



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 12:45 PM UTC

PDB ID : 3W1W / pdb_00003w1w
Title : Protein-drug complex
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Deposited on : 2012-11-21
Resolution : 2.01 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

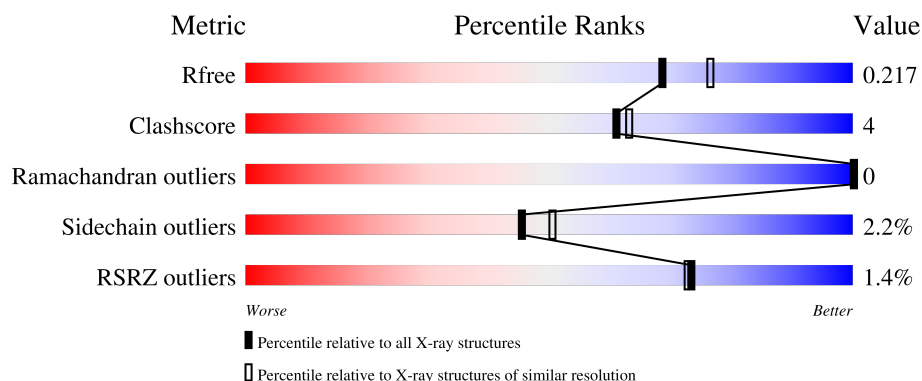
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.01 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	371	
1	B	371	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6474 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.

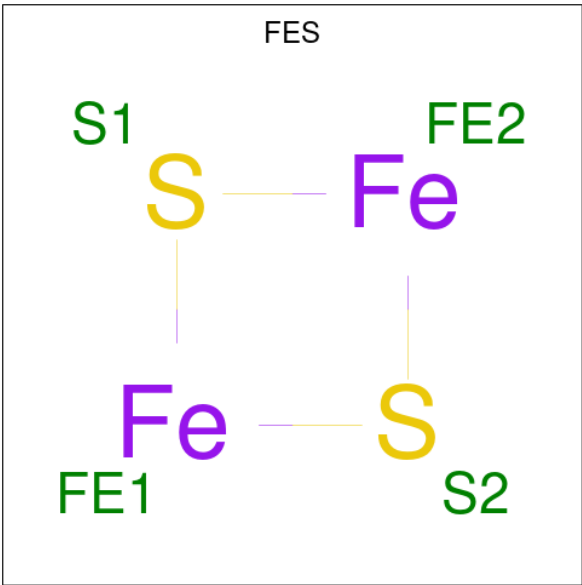
- Molecule 1 is a protein called Ferrochelatase, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	359	Total	C	N	O	S	0	5	0
			2905	1853	500	532	20			
1	B	359	Total	C	N	O	S	0	2	0
			2894	1845	500	531	18			

There are 18 discrepancies between the modelled and reference sequences:

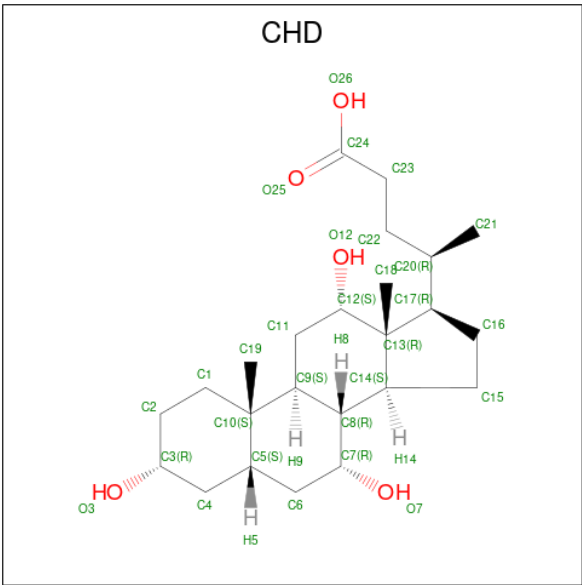
Chain	Residue	Modelled	Actual	Comment	Reference
A	53	MET	-	expression tag	UNP P22830
A	54	ALA	-	expression tag	UNP P22830
A	55	HIS	-	expression tag	UNP P22830
A	56	HIS	-	expression tag	UNP P22830
A	57	HIS	-	expression tag	UNP P22830
A	58	HIS	-	expression tag	UNP P22830
A	59	HIS	-	expression tag	UNP P22830
A	60	HIS	-	expression tag	UNP P22830
A	115	LEU	ARG	engineered mutation	UNP P22830
B	53	MET	-	expression tag	UNP P22830
B	54	ALA	-	expression tag	UNP P22830
B	55	HIS	-	expression tag	UNP P22830
B	56	HIS	-	expression tag	UNP P22830
B	57	HIS	-	expression tag	UNP P22830
B	58	HIS	-	expression tag	UNP P22830
B	59	HIS	-	expression tag	UNP P22830
B	60	HIS	-	expression tag	UNP P22830
B	115	LEU	ARG	engineered mutation	UNP P22830

- Molecule 2 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe₂S₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	Fe	S	0	0
			4	2	2		
2	B	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 3 is CHOLIC ACID (CCD ID: CHD) (formula: C₂₄H₄₀O₅).



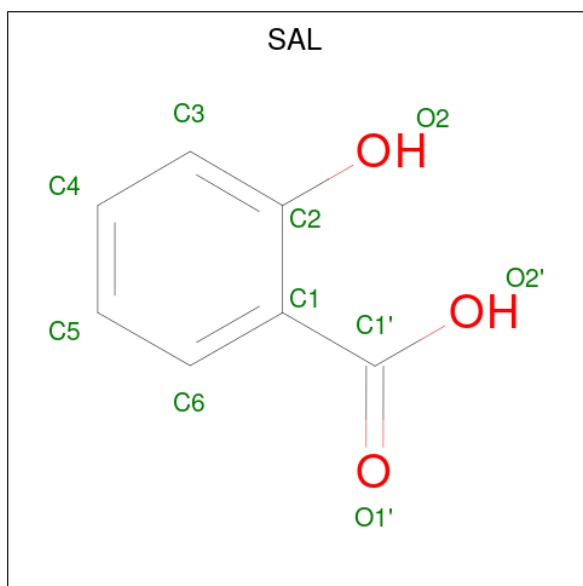
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			29	24	5		
3	A	1	Total	C	O	0	0
			29	24	5		

