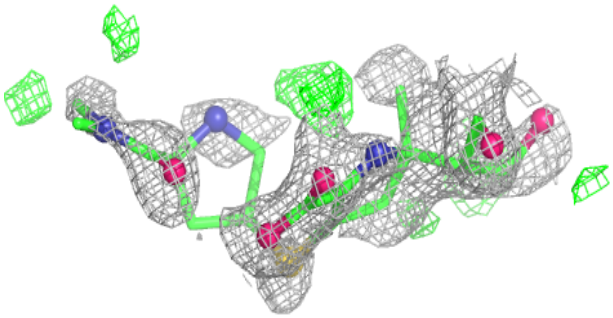
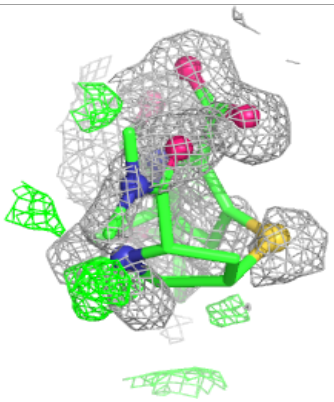
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

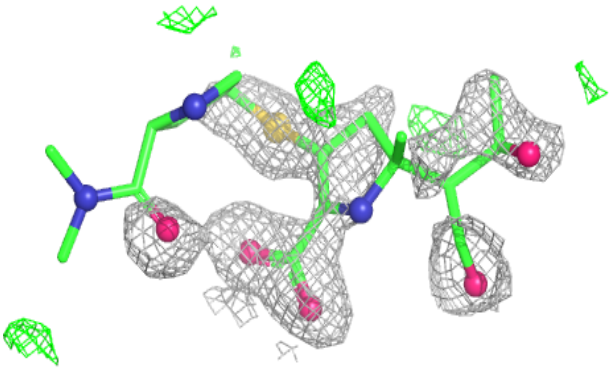


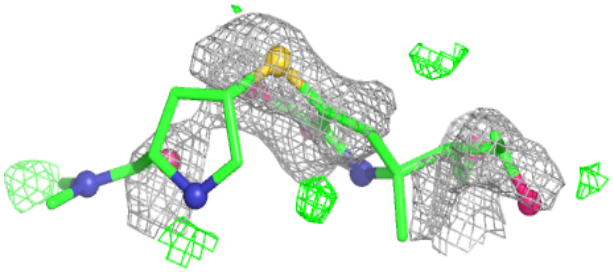


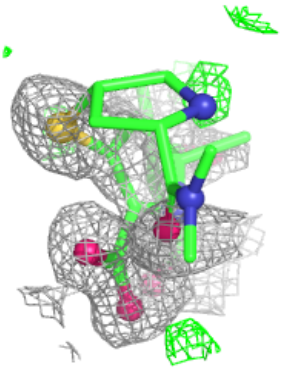


Electron density around Y33 C 301:

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







6.5 Other polymers (i)

There are no such residues in this entry.