



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 25, 2026 – 07:05 PM UTC

PDB ID : 5L13 / pdb_00005l13
Title : Structure of ALDH2 in complex with 2P3
Authors : Buchman, C.D.; Hurley, T.D.
Deposited on : 2016-07-28
Resolution : 2.40 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

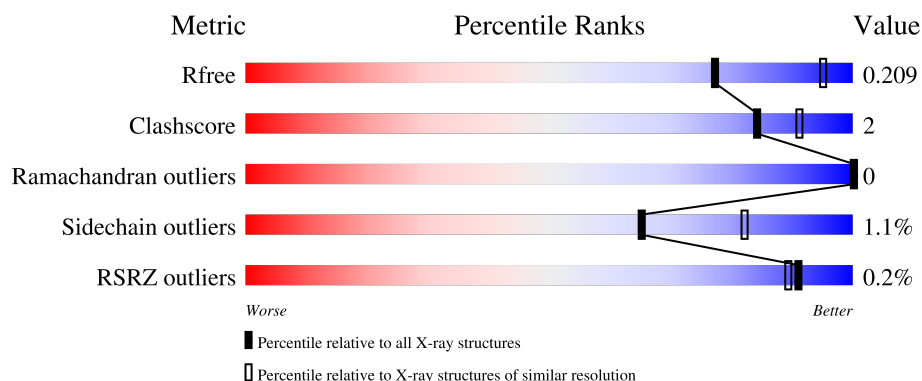
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	517	 91%
1	B	517	 92%
1	C	517	 91%
1	D	517	 91%
1	E	517	 89% 6%

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Mol	Chain	Length	Quality of chain
1	F	517	91%
1	G	517	90%
1	H	517	90%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 32476 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 Aldehyde dehydrogenase, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	494	Total	C	N	O	S	0	1	0
			3804	2419	649	718	18			
1	B	494	Total	C	N	O	S	0	1	0
			3803	2419	648	717	19			
1	C	494	Total	C	N	O	S	0	2	0
			3810	2423	649	719	19			
1	D	494	Total	C	N	O	S	0	3	0
			3816	2427	649	722	18			
1	E	495	Total	C	N	O	S	0	1	0
			3813	2424	651	720	18			
1	F	494	Total	C	N	O	S	0	1	0
			3804	2419	649	718	18			
1	G	494	Total	C	N	O	S	0	3	0
			3818	2428	652	720	18			
1	H	494	Total	C	N	O	S	0	2	0
			3817	2430	652	717	18			

- Molecule 2 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Na	0	0
			1	1		
2	B	1	Total	Na	0	0
			1	1		
2	C	1	Total	Na	0	0
			1	1		
2	D	1	Total	Na	0	0
			1	1		
2	E	1	Total	Na	0	0
			1	1		
2	F	1	Total	Na	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	1	Total	Na	0	0
			1	1		
2	H	1	Total	Na	0	0
			1	1		

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



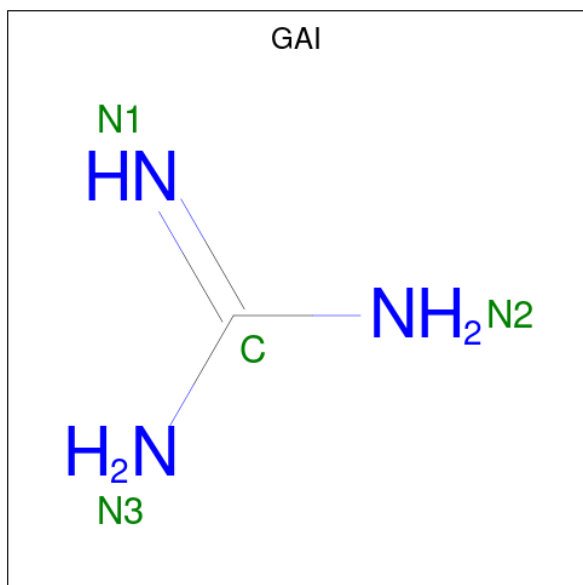
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		
3	E	1	Total	C	O	0	0
			4	2	2		
3	E	1	Total	C	O	0	0
			4	2	2		
3	F	1	Total	C	O	0	0
			4	2	2		
3	F	1	Total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

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

- Molecule 4 is GUANIDINE (CCD ID: GAI) (formula: CH_5N_3).



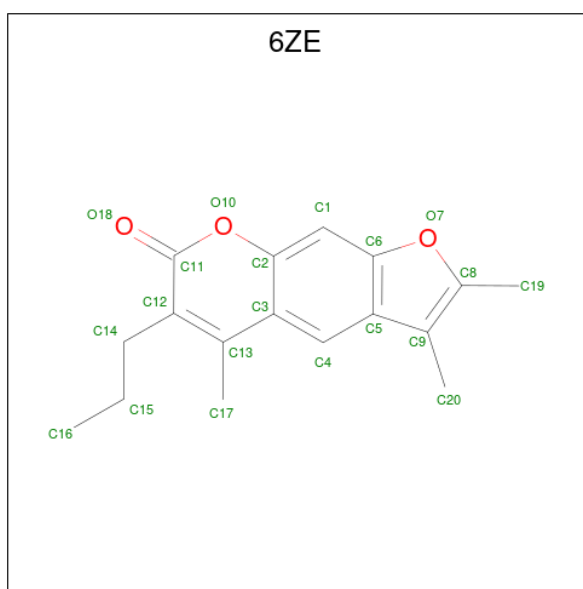
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	N	0	0
			4	1	3		
4	A	1	Total	C	N	0	0
			4	1	3		
4	B	1	Total	C	N	0	0
			4	1	3		
4	C	1	Total	C	N	0	0
			4	1	3		
4	D	1	Total	C	N	0	0
			4	1	3		
4	D	1	Total	C	N	0	0
			4	1	3		
4	D	1	Total	C	N	0	0
			4	1	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	E	1	Total	C	N	0	0
			4	1	3		
4	E	1	Total	C	N	0	0
			4	1	3		
4	E	1	Total	C	N	0	0
			4	1	3		
4	F	1	Total	C	N	0	0
			4	1	3		
4	G	1	Total	C	N	0	0
			4	1	3		
4	G	1	Total	C	N	0	0
			4	1	3		
4	G	1	Total	C	N	0	0
			4	1	3		
4	H	1	Total	C	N	0	0
			4	1	3		

- Molecule 5 is 2,3,5-trimethyl-6-propyl-7H-furo[3,2-g][1]benzopyran-7-one (CCD ID: 6ZE) (formula: C₁₇H₁₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			20	17	3		
5	B	1	Total	C	O	0	0
			20	17	3		
5	C	1	Total	C	O	0	0
			20	17	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	D	1	Total	C	O	0	0
			20	17	3		
5	E	1	Total	C	O	0	0
			20	17	3		
5	F	1	Total	C	O	0	0
			20	17	3		
5	G	1	Total	C	O	0	0
			20	17	3		
5	H	1	Total	C	O	0	0
			20	17	3		