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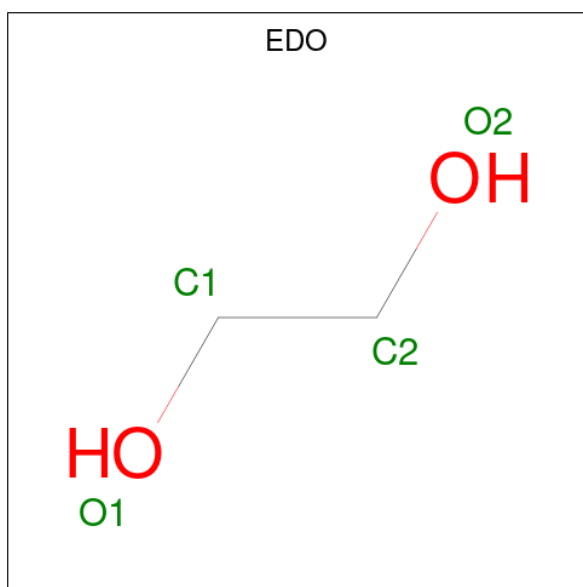
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			29	24	5		
3	A	1	Total	C	O	0	0
			29	24	5		
3	B	1	Total	C	O	0	0
			29	24	5		
3	B	1	Total	C	O	0	0
			29	24	5		
3	B	1	Total	C	O	0	0
			29	24	5		
3	B	1	Total	C	O	0	0
			29	24	5		

- Molecule 4 is 2-HYDROXYBENZOIC ACID (CCD ID: SAL) (formula: $C_7H_6O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			10	7	3		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

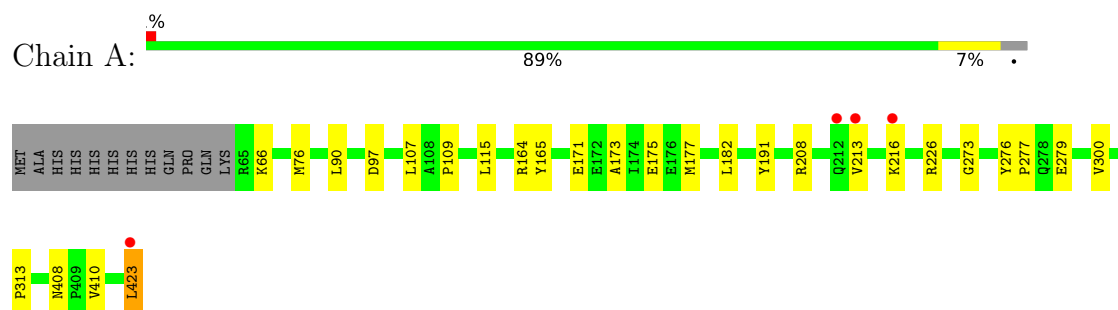
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	201	Total	O	0	0
			201	201		
6	B	216	Total	O	0	0
			216	216		

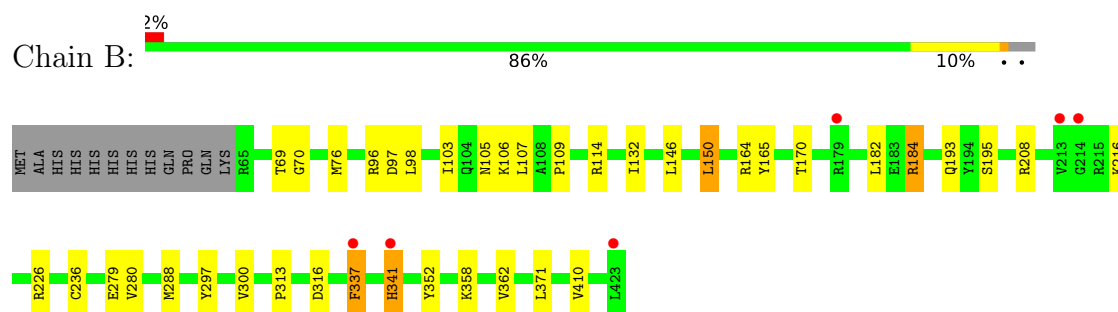
3 Residue-property plots [i](#)

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: Ferrochelatase, mitochondrial



- Molecule 1: Ferrochelatase, mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	87.53Å 93.63Å 110.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.28 – 2.01 34.28 – 2.01	Depositor EDS
% Data completeness (in resolution range)	99.1 (34.28-2.01) 99.2 (34.28-2.01)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 2.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.2_869)	Depositor
R, R_{free}	0.191 , 0.229 0.181 , 0.217	Depositor DCC
R_{free} test set	3081 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	21.0	Xtriage
Anisotropy	0.102	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6474	wwPDB-VP
Average B, all atoms (Å ²)	23.0	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 71.71 % 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 2.5040e-06. 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SAL, CHD, FES, EDO

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	0.47	0/2990	0.75	0/4050
1	B	0.47	0/2970	0.74	0/4024
All	All	0.47	0/5960	0.75	0/8074

There are no bond length outliers.

There are no bond angle outliers.

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	2905	0	2926	15	0
1	B	2894	0	2907	28	0
2	A	4	0	0	0	0
2	B	4	0	0	0	0
3	A	116	0	156	3	0
3	B	116	0	156	7	0
4	A	10	0	4	1	0
5	A	4	0	6	0	0
5	B	4	0	6	0	0
6	A	201	0	0	0	0
6	B	216	0	0	4	0
All	All	6474	0	6161	51	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 4.

