



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 11:16 PM UTC

PDB ID : 3QVI / pdb_00003qvi
Title : Crystal structure of KNI-10395 bound histo-aspartic protease (HAP) from Plasmodium falciparum
Authors : Bhaumik, P.; Gustchina, A.; Wlodawer, A.
Deposited on : 2011-02-25
Resolution : 2.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

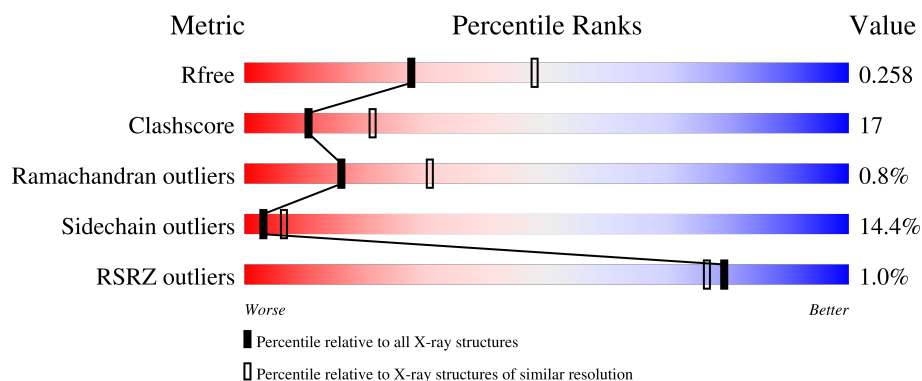
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	451	46%18%7%•28%
1	B	451	% 47%21%5%27%
1	C	451	% 47%21%• •27%
1	D	451	45%22%• •27%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

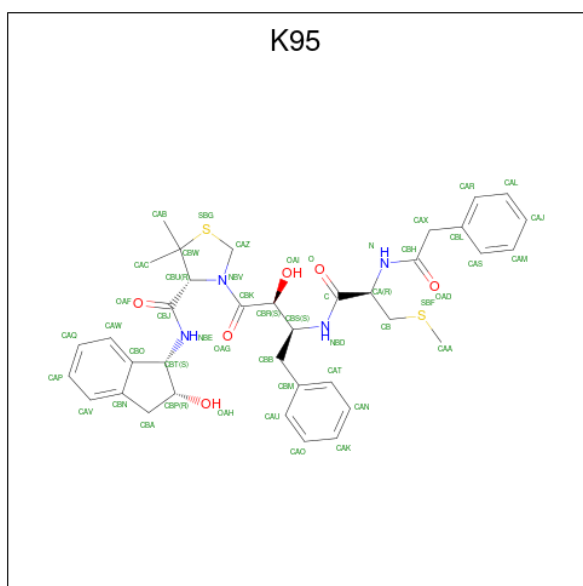
Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	EDO	A	331	-	-	X	-
3	EDO	B	329	-	-	X	-
3	EDO	C	331	-	-	X	-
3	EDO	D	330	-	-	X	-
3	EDO	D	332	-	-	X	-
6	PG5	B	330	-	-	X	-

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 Histo-aspartic protease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	323	Total 2599	C 1683	N 400	O 508	S 8	0	7	0
1	B	327	Total 2638	C 1711	N 408	O 511	S 8	0	6	0
1	C	327	Total 2630	C 1704	N 407	O 511	S 8	0	4	0
1	D	327	Total 2655	C 1726	N 410	O 511	S 8	0	9	0

- Molecule 2 is (4R)-N-[(1S,2R)-2-hydroxy-2,3-dihydro-1H-inden-1-yl]-3-[(2S,3S)-2-hydroxy-3-
-{[S-methyl-N-(phenylacetyl)-L-cysteinyl]amino}-4-phenylbutanoyl]-5,5-dimethyl-1,3-thiazolidine-4-carboxamide (CCD ID: K95) (formula: C₃₇H₄₄N₄O₆S₂).



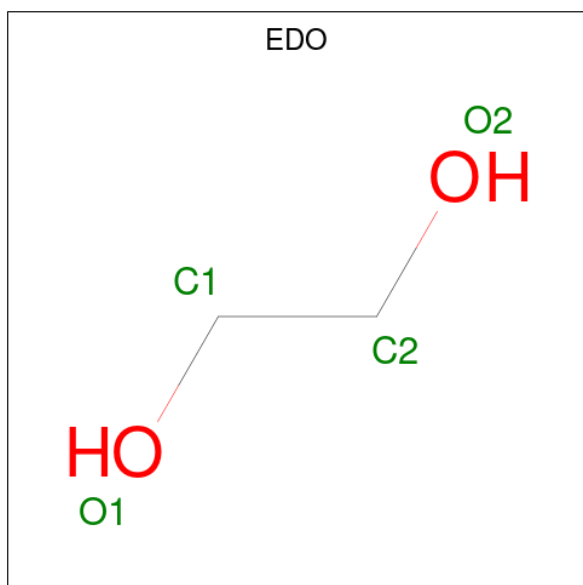
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			49	37	4	6	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	S	0	0
			49	37	4	6	2		
2	C	1	Total	C	N	O	S	0	0
			49	37	4	6	2		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