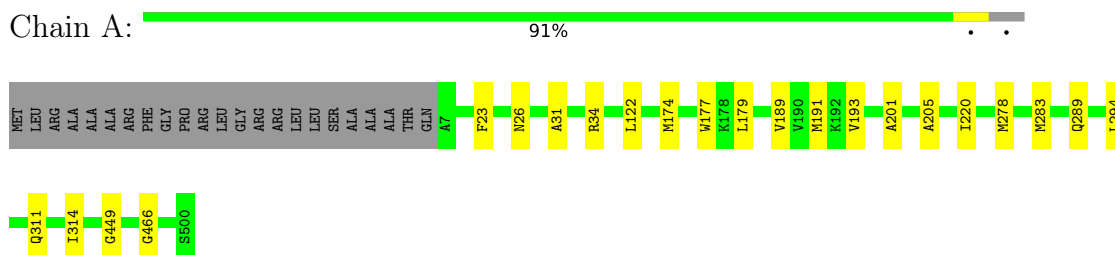
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	273	Total	O	0	0
			273	273		
6	B	244	Total	O	0	0
			244	244		
6	C	261	Total	O	0	0
			261	261		
6	D	279	Total	O	0	0
			279	279		
6	E	202	Total	O	0	0
			202	202		
6	F	148	Total	O	0	0
			148	148		
6	G	138	Total	O	0	0
			138	138		
6	H	166	Total	O	0	0
			166	166		

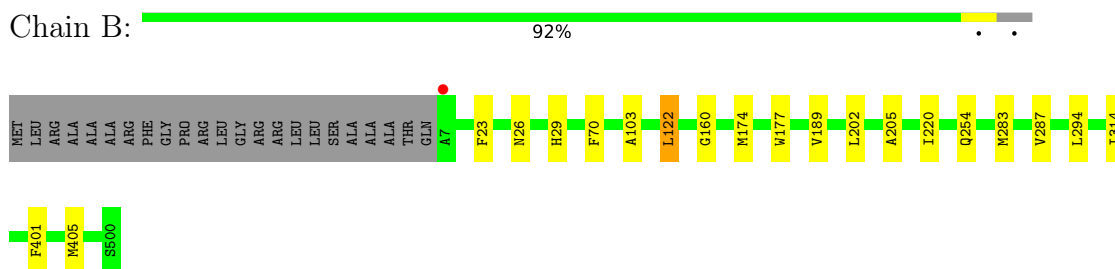
3 Residue-property plots

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.

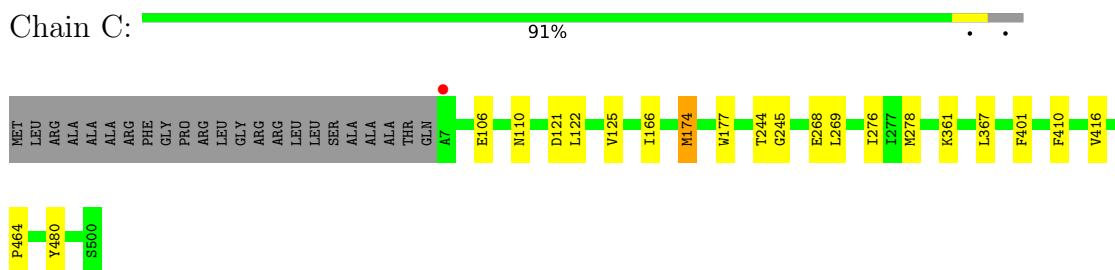
- Molecule 1: Aldehyde dehydrogenase, mitochondrial



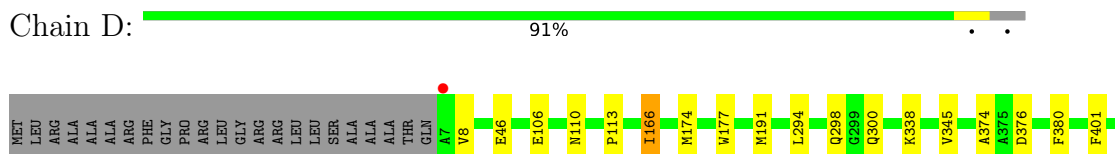
- Molecule 1: Aldehyde dehydrogenase, mitochondrial



- Molecule 1: Aldehyde dehydrogenase, mitochondrial



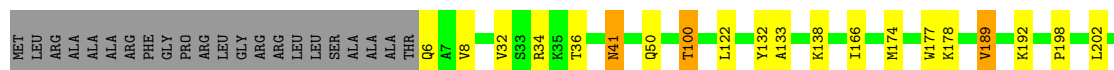
- Molecule 1: Aldehyde dehydrogenase, mitochondrial





- Molecule 1: Aldehyde dehydrogenase, mitochondrial

Chain E: 89% 6% . .



- Molecule 1: Aldehyde dehydrogenase, mitochondrial

Chain F: 91% . .



- Molecule 1: Aldehyde dehydrogenase, mitochondrial

Chain G: 90% 6% .



- Molecule 1: Aldehyde dehydrogenase, mitochondrial

Chain H: 90% 5% .



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	99.41Å 127.05Å 294.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.40 50.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	94.5 (50.00-2.40) 94.5 (50.00-2.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.61 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.155 , 0.206 0.162 , 0.209	Depositor DCC
R_{free} test set	6961 reflections (4.75%)	wwPDB-VP
Wilson B-factor (Å ²)	26.2	Xtriage
Anisotropy	0.081	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 31.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	32476	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.00% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, GAI, 6ZE, NA

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	0.67	0/3891	0.83	0/5279
1	B	0.66	0/3890	0.82	0/5277
1	C	0.67	0/3897	0.84	0/5287
1	D	0.73	1/3909 (0.0%)	0.83	1/5303 (0.0%)
1	E	0.69	0/3900	0.84	1/5291 (0.0%)
1	F	0.69	0/3891	0.84	0/5279
1	G	0.70	0/3911	0.84	0/5305
1	H	0.71	0/3909	0.86	0/5304
All	All	0.69	1/31198 (0.0%)	0.84	2/42325 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	453	VAL	C-O	-5.24	1.18	1.24

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	189	VAL	N-CA-C	5.34	117.56	108.86
1	D	8	VAL	N-CA-C	5.11	112.92	107.76

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3804	0	3753	14	0
1	B	3803	0	3754	12	0
1	C	3810	0	3760	18	0
1	D	3816	0	3765	15	0
1	E	3813	0	3760	26	0
1	F	3804	0	3753	14	0
1	G	3818	0	3772	19	0
1	H	3817	0	3768	22	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	8	0	12	0	0
3	B	8	0	12	0	0
3	D	4	0	6	0	0
3	E	8	0	12	0	0
3	F	8	0	12	0	0
3	G	12	0	18	0	0
4	A	8	0	8	0	0
4	B	4	0	4	0	0
4	C	4	0	4	0	0
4	D	16	0	16	0	0
4	E	12	0	12	0	0
4	F	4	0	4	0	0
4	G	12	0	12	0	0
4	H	4	0	4	0	0
5	A	20	0	0	1	0
5	B	20	0	0	1	0
5	C	20	0	0	0	0
5	D	20	0	0	1	0
5	E	20	0	0	1	0
5	F	20	0	0	1	0
5	G	20	0	0	1	0
5	H	20	0	0	1	0
6	A	273	0	0	3	1
6	B	244	0	0	1	0
6	C	261	0	0	1	0
6	D	279	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	E	202	0	0	3	0
6	F	148	0	0	1	1
6	G	138	0	0	2	0
6	H	166	0	0	0	0
All	All	32476	0	30221	138	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 2.