All (51) 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)
4:A:1505:SAL:O1'	4:A:1505:SAL:O2	2.14	0.64
1:A:300:VAL:HG12	1:A:313:PRO:HG2	1.80	0.63
1:B:341:HIS:HB2	6:B:602:HOH:O	2.01	0.59
1:B:337:PHE:CZ	1:B:341:HIS:HE1	2.20	0.58
1:B:337:PHE:CE1	1:B:341:HIS:HE1	2.25	0.54
1:B:195:SER:OG	6:B:801:HOH:O	2.18	0.54
1:A:76[A]:MET:HB2	1:A:191:TYR:OH	2.09	0.53
1:B:208:ARG:NH2	1:B:410:VAL:HG21	2.24	0.52
1:A:97:ASP:OD2	1:A:208:ARG:NH1	2.41	0.52
1:A:173:ALA:O	1:A:177:MET:HG3	2.11	0.51
1:A:226:ARG:HD3	1:A:279:GLU:OE1	2.11	0.51
1:B:96:ARG:NH2	1:B:105:ASN:OD1	2.41	0.50
1:B:300:VAL:HG12	1:B:313:PRO:HG2	1.93	0.50
1:B:98:LEU:HD11	3:B:504:CHD:H222	1.95	0.49
1:B:164:ARG:HG3	1:B:165:TYR:CE1	2.48	0.48
1:B:337:PHE:CE1	1:B:341:HIS:CE1	3.02	0.47
3:B:504:CHD:H231	3:B:504:CHD:H211	1.46	0.47
1:B:69:THR:HG23	1:B:184:ARG:HG2	1.98	0.46
1:A:164:ARG:HG3	1:A:165:TYR:CE1	2.50	0.46
3:A:1502:CHD:H183	3:A:1502:CHD:H20	1.80	0.44
1:B:132:ILE:HD11	1:B:341:HIS:HD2	1.81	0.44
1:B:103:ILE:HG13	1:B:107:LEU:HG	1.98	0.44
1:A:177:MET:HB3	1:A:182:LEU:HD12	1.99	0.44
1:B:70:GLY:HA3	1:B:182:LEU:HD13	2.00	0.44
1:B:132:ILE:HD11	1:B:341:HIS:CD2	2.53	0.43
1:B:341:HIS:CD2	6:B:812:HOH:O	2.72	0.43
1:B:226:ARG:HD3	1:B:279:GLU:OE1	2.19	0.43
1:B:316:ASP:HB3	1:B:352:TYR:CE1	2.54	0.43
1:B:106:LYS:O	1:B:109:PRO:HD2	2.19	0.42
1:A:273:GLY:HA2	1:B:313:PRO:HG3	2.01	0.42
3:B:502:CHD:H213	3:B:502:CHD:H231	1.78	0.42
1:A:276:TYR:HB3	1:A:277:PRO:HD3	2.01	0.42
1:B:69:THR:HG23	1:B:184:ARG:CG	2.50	0.42
3:A:1502:CHD:H211	3:A:1502:CHD:H231	1.57	0.42
1:B:164:ARG:NH1	6:B:683:HOH:O	2.40	0.42
1:A:408:ASN:OD1	1:A:410:VAL:HG12	2.18	0.42
3:B:503:CHD:H162	3:B:503:CHD:H222	1.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:76:MET:HG3	1:B:165:TYR:CD2	2.55	0.41
1:B:97:ASP:OD2	1:B:208:ARG:NH1	2.46	0.41
3:B:503:CHD:H112	3:B:503:CHD:H12A	1.87	0.41
1:B:288:MET:HG3	1:B:297:TYR:CD1	2.55	0.41
1:B:146:LEU:O	1:B:150:LEU:HG	2.20	0.41
3:B:504:CHD:H183	3:B:504:CHD:H20	1.63	0.41
1:A:115:LEU:HD11	3:A:1503:CHD:H222	2.02	0.41
1:A:171:GLU:O	1:A:175:GLU:HG3	2.21	0.41
1:A:76[B]:MET:HE3	1:A:76[B]:MET:HB2	2.00	0.40
1:A:90:LEU:HD13	1:A:109:PRO:HA	2.02	0.40
3:B:506:CHD:H213	3:B:506:CHD:H232	1.89	0.40
1:B:193:GLN:HG2	1:B:280:VAL:HA	2.03	0.40
1:B:236:CYS:HB3	1:B:371:LEU:HD22	2.02	0.40
1:A:423:LEU:HD13	1:A:423:LEU:HA	1.90	0.40

There are no symmetry-related clashes.

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	362/371 (98%)	353 (98%)	9 (2%)	0	100	100
1	B	359/371 (97%)	349 (97%)	10 (3%)	0	100	100
All	All	721/742 (97%)	702 (97%)	19 (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	329/335 (98%)	324 (98%)	5 (2%)	57	64
1	B	326/335 (97%)	317 (97%)	9 (3%)	38	41
All	All	655/670 (98%)	641 (98%)	14 (2%)	45	52

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	LYS
1	A	107	LEU
1	A	213	VAL
1	A	216	LYS
1	A	423	LEU
1	B	114	ARG
1	B	150	LEU
1	B	170	THR
1	B	184	ARG
1	B	216	LYS
1	B	337	PHE
1	B	341	HIS
1	B	358	LYS
1	B	362	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	341	HIS
1	B	354	GLN
1	B	364	ASN
1	B	386	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

13 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	FES	A	1501	1	0,4,4	-	-	-		
3	CHD	B	504	-	32,32,32	0.77	0	51,51,51	1.69	7 (13%)
3	CHD	B	502	-	32,32,32	0.77	0	51,51,51	1.23	4 (7%)
3	CHD	A	1503	-	32,32,32	0.75	0	51,51,51	1.33	8 (15%)
2	FES	B	501	1	0,4,4	-	-	-		
5	EDO	B	505	-	3,3,3	0.51	0	2,2,2	0.23	0
3	CHD	A	1502	-	32,32,32	0.78	1 (3%)	51,51,51	1.58	9 (17%)
3	CHD	A	1507	-	32,32,32	0.75	0	51,51,51	1.26	5 (9%)
3	CHD	A	1504	-	32,32,32	0.80	1 (3%)	51,51,51	1.11	2 (3%)
3	CHD	B	503	-	32,32,32	0.82	0	51,51,51	1.24	6 (11%)
5	EDO	A	1506	-	3,3,3	0.51	0	2,2,2	0.26	0
3	CHD	B	506	-	32,32,32	0.70	0	51,51,51	1.01	2 (3%)
4	SAL	A	1505	-	10,10,10	1.67	1 (10%)	13,13,13	2.56	5 (38%)