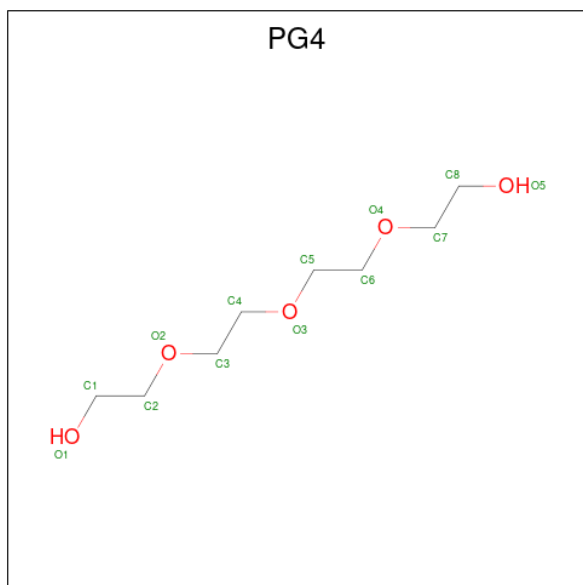
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		

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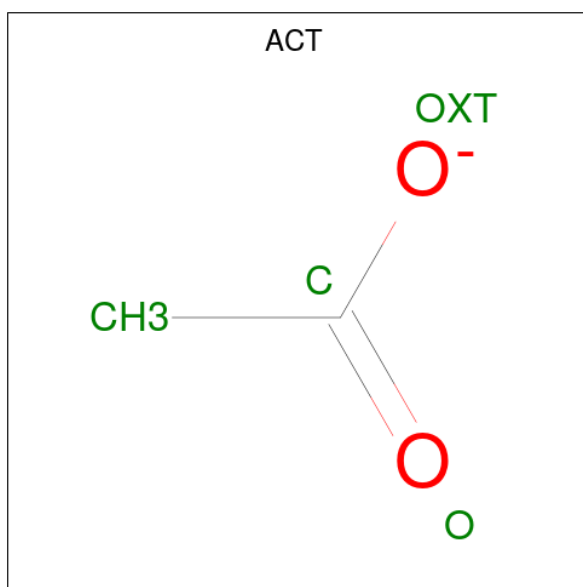
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).



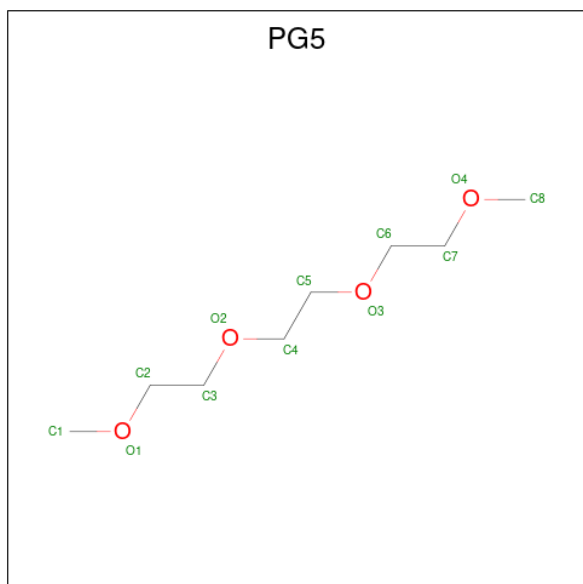
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	8	5		
4	A	1	Total	C	O	0	0
			10	6	4		
4	A	1	Total	C	O	0	0
			10	6	4		
4	D	1	Total	C	O	0	0
			10	6	4		

- Molecule 5 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 6 is 1-METHOXY-2-[2-(2-METHOXY-ETHOXY)]-ETHANE (CCD ID: PG5) (formula: C₈H₁₈O₄).



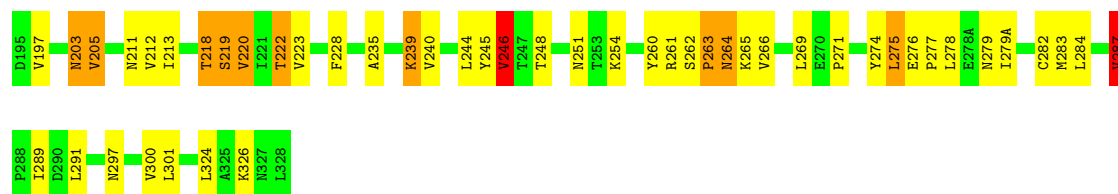
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			12	8	4		

- Molecule 7 is SODIUM ION (CCD ID: NA) (formula: Na).

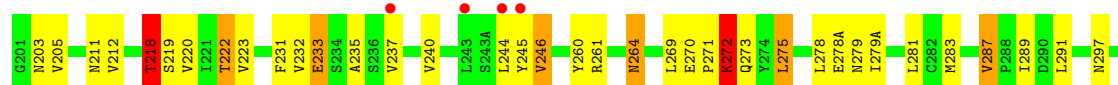
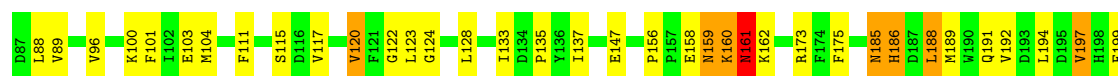
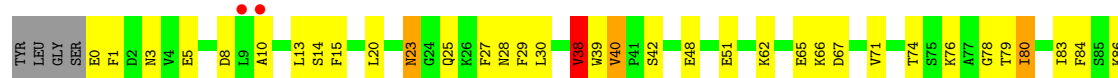
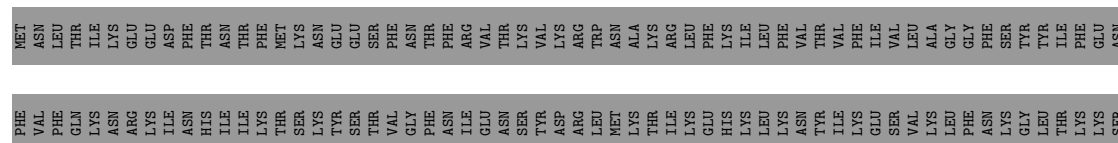
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	D	1	Total 1	Na 1	0	0

- Molecule 8 is water.