The worst 5 of 138 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:H:86[B]:ARG:HH21	1:H:86[B]:ARG:CG	1.68	1.07
1:H:86[B]:ARG:HG3	1:H:86[B]:ARG:NH2	1.52	0.94
1:H:86[B]:ARG:HH21	1:H:86[B]:ARG:HG3	0.76	0.85
1:C:174[A]:MET:HE2	1:C:174[A]:MET:HA	1.63	0.80
1:C:276:ILE:HG22	1:C:278:MET:CE	2.12	0.79

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)
6:A:927:HOH:O	6:F:814:HOH:O[1_565]	2.11	0.09

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	493/517 (95%)	478 (97%)	15 (3%)	0	100	100
1	B	493/517 (95%)	474 (96%)	19 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	494/517 (96%)	480 (97%)	14 (3%)	0	100	100
1	D	495/517 (96%)	480 (97%)	15 (3%)	0	100	100
1	E	493/517 (95%)	479 (97%)	14 (3%)	0	100	100
1	F	493/517 (95%)	478 (97%)	15 (3%)	0	100	100
1	G	495/517 (96%)	477 (96%)	18 (4%)	0	100	100
1	H	494/517 (96%)	475 (96%)	19 (4%)	0	100	100
All	All	3950/4136 (96%)	3821 (97%)	129 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	400/414 (97%)	397 (99%)	3 (1%)	73	86
1	B	400/414 (97%)	395 (99%)	5 (1%)	61	80
1	C	401/414 (97%)	397 (99%)	4 (1%)	68	84
1	D	402/414 (97%)	398 (99%)	4 (1%)	68	84
1	E	401/414 (97%)	396 (99%)	5 (1%)	63	81
1	F	400/414 (97%)	394 (98%)	6 (2%)	57	77
1	G	402/414 (97%)	398 (99%)	4 (1%)	68	84
1	H	401/414 (97%)	397 (99%)	4 (1%)	68	84
All	All	3207/3312 (97%)	3172 (99%)	35 (1%)	65	82

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	192	LYS
1	G	268	GLU
1	H	248	GLU
1	D	46	GLU

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Mol	Chain	Res	Type
1	C	401	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	50	GLN
1	H	175	GLN
1	G	164	GLN
1	H	25	ASN
1	C	358	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 44 ligands modelled in this entry, 8 are monoatomic - leaving 36 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	A	603	-	3,3,3	0.32	0	2,2,2	0.51	0
3	EDO	G	603	-	3,3,3	0.45	0	2,2,2	0.39	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	GAI	D	604	-	3,3,3	2.30	1 (33%)	3,3,3	1.32	0
4	GAI	D	605	-	3,3,3	0.89	0	3,3,3	1.30	0
4	GAI	A	604	-	3,3,3	2.19	1 (33%)	3,3,3	1.13	0
5	6ZE	B	605	-	21,22,22	2.84	5 (23%)	27,33,33	2.37	12 (44%)
5	6ZE	D	607	-	21,22,22	2.66	5 (23%)	27,33,33	2.22	12 (44%)
5	6ZE	E	607	-	21,22,22	2.78	5 (23%)	27,33,33	2.11	13 (48%)
4	GAI	G	606	-	3,3,3	2.11	1 (33%)	3,3,3	0.82	0
4	GAI	A	605	-	3,3,3	2.18	1 (33%)	3,3,3	1.15	0
3	EDO	D	602	-	3,3,3	0.38	0	2,2,2	0.77	0
3	EDO	A	602	-	3,3,3	0.46	0	2,2,2	0.21	0
3	EDO	E	603	-	3,3,3	0.37	0	2,2,2	0.59	0
5	6ZE	G	608	-	21,22,22	2.74	6 (28%)	27,33,33	2.19	12 (44%)
3	EDO	G	604	-	3,3,3	0.49	0	2,2,2	0.33	0
5	6ZE	A	606	-	21,22,22	2.58	5 (23%)	27,33,33	2.16	14 (51%)
4	GAI	E	605	-	3,3,3	2.16	1 (33%)	3,3,3	1.12	0
4	GAI	G	607	-	3,3,3	1.38	0	3,3,3	1.07	0
4	GAI	B	604	-	3,3,3	2.07	1 (33%)	3,3,3	1.24	0
4	GAI	H	602	-	3,3,3	1.12	0	3,3,3	1.07	0
3	EDO	E	602	-	3,3,3	0.37	0	2,2,2	0.52	0
5	6ZE	C	603	-	21,22,22	2.72	5 (23%)	27,33,33	2.59	14 (51%)
5	6ZE	F	605	-	21,22,22	2.81	6 (28%)	27,33,33	2.16	13 (48%)
3	EDO	B	602	-	3,3,3	0.39	0	2,2,2	0.57	0
4	GAI	D	603	-	3,3,3	2.08	1 (33%)	3,3,3	1.09	0
4	GAI	E	604	-	3,3,3	2.21	1 (33%)	3,3,3	1.00	0
3	EDO	B	603	-	3,3,3	0.45	0	2,2,2	0.45	0
3	EDO	G	602	-	3,3,3	0.40	0	2,2,2	0.61	0
4	GAI	D	606	-	3,3,3	2.07	1 (33%)	3,3,3	1.00	0
5	6ZE	H	603	-	21,22,22	2.67	6 (28%)	27,33,33	2.40	12 (44%)
4	GAI	F	604	-	3,3,3	2.10	1 (33%)	3,3,3	1.15	0
4	GAI	G	605	-	3,3,3	2.18	1 (33%)	3,3,3	1.47	1 (33%)
4	GAI	C	602	-	3,3,3	2.08	1 (33%)	3,3,3	1.50	1 (33%)
3	EDO	F	602	-	3,3,3	0.47	0	2,2,2	0.32	0
4	GAI	E	606	-	3,3,3	2.05	1 (33%)	3,3,3	1.33	0
3	EDO	F	603	-	3,3,3	0.37	0	2,2,2	0.56	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	A	603	-	-	0/1/1/1	-
3	EDO	G	603	-	-	0/1/1/1	-
5	6ZE	B	605	-	-	0/3/3/3	0/3/3/3
5	6ZE	D	607	-	-	0/3/3/3	0/3/3/3
5	6ZE	E	607	-	-	1/3/3/3	0/3/3/3
3	EDO	D	602	-	-	1/1/1/1	-
3	EDO	A	602	-	-	1/1/1/1	-
3	EDO	E	603	-	-	1/1/1/1	-
5	6ZE	G	608	-	-	0/3/3/3	0/3/3/3
3	EDO	G	604	-	-	0/1/1/1	-
5	6ZE	A	606	-	-	1/3/3/3	0/3/3/3
5	6ZE	C	603	-	-	0/3/3/3	0/3/3/3
3	EDO	E	602	-	-	0/1/1/1	-
5	6ZE	F	605	-	-	0/3/3/3	0/3/3/3
3	EDO	B	602	-	-	1/1/1/1	-
3	EDO	B	603	-	-	1/1/1/1	-
3	EDO	G	602	-	-	0/1/1/1	-
5	6ZE	H	603	-	-	1/3/3/3	0/3/3/3
3	EDO	F	602	-	-	0/1/1/1	-
3	EDO	F	603	-	-	0/1/1/1	-