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	FES	A	1501	1	-	-	0/1/1/1
3	CHD	B	504	-	-	8/9/74/74	0/4/4/4
3	CHD	B	502	-	-	2/9/74/74	0/4/4/4
3	CHD	A	1503	-	-	3/9/74/74	0/4/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	B	505	-	-	1/1/1/1	-
2	FES	B	501	1	-	-	0/1/1/1
3	CHD	A	1502	-	-	6/9/74/74	0/4/4/4
3	CHD	A	1507	-	-	3/9/74/74	0/4/4/4
3	CHD	A	1504	-	-	3/9/74/74	0/4/4/4
3	CHD	B	503	-	-	5/9/74/74	0/4/4/4
5	EDO	A	1506	-	-	0/1/1/1	-
3	CHD	B	506	-	-	7/9/74/74	0/4/4/4
4	SAL	A	1505	-	-	0/4/4/4	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1505	SAL	C1-C2	4.46	1.47	1.40
3	A	1502	CHD	C13-C14	-2.17	1.51	1.55
3	A	1504	CHD	C13-C14	-2.09	1.52	1.55

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	504	CHD	C13-C17-C20	-6.40	111.73	119.48
4	A	1505	SAL	C2-C1-C1'	-6.26	113.59	120.00
3	A	1502	CHD	C13-C17-C20	-5.00	113.43	119.48
3	A	1507	CHD	C13-C17-C20	-4.38	114.18	119.48
3	B	504	CHD	C16-C17-C20	4.16	118.47	112.18
3	A	1502	CHD	C16-C17-C20	3.94	118.13	112.18
3	B	504	CHD	C22-C20-C17	3.85	118.32	110.33
3	B	503	CHD	C13-C17-C20	-3.54	115.20	119.48
3	A	1502	CHD	C22-C20-C17	3.38	117.34	110.33
4	A	1505	SAL	C6-C1-C1'	3.16	125.90	118.64
3	A	1503	CHD	C11-C9-C10	-3.14	110.52	113.70
4	A	1505	SAL	O1'-C1'-C1	-3.05	114.68	121.97
3	B	504	CHD	C18-C13-C17	-3.05	106.43	111.20
3	A	1503	CHD	C13-C17-C20	-3.02	115.82	119.48
4	A	1505	SAL	O2-C2-C1	-2.89	116.34	121.71
3	A	1503	CHD	C17-C13-C14	2.79	102.91	100.11
3	B	502	CHD	C11-C9-C10	-2.79	110.88	113.70
3	B	503	CHD	C11-C9-C10	-2.76	110.90	113.70
3	A	1502	CHD	C18-C13-C12	2.59	111.64	109.06
3	B	504	CHD	C17-C13-C14	2.53	102.65	100.11
3	B	502	CHD	C13-C17-C20	-2.45	116.52	119.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1502	CHD	C17-C13-C12	-2.43	115.48	117.67
3	B	506	CHD	C13-C17-C20	-2.42	116.55	119.48
3	A	1503	CHD	C18-C13-C12	2.41	111.47	109.06
3	A	1503	CHD	C13-C14-C8	-2.41	111.67	114.72
3	B	502	CHD	C1-C10-C5	2.39	111.18	107.75
3	A	1507	CHD	O12-C12-C13	-2.31	107.11	111.02
3	B	503	CHD	C23-C22-C20	-2.31	110.14	114.46
3	B	503	CHD	C13-C14-C8	-2.31	111.79	114.72
3	A	1502	CHD	O12-C12-C13	-2.29	107.15	111.02
4	A	1505	SAL	O2'-C1'-C1	2.24	121.64	115.28
3	A	1504	CHD	C13-C14-C8	-2.24	111.89	114.72
3	A	1502	CHD	C6-C5-C4	-2.23	108.68	111.23
3	A	1502	CHD	C13-C14-C8	-2.23	111.90	114.72
3	A	1504	CHD	C11-C9-C10	-2.20	111.47	113.70
3	A	1503	CHD	C1-C10-C5	2.17	110.86	107.75
3	B	506	CHD	O25-C24-C23	-2.16	116.23	123.09
3	A	1502	CHD	C18-C13-C17	-2.15	107.83	111.20
3	B	503	CHD	C11-C12-C13	-2.14	109.09	111.26
3	B	503	CHD	C1-C10-C5	2.13	110.80	107.75
3	B	504	CHD	C23-C22-C20	-2.08	110.57	114.46
3	A	1507	CHD	C17-C13-C14	2.08	102.19	100.11
3	B	502	CHD	C13-C14-C8	-2.07	112.10	114.72
3	B	504	CHD	C17-C13-C12	-2.05	115.82	117.67
3	A	1507	CHD	C11-C9-C10	-2.04	111.64	113.70
3	A	1507	CHD	C1-C10-C5	2.01	110.64	107.75
3	A	1503	CHD	C19-C10-C9	-2.01	108.48	111.18
3	A	1503	CHD	C21-C20-C22	-2.00	107.24	110.34

There are no chirality outliers.

All (38) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1502	CHD	C13-C17-C20-C21
3	A	1502	CHD	C16-C17-C20-C21
3	B	504	CHD	C16-C17-C20-C21
3	B	504	CHD	C13-C17-C20-C21
3	B	506	CHD	C21-C20-C22-C23
3	A	1502	CHD	C16-C17-C20-C22
3	A	1502	CHD	C13-C17-C20-C22
3	B	504	CHD	C13-C17-C20-C22
3	B	504	CHD	C16-C17-C20-C22
3	B	506	CHD	C17-C20-C22-C23

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Mol	Chain	Res	Type	Atoms
3	A	1504	CHD	C20-C22-C23-C24
3	B	504	CHD	C20-C22-C23-C24
3	A	1503	CHD	C17-C20-C22-C23
3	B	503	CHD	C20-C22-C23-C24
3	B	503	CHD	C13-C17-C20-C22
3	B	503	CHD	C13-C17-C20-C21
3	B	503	CHD	C16-C17-C20-C22
3	B	503	CHD	C16-C17-C20-C21
3	A	1502	CHD	C20-C22-C23-C24
3	B	502	CHD	C22-C23-C24-O26
5	B	505	EDO	O1-C1-C2-O2
3	B	504	CHD	C22-C23-C24-O25
3	A	1507	CHD	C13-C17-C20-C21
3	B	504	CHD	C22-C23-C24-O26
3	B	504	CHD	C21-C20-C22-C23
3	B	502	CHD	C22-C23-C24-O25
3	A	1504	CHD	C22-C23-C24-O25
3	A	1504	CHD	C22-C23-C24-O26
3	A	1503	CHD	C22-C23-C24-O26
3	B	506	CHD	C13-C17-C20-C22
3	B	506	CHD	C22-C23-C24-O26
3	B	506	CHD	C13-C17-C20-C21
3	A	1507	CHD	C13-C17-C20-C22
3	A	1507	CHD	C17-C20-C22-C23
3	A	1503	CHD	C22-C23-C24-O25
3	A	1502	CHD	C22-C23-C24-O25
3	B	506	CHD	C16-C17-C20-C22
3	B	506	CHD	C22-C23-C24-O25