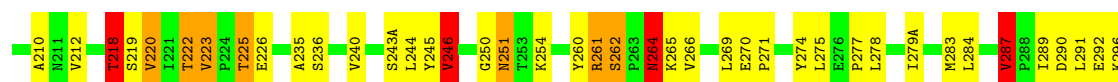
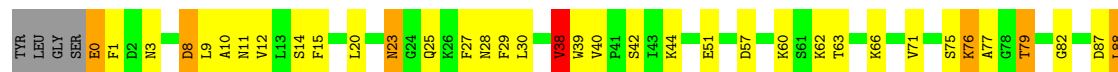
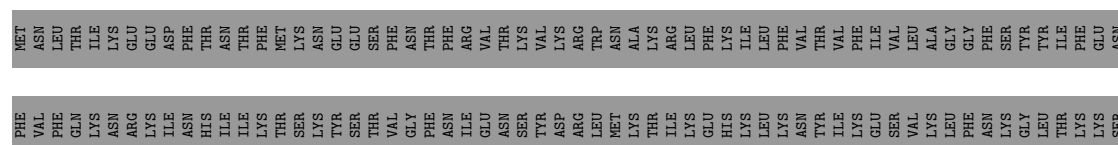
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	138	Total 138	O 138	0	0
8	B	95	Total 95	O 95	0	0
8	C	128	Total 128	O 128	0	0
8	D	147	Total 147	O 147	0	0



• Molecule 1: Histo-aspartic protease



• Molecule 1: Histo-aspartic protease



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	88.43Å 90.51Å 192.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.72 – 2.50 39.72 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (39.72-2.50) 100.0 (39.72-2.50)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.43 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.5.0104	Depositor
R, R_{free}	0.175 , 0.252 0.188 , 0.258	Depositor DCC
R_{free} test set	2712 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	36.5	Xtriage
Anisotropy	0.405	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 43.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.023 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11285	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.38% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NA, ACT, PG5, PG4, EDO, K95

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	1.04	0/2682	1.20	14/3639 (0.4%)
1	B	0.94	4/2722 (0.1%)	1.11	10/3693 (0.3%)
1	C	1.05	2/2704 (0.1%)	1.17	15/3668 (0.4%)
1	D	1.06	3/2748 (0.1%)	1.18	8/3725 (0.2%)
All	All	1.03	9/10856 (0.1%)	1.16	47/14725 (0.3%)

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	C	0	1

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	246	VAL	CA-CB	7.12	1.62	1.54
1	C	300	VAL	CA-CB	6.96	1.63	1.54
1	B	205	VAL	CA-CB	6.29	1.62	1.54
1	D	303	ASP	C-O	-6.21	1.18	1.24
1	B	287	VAL	CA-CB	5.83	1.61	1.54

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	287	VAL	N-CA-C	9.11	118.11	107.73
1	D	246	VAL	N-CA-C	8.07	119.89	108.36
1	C	246	VAL	N-CA-C	7.64	119.28	108.36
1	B	162	LYS	N-CA-C	7.41	120.41	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	287	VAL	N-CA-C	7.20	115.74	107.89

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	159	ASN	Peptide

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	2599	0	2560	94	0
1	B	2638	0	2602	98	1
1	C	2630	0	2588	91	0
1	D	2655	0	2639	100	0
2	A	49	0	44	4	0
2	C	98	0	88	6	0
3	A	12	0	18	4	0
3	B	4	0	6	5	0
3	C	16	0	24	4	0
3	D	16	0	24	13	0
4	A	33	0	44	5	0
4	D	10	0	13	4	0
5	A	4	0	3	0	0
6	B	12	0	18	8	0
7	D	1	0	0	0	0
8	A	138	0	0	19	2
8	B	95	0	0	15	1
8	C	128	0	0	17	0
8	D	147	0	0	19	0
All	All	11285	0	10671	360	2

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 17.

The worst 5 of 360 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)
2:C:330:K95:CAZ	3:D:332:EDO:H21	1.57	1.31
1:D:186[B]:HIS:HE1	8:D:610:HOH:O	1.06	1.28
2:C:330:K95:HAZ	3:D:332:EDO:C2	1.79	1.11
1:C:278:LEU:O	1:D:218:THR:HG22	1.55	1.06
1:B:235:ALA:HB1	1:B:240:VAL:CG1	1.92	1.00

All (2) 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)
8:A:873:HOH:O	8:B:874:HOH:O[4_445]	1.65	0.55
1:B:239:LYS:CE	8:A:397:HOH:O[4_545]	1.82	0.38

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	326/451 (72%)	308 (94%)	15 (5%)	3 (1%)	14	27
1	B	331/451 (73%)	313 (95%)	17 (5%)	1 (0%)	36	55
1	C	329/451 (73%)	312 (95%)	14 (4%)	3 (1%)	14	27
1	D	334/451 (74%)	323 (97%)	8 (2%)	3 (1%)	14	27
All	All	1320/1804 (73%)	1256 (95%)	54 (4%)	10 (1%)	16	31