The worst 5 of 56 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	605	6ZE	C5-C6	7.96	1.49	1.39
5	G	608	6ZE	C12-C13	7.81	1.49	1.35
5	E	607	6ZE	C12-C13	7.66	1.48	1.35
5	C	603	6ZE	C12-C13	7.62	1.48	1.35
5	D	607	6ZE	C12-C13	7.52	1.48	1.35

The worst 5 of 104 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	603	6ZE	C11-C12-C13	-5.38	116.61	120.35
5	H	603	6ZE	C20-C9-C5	-5.12	115.71	124.76
5	B	605	6ZE	C1-C6-C5	-5.09	118.88	124.70
5	B	605	6ZE	C4-C5-C6	4.72	123.92	119.28
5	B	605	6ZE	C20-C9-C5	-4.69	116.48	124.76

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

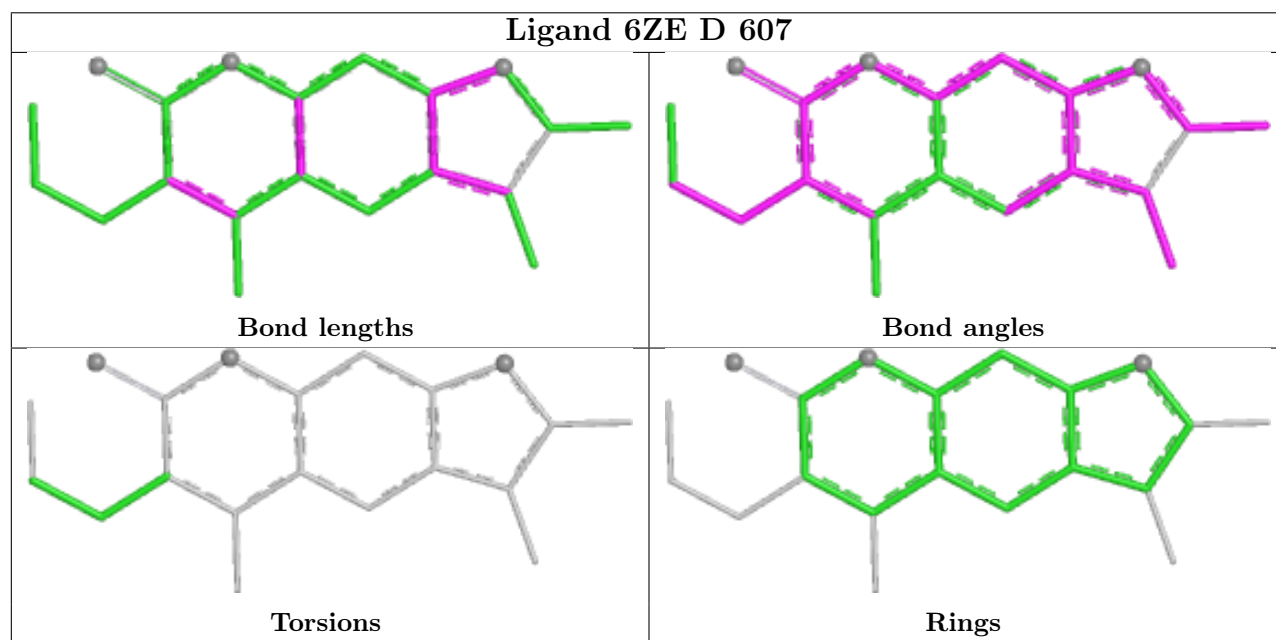
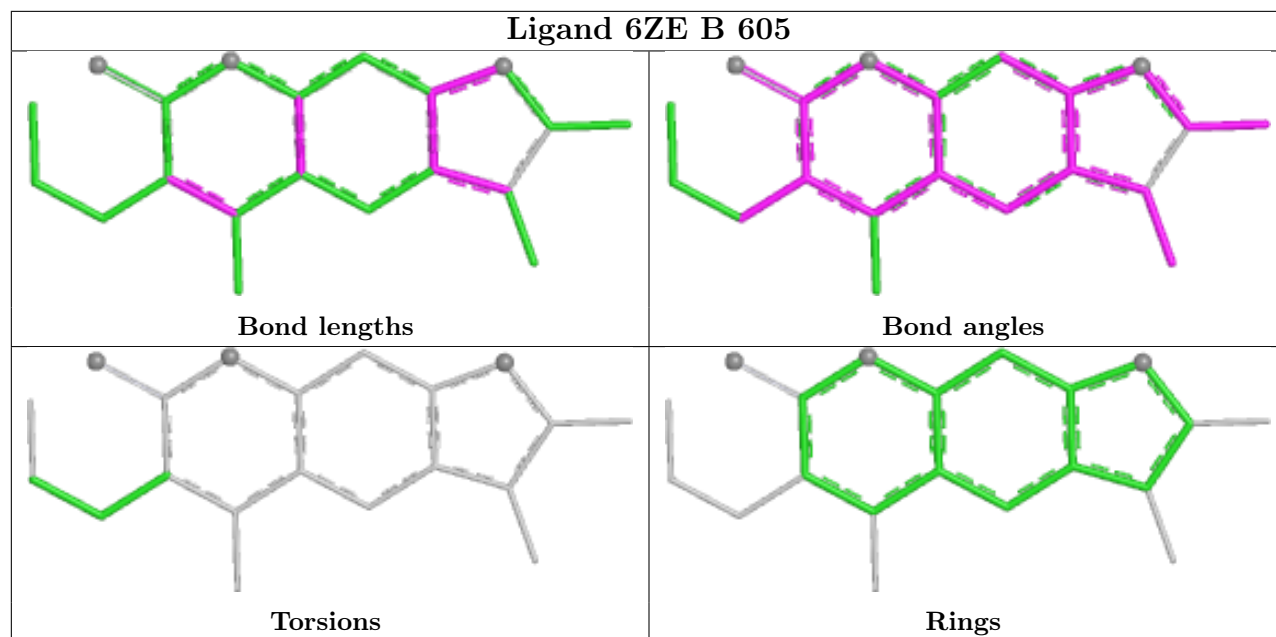
Mol	Chain	Res	Type	Atoms
5	H	603	6ZE	C12-C14-C15-C16
5	E	607	6ZE	C12-C14-C15-C16
3	E	603	EDO	O1-C1-C2-O2
5	A	606	6ZE	C12-C14-C15-C16
3	B	602	EDO	O1-C1-C2-O2