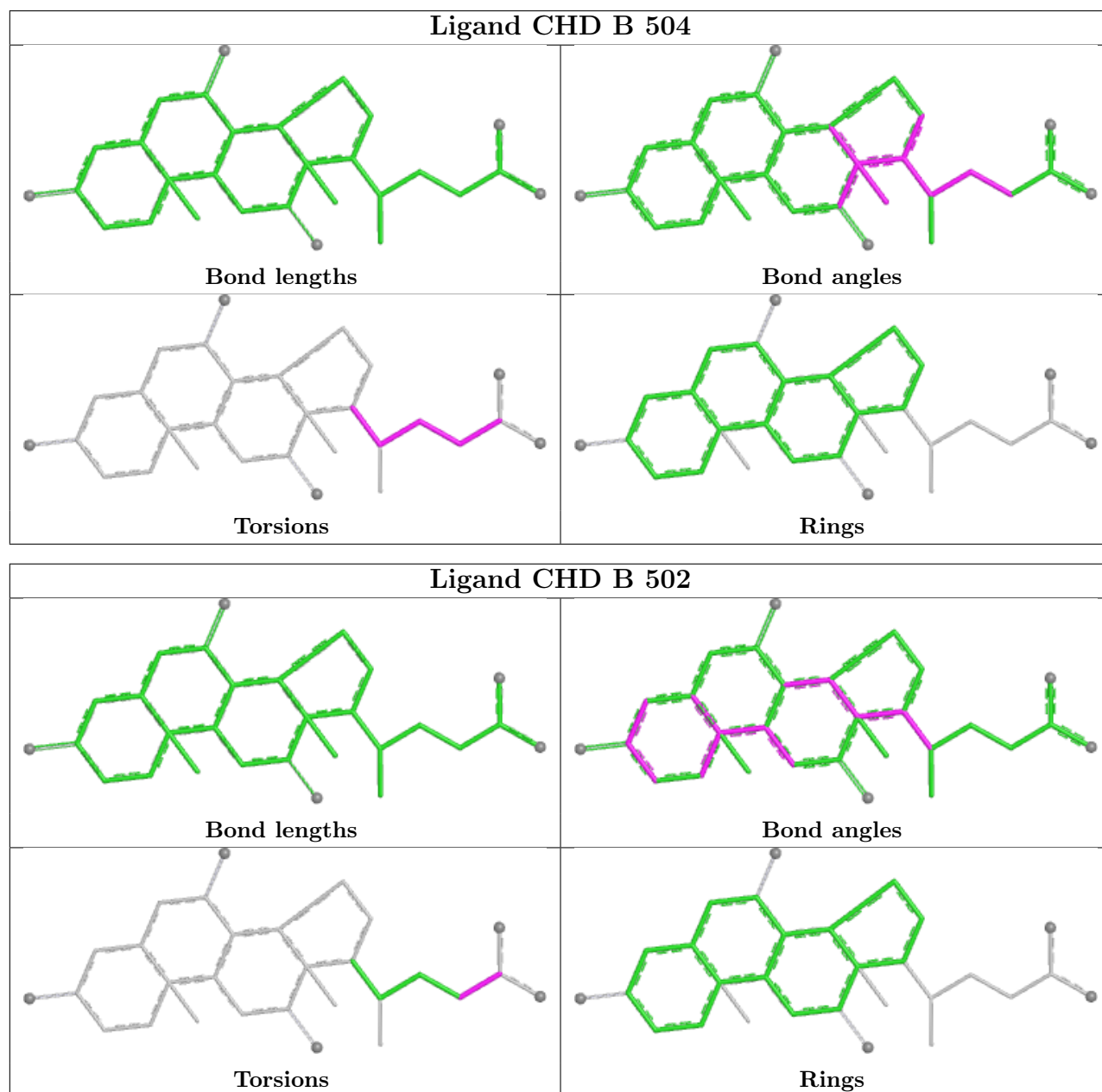
There are no ring outliers.

7 monomers are involved in 11 short contacts:

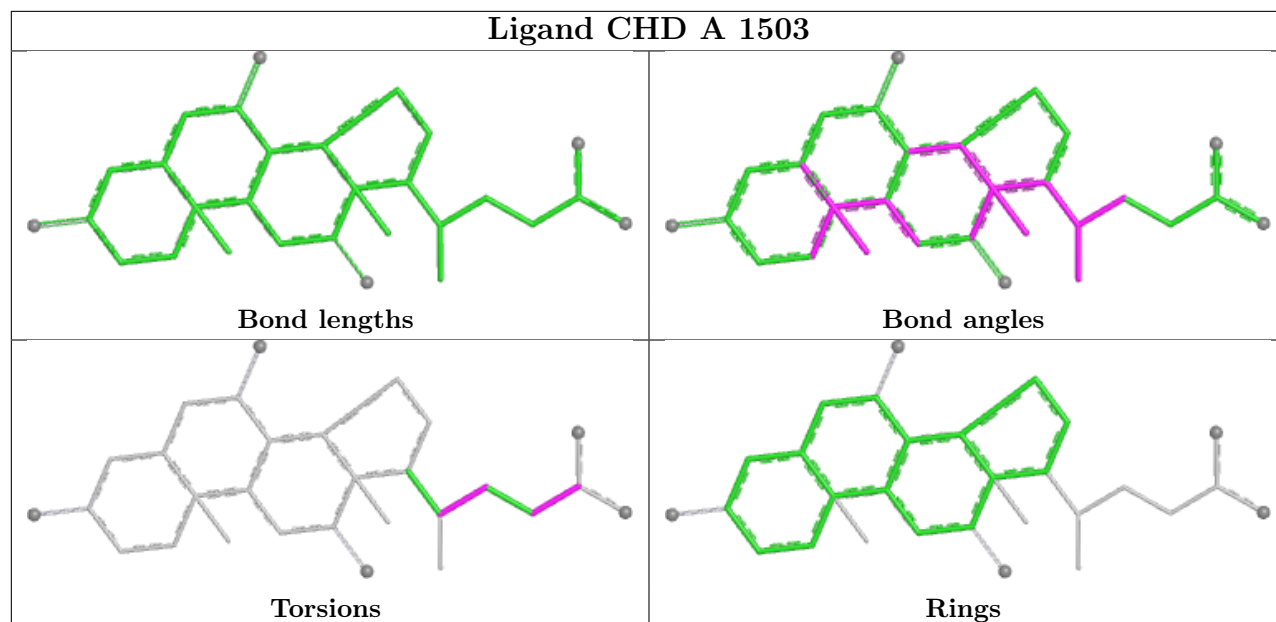
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	504	CHD	3	0
3	B	502	CHD	1	0
3	A	1503	CHD	1	0
3	A	1502	CHD	2	0
3	B	503	CHD	2	0
3	B	506	CHD	1	0
4	A	1505	SAL	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