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	161	ASN
1	C	160	LYS
1	C	161	ASN
1	C	272	LYS
1	D	76	LYS

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	300/414 (72%)	245 (82%)	55 (18%)	2	3
1	B	303/414 (73%)	264 (87%)	39 (13%)	4	9
1	C	301/414 (73%)	263 (87%)	38 (13%)	4	9
1	D	306/414 (74%)	262 (86%)	44 (14%)	3	6
All	All	1210/1656 (73%)	1034 (86%)	176 (14%)	3	6

5 of 176 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	218	THR
1	D	117	VAL
1	C	232	VAL
1	C	291	LEU
1	D	186[A]	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	203	ASN
1	D	159	ASN
1	C	211	ASN
1	C	318	HIS
1	D	251	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 22 ligands modelled in this entry, 1 is monoatomic - leaving 21 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	EDO	C	334	-	3,3,3	0.41	0	2,2,2	0.49	0
4	PG4	A	335	-	9,9,12	0.51	0	8,8,11	0.61	0
3	EDO	A	331	-	3,3,3	0.57	0	2,2,2	0.26	0
3	EDO	D	330	-	3,3,3	0.50	0	2,2,2	0.13	0
5	ACT	A	336	-	3,3,3	0.88	0	3,3,3	1.52	1 (33%)
3	EDO	A	332	-	3,3,3	0.55	0	2,2,2	0.34	0
3	EDO	C	333	-	3,3,3	0.50	0	2,2,2	0.29	0
2	K95	C	330	-	53,53,53	1.77	10 (18%)	66,75,75	1.34	9 (13%)
3	EDO	D	332	-	3,3,3	0.42	0	2,2,2	0.43	0
4	PG4	A	333	-	12,12,12	0.69	0	11,11,11	0.55	0
4	PG4	D	334	-	9,9,12	0.50	0	8,8,11	0.59	0
3	EDO	A	330	-	3,3,3	0.49	0	2,2,2	0.33	0
2	K95	A	329	-	53,53,53	1.65	9 (16%)	66,75,75	1.61	13 (19%)
3	EDO	B	329	-	3,3,3	0.38	0	2,2,2	0.39	0
4	PG4	A	334	-	9,9,12	0.63	0	8,8,11	0.48	0
3	EDO	D	331	-	3,3,3	0.28	0	2,2,2	0.69	0
3	EDO	D	333	-	3,3,3	0.23	0	2,2,2	1.03	0
6	PG5	B	330	-	11,11,11	0.56	0	10,10,10	0.33	0
3	EDO	C	331	-	3,3,3	0.24	0	2,2,2	0.31	0
2	K95	C	329	-	53,53,53	1.55	6 (11%)	66,75,75	1.28	6 (9%)
3	EDO	C	332	-	3,3,3	0.31	0	2,2,2	0.71	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	C	334	-	-	0/1/1/1	-
4	PG4	A	335	-	-	4/7/7/10	-
3	EDO	A	331	-	-	1/1/1/1	-
3	EDO	D	330	-	-	0/1/1/1	-
3	EDO	A	332	-	-	1/1/1/1	-
3	EDO	C	333	-	-	1/1/1/1	-
2	K95	C	330	-	-	8/43/71/71	0/5/5/5
3	EDO	D	332	-	-	1/1/1/1	-
4	PG4	A	333	-	-	6/10/10/10	-
4	PG4	D	334	-	-	5/7/7/10	-
3	EDO	A	330	-	-	0/1/1/1	-
2	K95	A	329	-	-	4/43/71/71	0/5/5/5
3	EDO	B	329	-	-	0/1/1/1	-
4	PG4	A	334	-	-	4/7/7/10	-
3	EDO	D	331	-	-	1/1/1/1	-
3	EDO	D	333	-	-	0/1/1/1	-
6	PG5	B	330	-	-	6/9/9/9	-
3	EDO	C	331	-	-	1/1/1/1	-
2	K95	C	329	-	-	3/43/71/71	0/5/5/5
3	EDO	C	332	-	-	1/1/1/1	-

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	329	K95	CBU-NBV	7.12	1.52	1.46
2	C	330	K95	CBU-NBV	6.59	1.52	1.46
2	C	329	K95	CBU-NBV	5.69	1.51	1.46
2	C	329	K95	CBR-CBS	4.45	1.59	1.54
2	C	330	K95	CBU-CBJ	4.17	1.60	1.53

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	330	K95	OAI-CBR-CBK	4.94	116.01	108.54
2	C	329	K95	CBO-CBT-CBP	4.30	105.62	102.48
2	A	329	K95	CBA-CBP-CBT	-3.83	100.10	103.70
2	A	329	K95	CAX-CBH-N	-3.83	109.92	115.88
2	A	329	K95	CAA-SBF-CB	-3.77	81.46	101.71

There are no chirality outliers.

5 of 47 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	329	K95	CA-CB-SBF-CAA
2	C	329	K95	CA-CB-SBF-CAA
2	C	330	K95	CBM-CBB-CBS-NBD
4	A	335	PG4	O4-C7-C8-O5
6	B	330	PG5	O3-C6-C7-O4

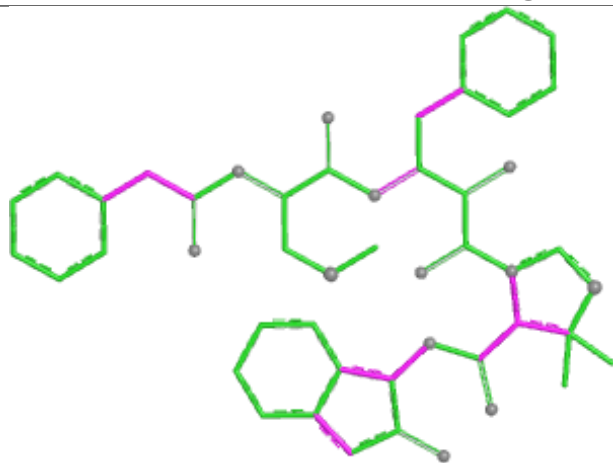
There are no ring outliers.