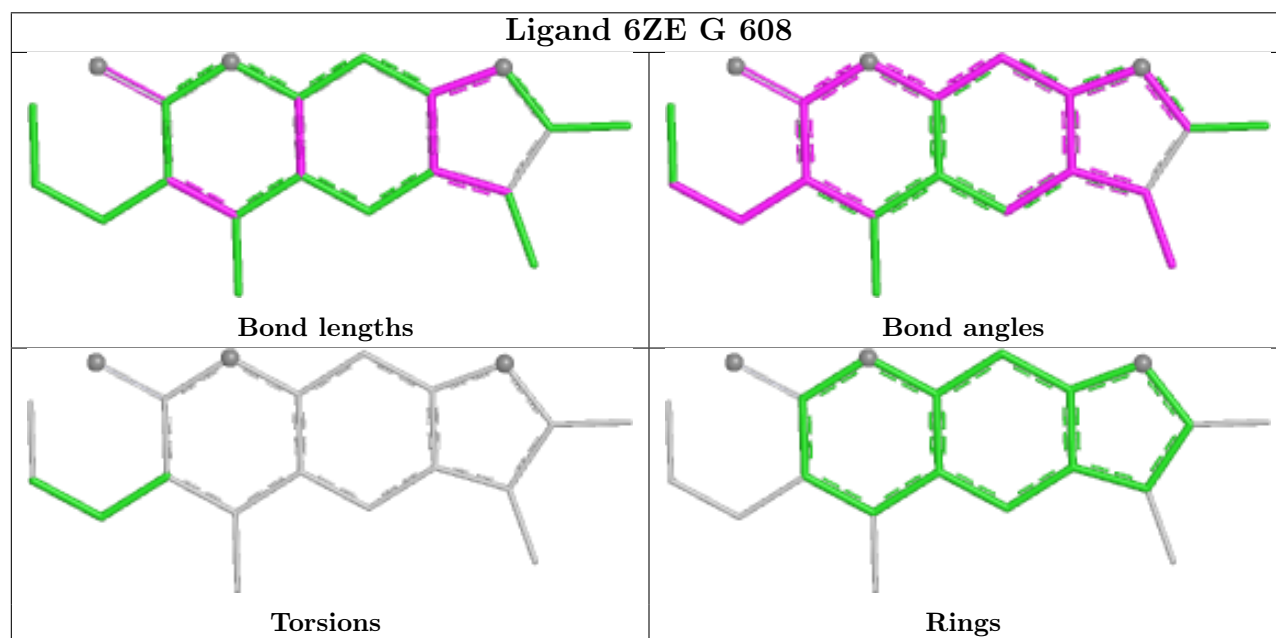
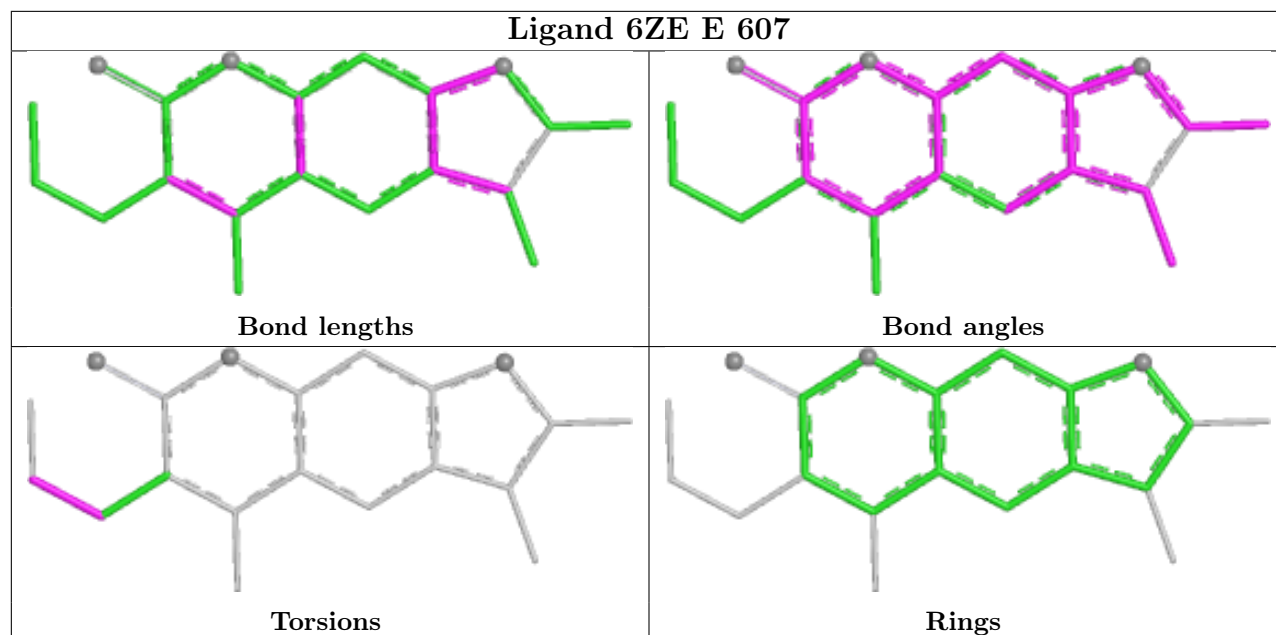
There are no ring outliers.