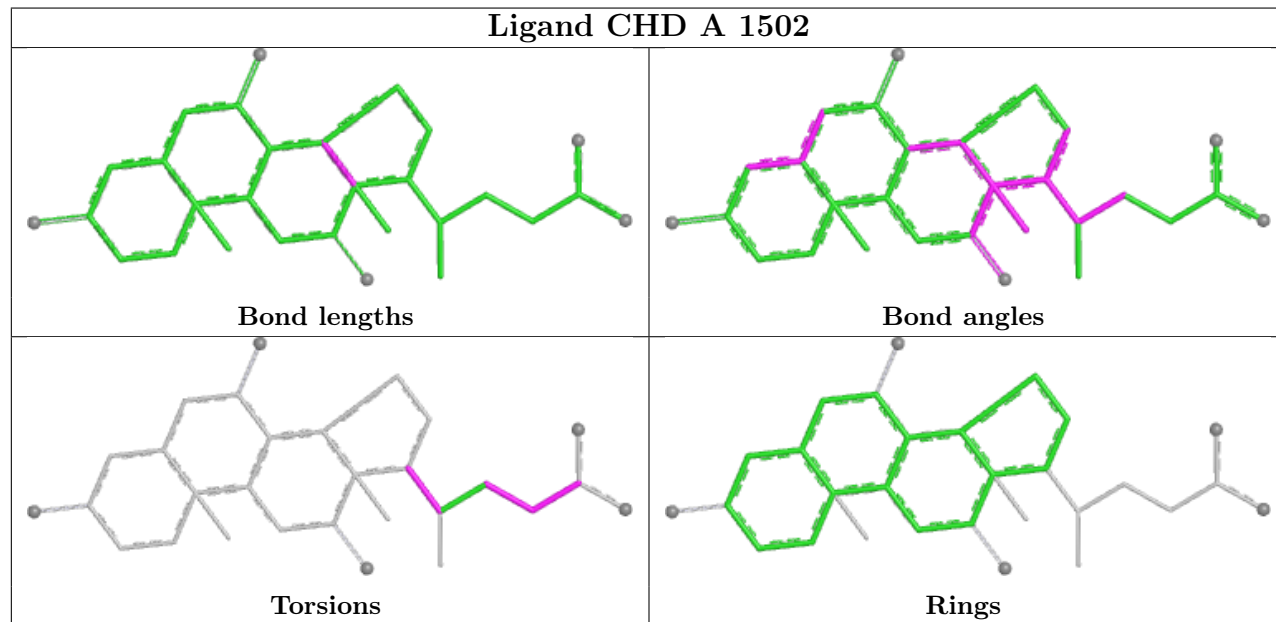
bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 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.