13 monomers are involved in 44 short contacts:

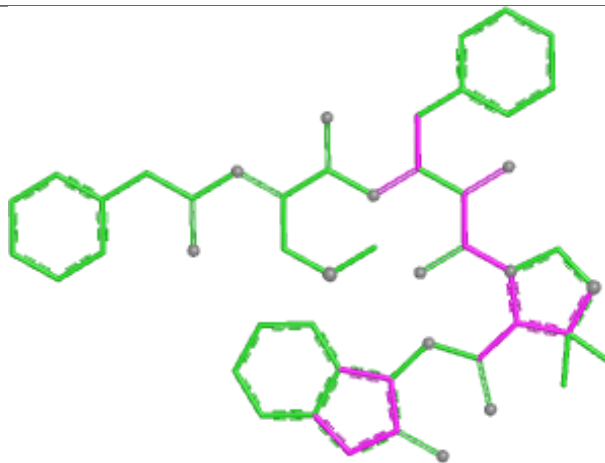
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	335	PG4	2	0
3	A	331	EDO	4	0
3	D	330	EDO	6	0
2	C	330	K95	6	0
3	D	332	EDO	6	0
4	A	333	PG4	2	0
4	D	334	PG4	4	0
2	A	329	K95	4	0
3	B	329	EDO	5	0
4	A	334	PG4	1	0
3	D	331	EDO	1	0
6	B	330	PG5	8	0
3	C	331	EDO	4	0

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.