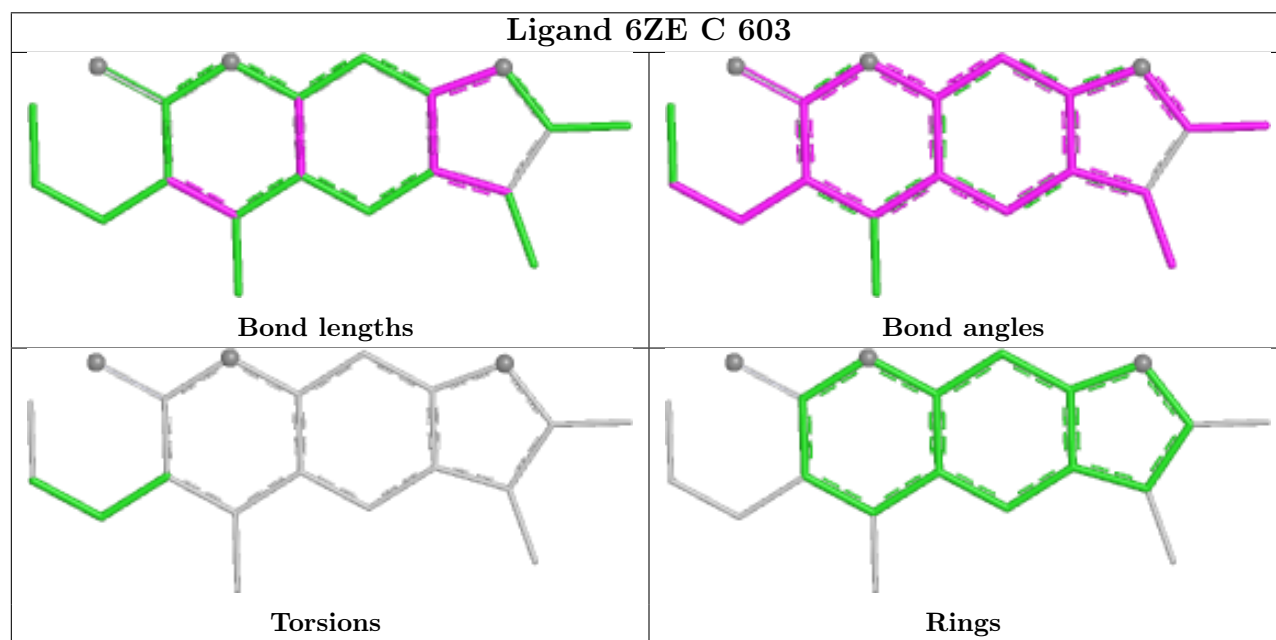
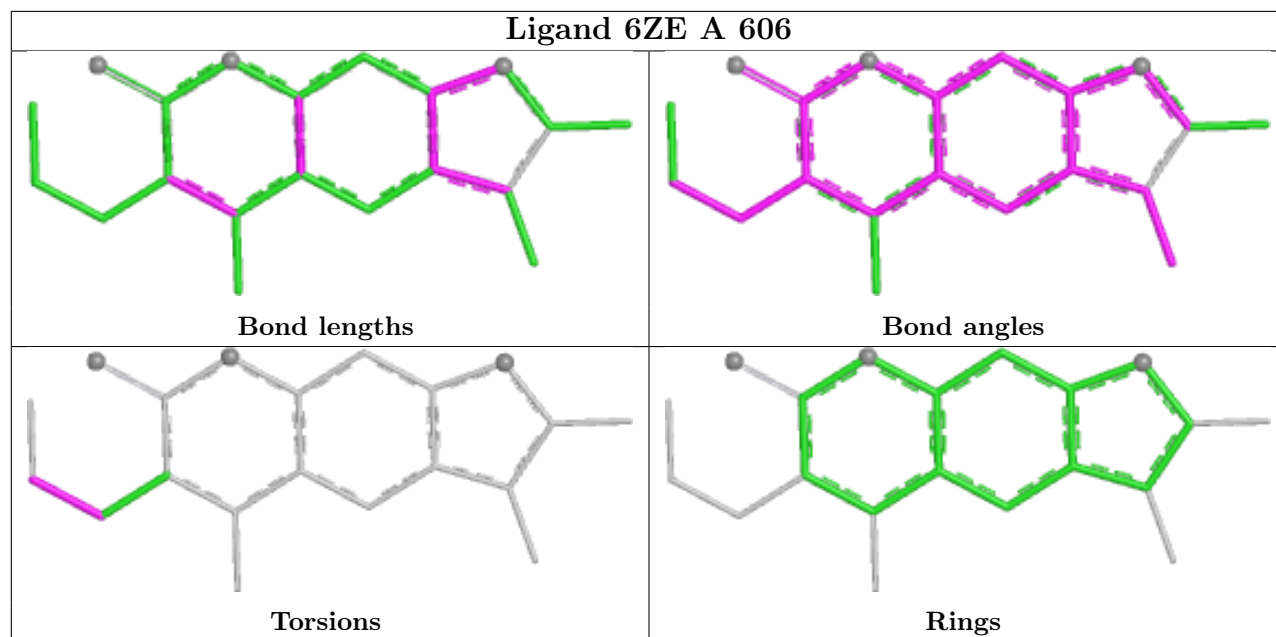
7 monomers are involved in 7 short contacts:

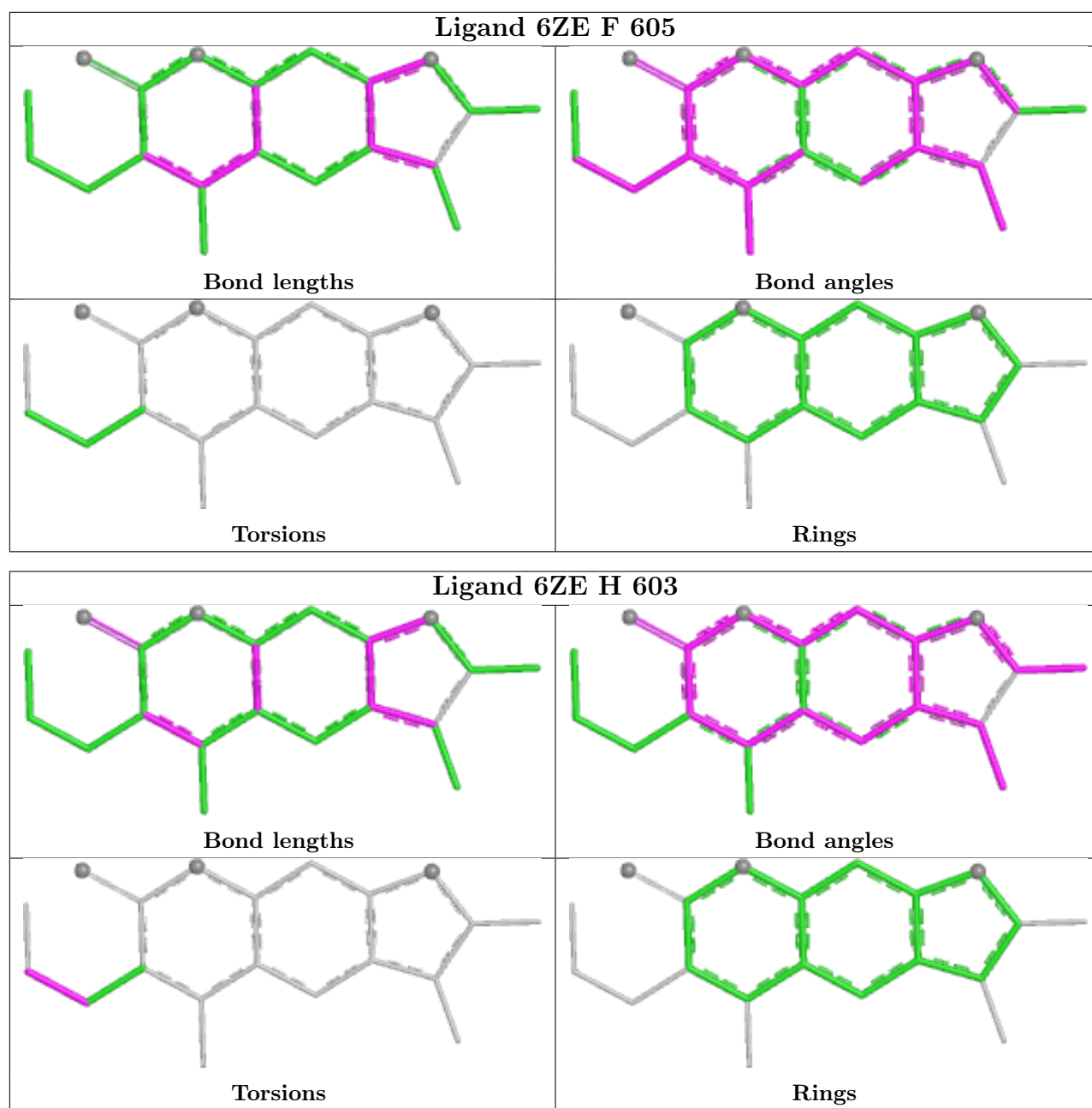
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	605	6ZE	1	0
5	D	607	6ZE	1	0
5	E	607	6ZE	1	0
5	G	608	6ZE	1	0
5	A	606	6ZE	1	0
5	F	605	6ZE	1	0
5	H	603	6ZE	1	0