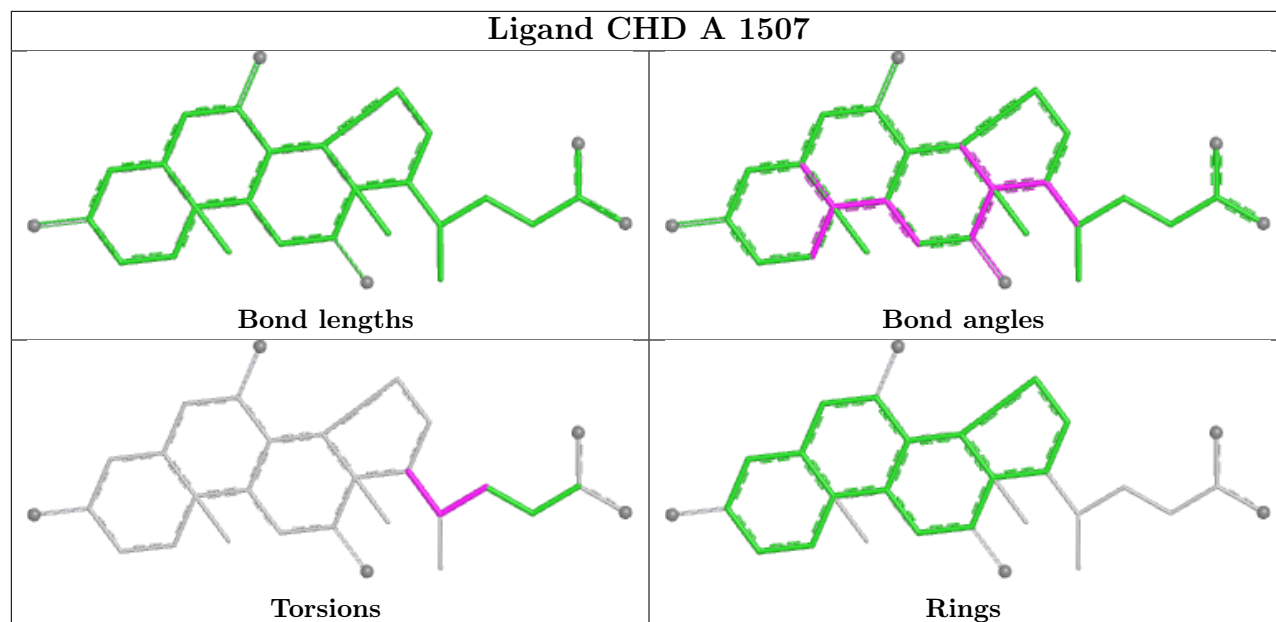
Ligand CHD A 1503



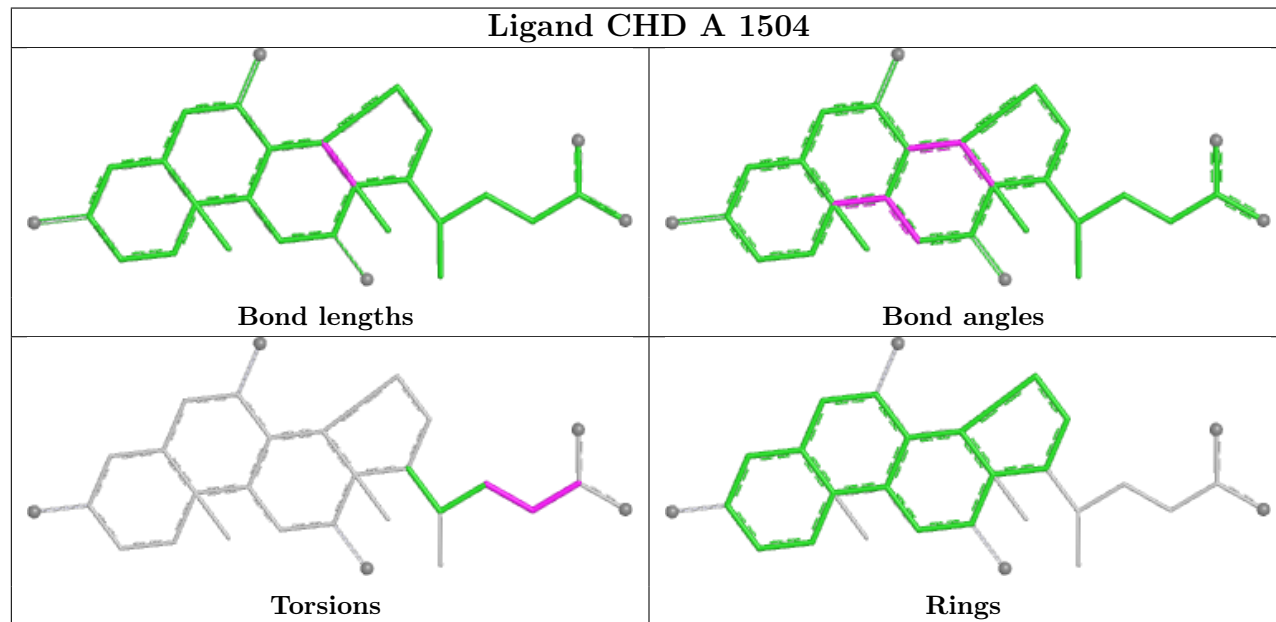
Ligand CHD A 1502

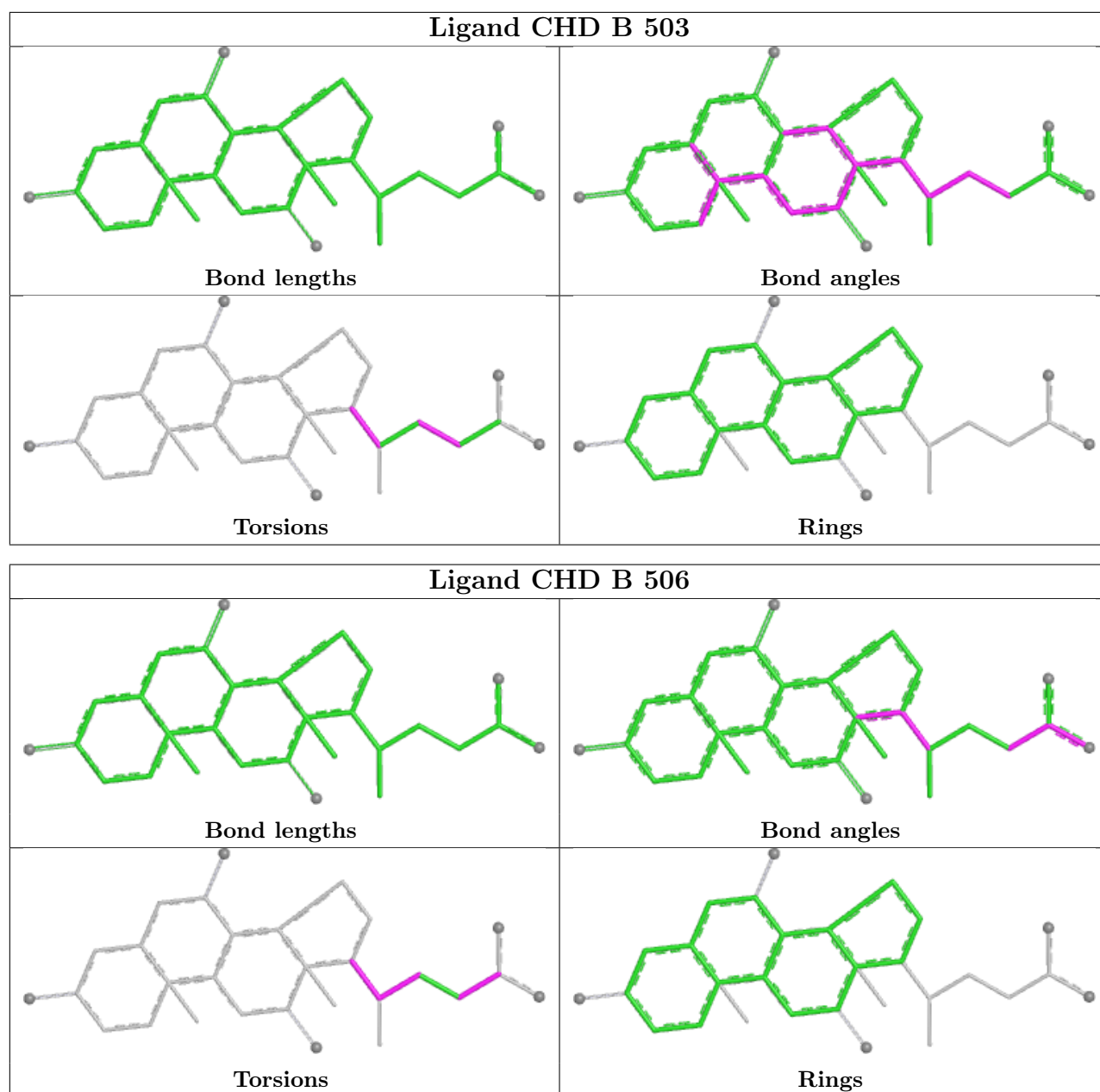


Ligand CHD A 1507



Ligand CHD A 1504





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	359/371 (96%)	-0.21	4 (1%) 78 77	9, 21, 38, 60	8 (2%)
1	B	359/371 (96%)	-0.27	6 (1%) 69 68	10, 20, 37, 56	7 (1%)
All	All	718/742 (96%)	-0.24	10 (1%) 73 73	9, 21, 38, 60	15 (2%)

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	213	VAL	3.8
1	B	213	VAL	3.4
1	B	179	ARG	2.7
1	A	216	LYS	2.3
1	B	337	PHE	2.2
1	B	423	LEU	2.1
1	B	214	GLY	2.1
1	B	341	HIS	2.1
1	A	423	LEU	2.0
1	A	212	GLN	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

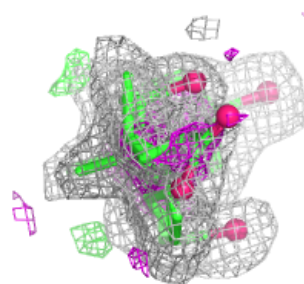
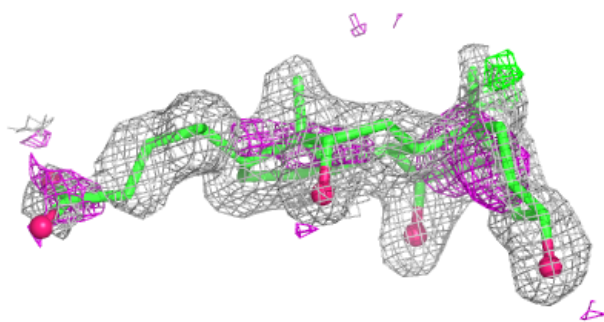
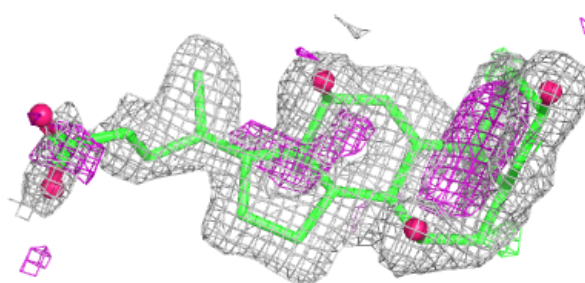