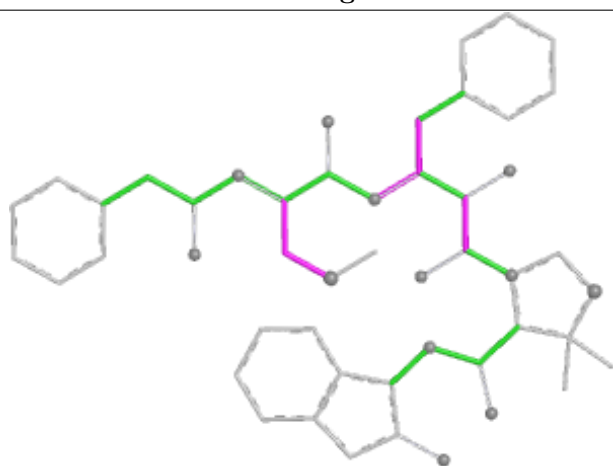
Ligand K95 C 330



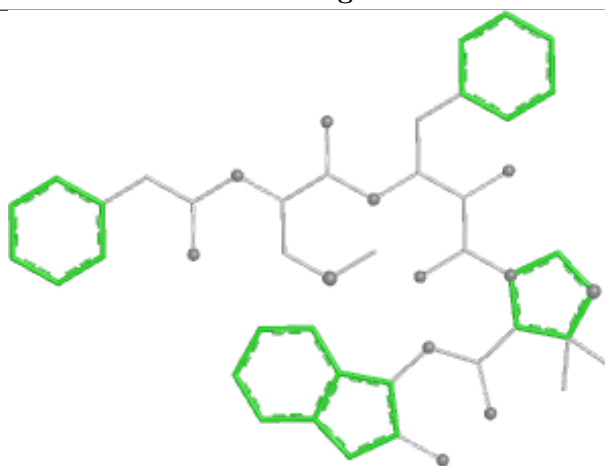
Bond lengths



Bond angles

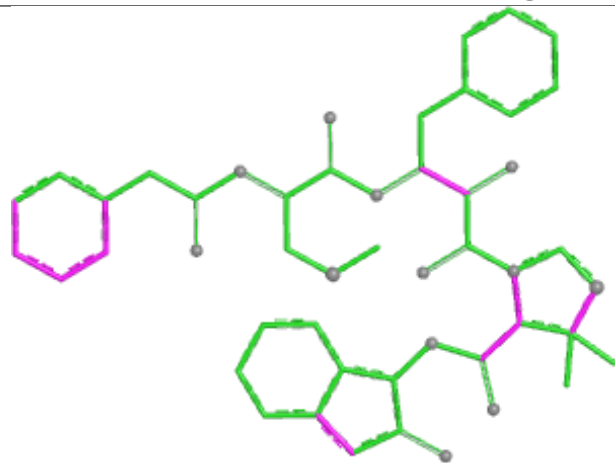


Torsions

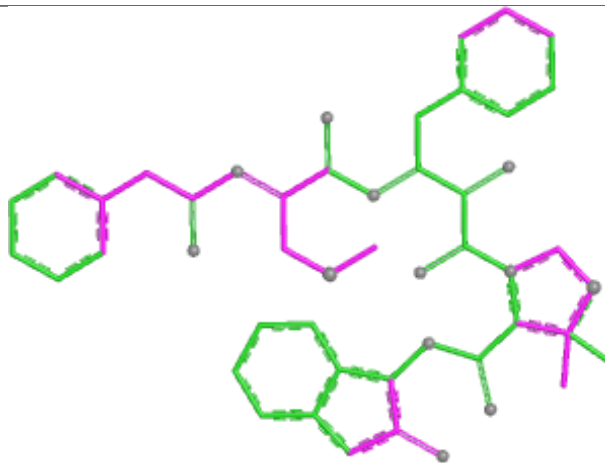


Rings

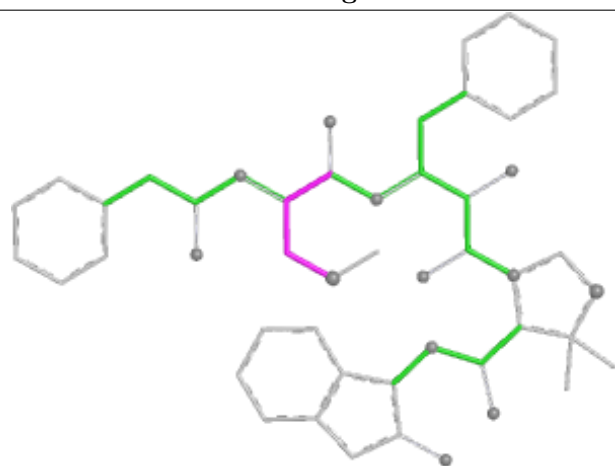
Ligand K95 A 329



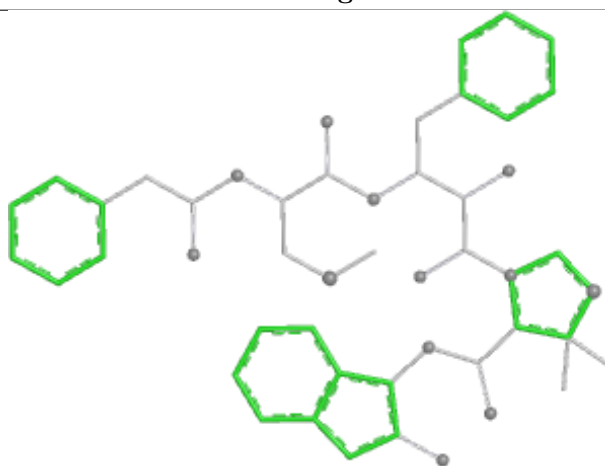
Bond lengths



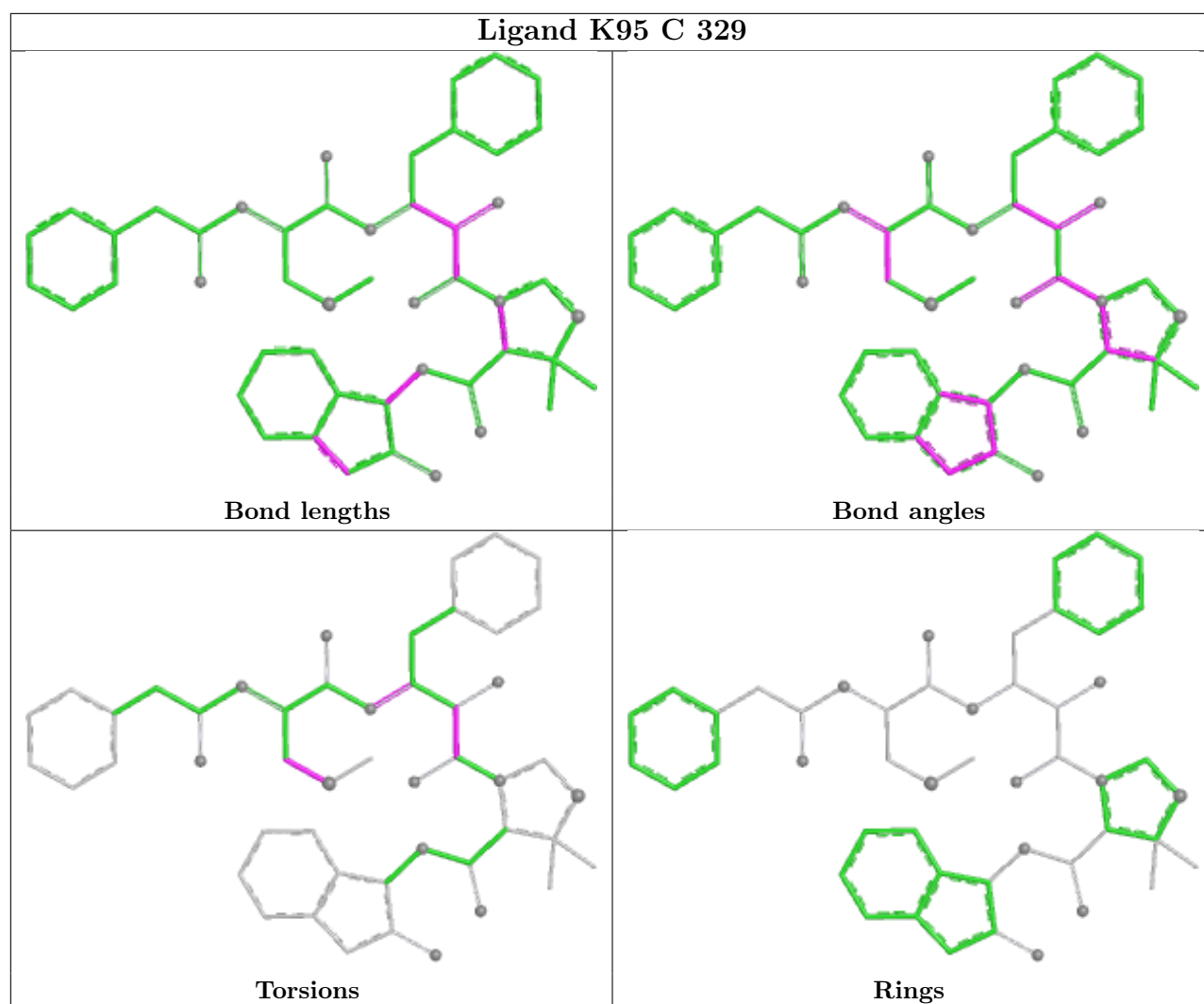
Bond angles



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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	323/451 (71%)	-0.42	2 (0%) 85 83	14, 34, 61, 95	7 (2%)
1	B	327/451 (72%)	0.03	5 (1%) 72 68	15, 53, 85, 97	6 (1%)
1	C	327/451 (72%)	-0.38	6 (1%) 67 64	14, 36, 64, 94	4 (1%)
1	D	327/451 (72%)	-0.53	0 100 100	14, 29, 52, 84	9 (2%)
All	All	1304/1804 (72%)	-0.32	13 (0%) 79 76	14, 35, 77, 97	26 (1%)

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	10	ALA	4.2
1	C	245	TYR	3.6
1	C	244	LEU	3.1
1	A	243	LEU	2.9
1	C	10	ALA	2.4

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](#)

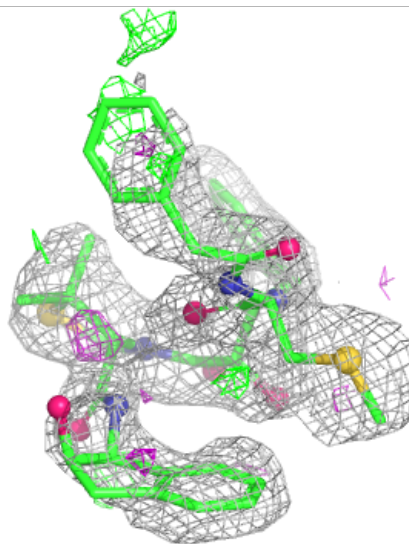
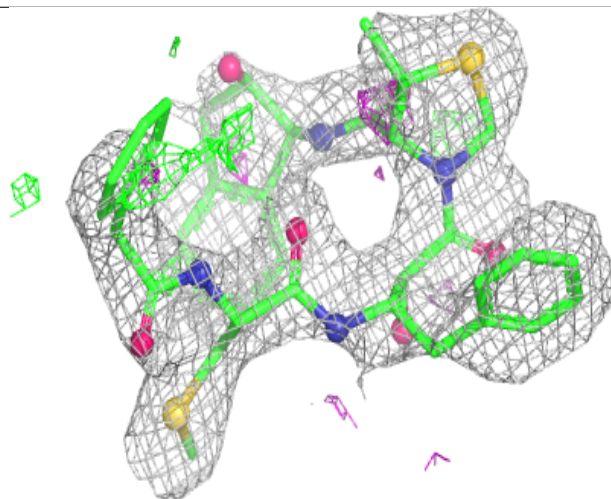