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 than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	494/517 (95%)	-0.52	0	100 100	14, 25, 39, 55	1 (0%)
1	B	494/517 (95%)	-0.42	1 (0%)	91 89	15, 28, 43, 63	2 (0%)
1	C	494/517 (95%)	-0.52	1 (0%)	91 89	14, 25, 42, 62	2 (0%)
1	D	494/517 (95%)	-0.54	1 (0%)	91 89	11, 23, 37, 63	4 (0%)
1	E	495/517 (95%)	-0.37	1 (0%)	91 89	15, 27, 44, 69	1 (0%)
1	F	494/517 (95%)	-0.42	1 (0%)	91 89	14, 28, 43, 69	1 (0%)
1	G	494/517 (95%)	-0.48	1 (0%)	91 89	13, 26, 41, 56	3 (0%)
1	H	494/517 (95%)	-0.49	1 (0%)	91 89	11, 24, 38, 65	2 (0%)
All	All	3953/4136 (95%)	-0.47	7 (0%)	91 89	11, 26, 41, 69	16 (0%)

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	7	ALA	3.3
1	B	7	ALA	3.1
1	D	7	ALA	2.6
1	E	362	GLN	2.3
1	F	7	ALA	2.2

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 ⓘ

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
3	EDO	F	603	4/4	0.79	0.18	52,54,54,56	0
3	EDO	E	603	4/4	0.80	0.15	48,49,49,52	0
4	GAI	E	606	4/4	0.81	0.14	38,38,38,39	0
3	EDO	F	602	4/4	0.83	0.19	55,58,61,62	0
2	NA	G	601	1/1	0.84	0.07	33,33,33,33	0
3	EDO	D	602	4/4	0.84	0.17	52,54,56,60	0
2	NA	C	601	1/1	0.84	0.06	31,31,31,31	0
3	EDO	A	603	4/4	0.87	0.11	47,47,49,49	0
3	EDO	E	602	4/4	0.87	0.16	50,55,57,59	0
4	GAI	D	606	4/4	0.88	0.11	38,38,39,41	0
3	EDO	B	603	4/4	0.88	0.15	49,51,54,55	0
4	GAI	A	605	4/4	0.89	0.12	37,37,37,38	0
4	GAI	C	602	4/4	0.89	0.13	44,45,46,47	0
4	GAI	D	605	4/4	0.89	0.12	43,43,43,45	0
3	EDO	G	602	4/4	0.89	0.13	43,48,51,53	0
3	EDO	G	604	4/4	0.89	0.11	36,38,38,39	0
3	EDO	A	602	4/4	0.90	0.12	49,53,54,54	0
3	EDO	B	602	4/4	0.91	0.12	41,43,44,44	0
3	EDO	G	603	4/4	0.91	0.11	42,45,47,51	0
4	GAI	F	604	4/4	0.91	0.12	37,39,40,40	0
4	GAI	E	604	4/4	0.93	0.08	28,29,29,31	0
4	GAI	E	605	4/4	0.93	0.11	40,41,42,43	0
5	6ZE	F	605	20/20	0.93	0.09	35,38,42,42	0
4	GAI	A	604	4/4	0.94	0.10	37,39,39,39	0
4	GAI	D	603	4/4	0.94	0.06	36,36,36,37	0
4	GAI	G	605	4/4	0.94	0.08	43,43,45,47	0
5	6ZE	B	605	20/20	0.94	0.08	30,32,36,40	0
5	6ZE	C	603	20/20	0.94	0.08	26,28,32,35	0
5	6ZE	D	607	20/20	0.94	0.08	24,24,33,33	0
4	GAI	B	604	4/4	0.94	0.08	30,31,33,33	0
5	6ZE	G	608	20/20	0.94	0.07	30,33,40,41	0
2	NA	F	601	1/1	0.95	0.04	31,31,31,31	0
4	GAI	G	606	4/4	0.95	0.08	38,39,39,42	0
4	GAI	G	607	4/4	0.95	0.09	43,43,44,45	0
5	6ZE	E	607	20/20	0.95	0.07	25,26,31,33	0
4	GAI	H	602	4/4	0.95	0.07	36,38,38,38	0
5	6ZE	A	606	20/20	0.95	0.07	23,25,31,33	0

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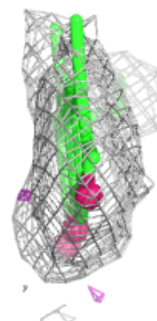
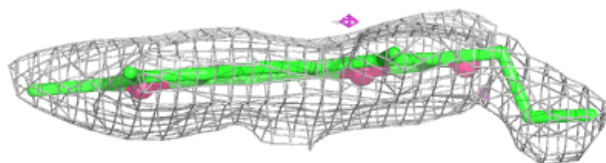
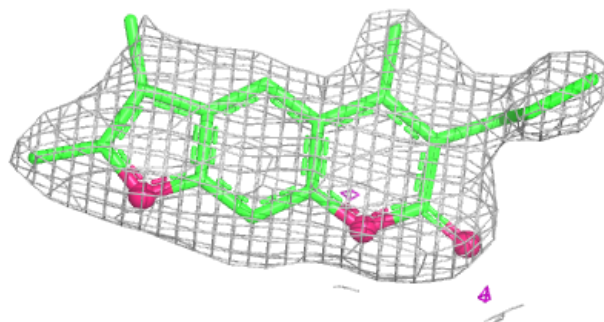
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NA	D	601	1/1	0.96	0.04	26,26,26,26	0
2	NA	H	601	1/1	0.96	0.05	28,28,28,28	0
2	NA	A	601	1/1	0.96	0.03	32,32,32,32	0
5	6ZE	H	603	20/20	0.96	0.06	26,27,30,32	0
2	NA	B	601	1/1	0.97	0.04	32,32,32,32	0
2	NA	E	601	1/1	0.97	0.08	21,21,21,21	0
4	GAI	D	604	4/4	0.97	0.05	29,31,31,32	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.

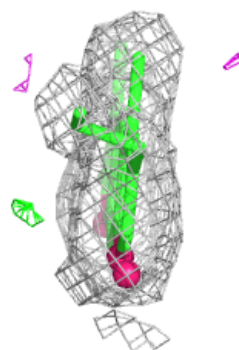
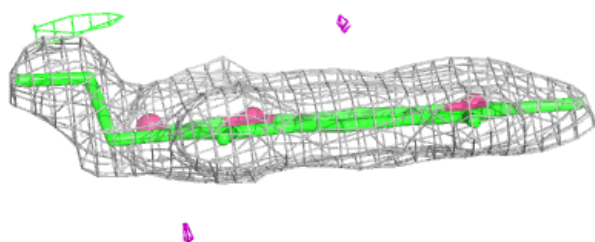
Electron density around 6ZE F 605:

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

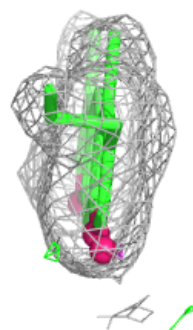
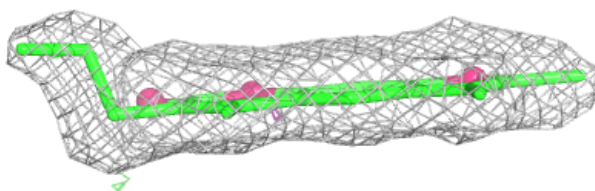
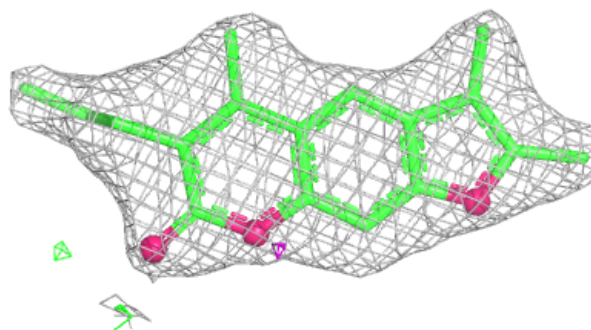