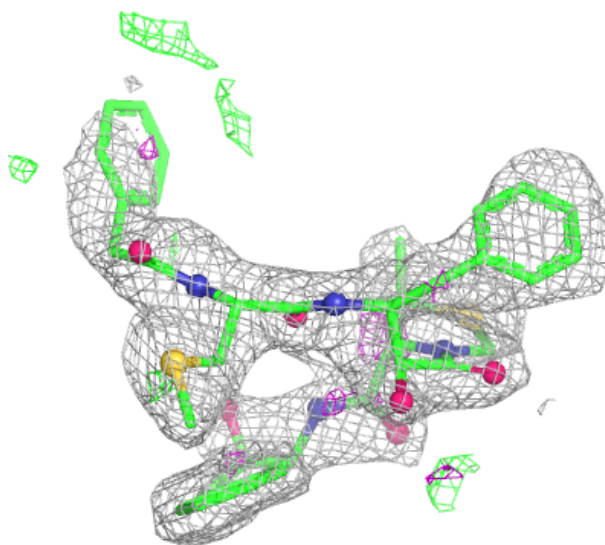
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	ACT	A	336	4/4	0.70	0.17	75,75,75,75	0
4	PG4	A	335	10/13	0.75	0.19	65,75,80,80	0
4	PG4	A	333	13/13	0.81	0.16	67,73,75,76	0
3	EDO	A	331	4/4	0.82	0.16	60,60,60,61	0
6	PG5	B	330	12/12	0.82	0.17	73,75,76,76	0
2	K95	C	330	49/49	0.83	0.14	49,64,73,75	0
4	PG4	D	334	10/13	0.84	0.17	63,65,66,67	0
2	K95	C	329	49/49	0.87	0.13	38,56,65,66	0
4	PG4	A	334	10/13	0.87	0.12	56,60,63,64	0
3	EDO	A	332	4/4	0.88	0.11	44,46,47,49	0
3	EDO	C	332	4/4	0.89	0.10	52,52,53,53	0
3	EDO	C	333	4/4	0.89	0.12	46,46,46,49	0
3	EDO	D	330	4/4	0.90	0.18	37,40,41,41	0
3	EDO	C	334	4/4	0.91	0.13	44,48,52,56	0
3	EDO	D	333	4/4	0.91	0.12	46,47,48,50	0
3	EDO	C	331	4/4	0.92	0.23	31,32,34,36	0
3	EDO	D	332	4/4	0.92	0.16	60,61,61,63	0
3	EDO	A	330	4/4	0.92	0.09	46,46,47,50	0
3	EDO	D	331	4/4	0.93	0.07	50,50,50,52	0
2	K95	A	329	49/49	0.94	0.08	22,35,42,44	0
3	EDO	B	329	4/4	0.94	0.13	37,43,46,48	0
7	NA	D	329	1/1	0.96	0.21	22,22,22,22	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.

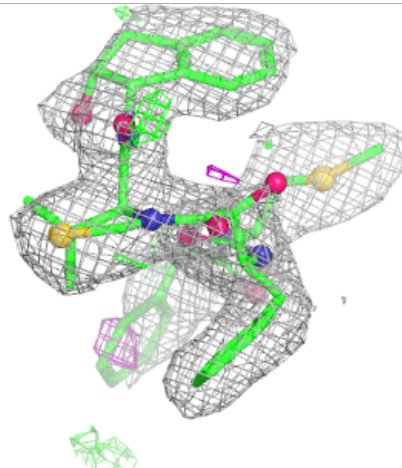
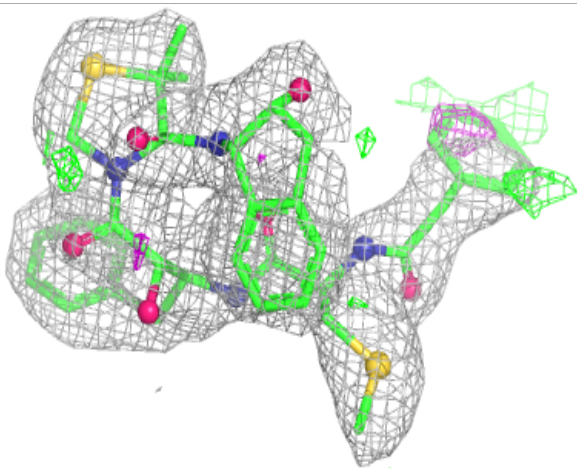
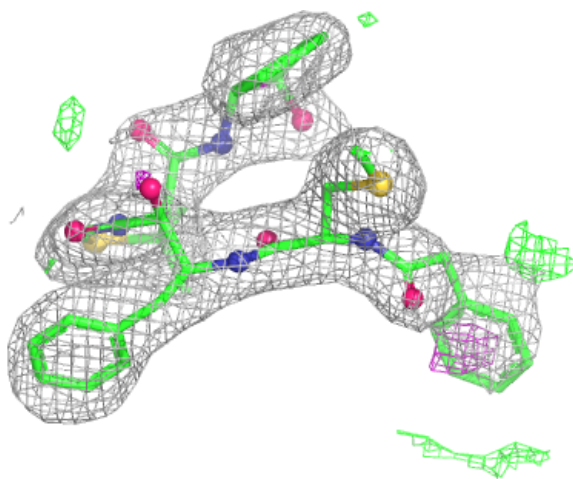
Electron density around K95 C 330:

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



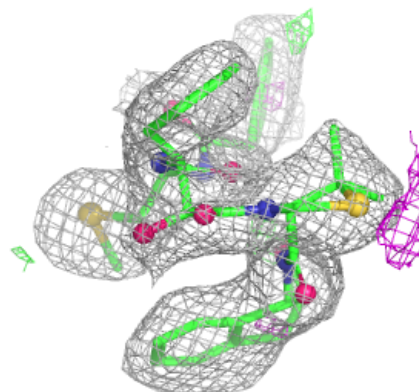
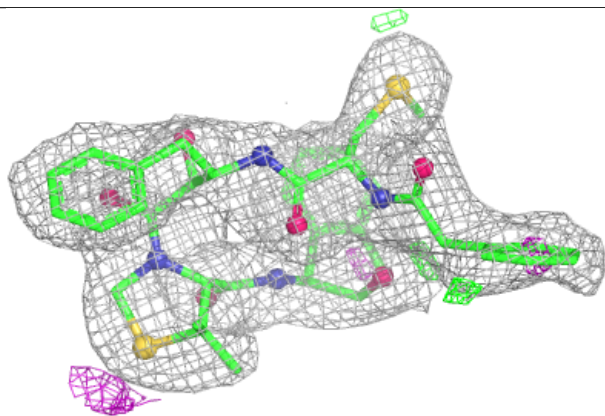
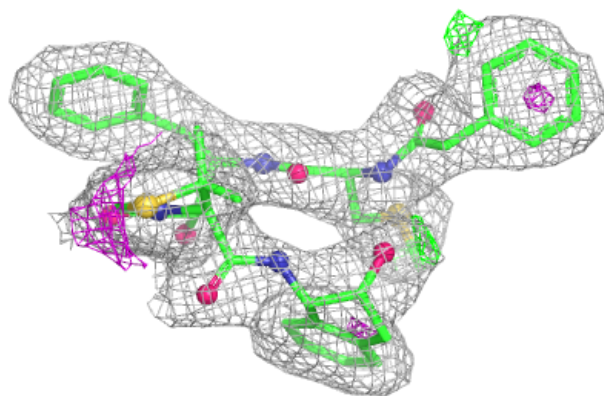
Electron density around K95 C 329:

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



Electron density around K95 A 329:

$2mF_o-DF_c$ (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.