Electron density around 6ZE B 605:

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

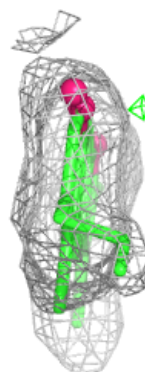
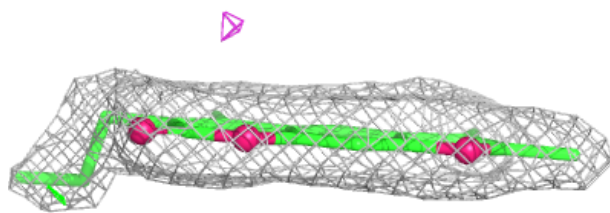
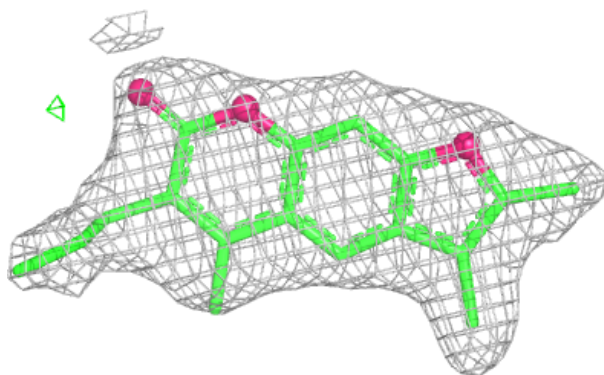
**Electron density around 6ZE C 603:**

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

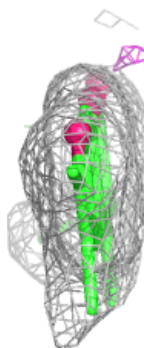
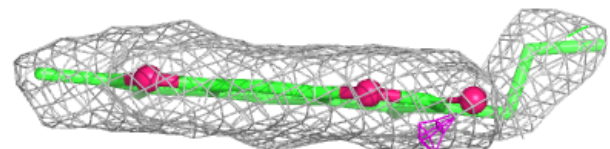
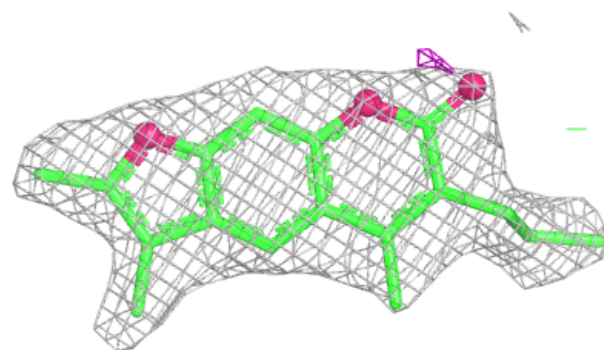


Electron density around 6ZE D 607:

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

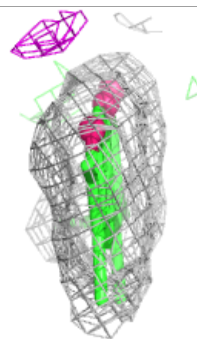
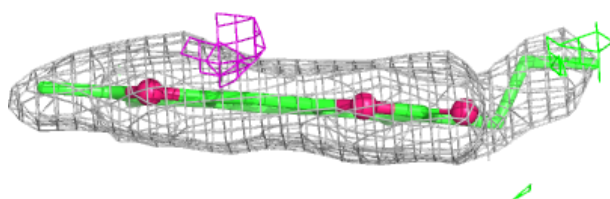
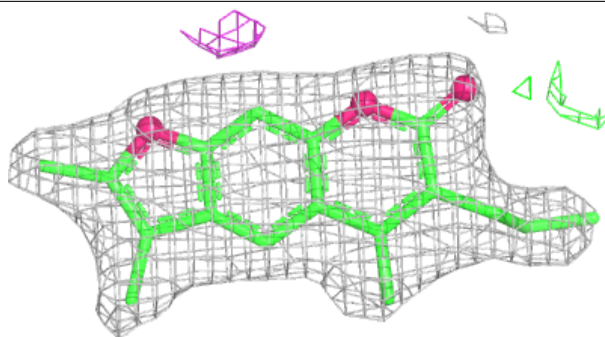
**Electron density around 6ZE G 608:**

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

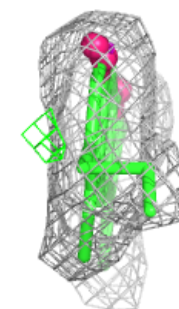
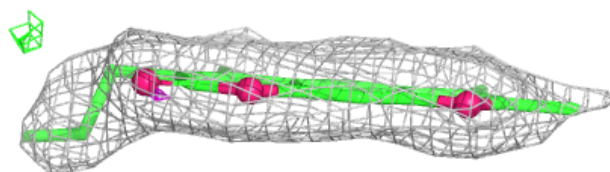
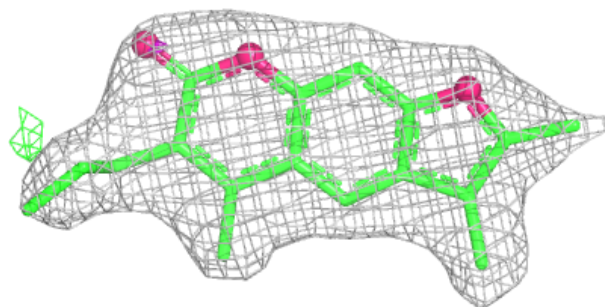


Electron density around 6ZE E 607:

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

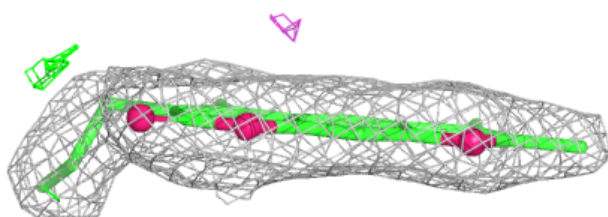
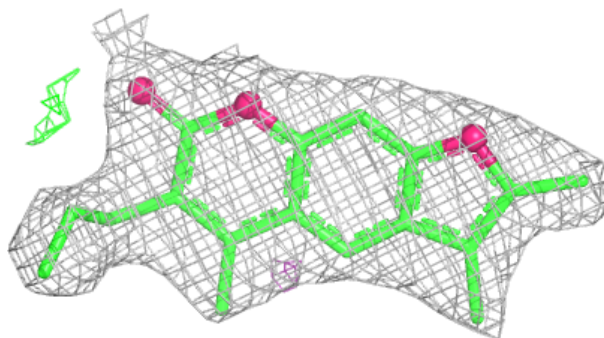
**Electron density around 6ZE A 606:**

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



Electron density around 6ZE H 603:

$2mF_o - DF_c$ (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.