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	CHD	A	1507	29/29	0.75	0.14	25,33,48,52	0
3	CHD	B	506	29/29	0.78	0.14	25,30,46,50	0
3	CHD	B	503	29/29	0.79	0.15	41,46,61,66	0
3	CHD	A	1504	29/29	0.84	0.13	30,38,51,52	0
3	CHD	B	502	29/29	0.89	0.11	22,30,49,58	0
3	CHD	A	1503	29/29	0.90	0.10	20,28,43,54	0
5	EDO	B	505	4/4	0.91	0.09	25,26,26,26	0
4	SAL	A	1505	10/10	0.92	0.08	11,17,19,24	0
3	CHD	B	504	29/29	0.93	0.08	15,19,30,42	0
3	CHD	A	1502	29/29	0.93	0.09	15,21,36,45	0
5	EDO	A	1506	4/4	0.94	0.08	21,22,24,28	0
2	FES	B	501	4/4	0.99	0.03	15,17,17,18	0
2	FES	A	1501	4/4	0.99	0.03	16,17,18,18	0

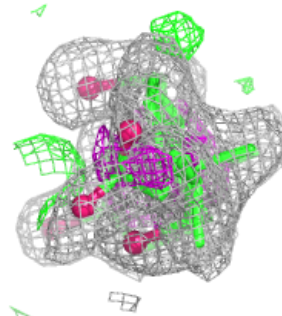
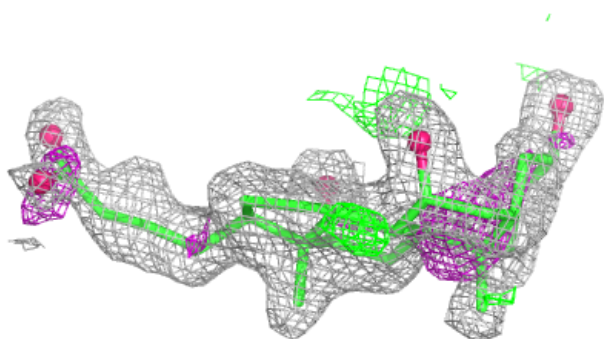
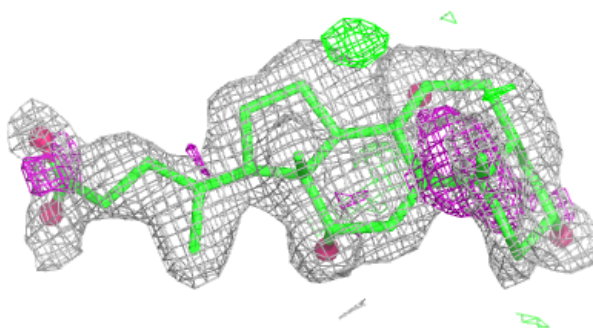
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around CHD A 1507:

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

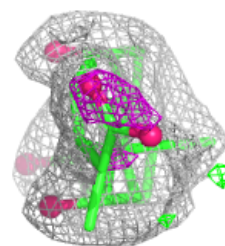
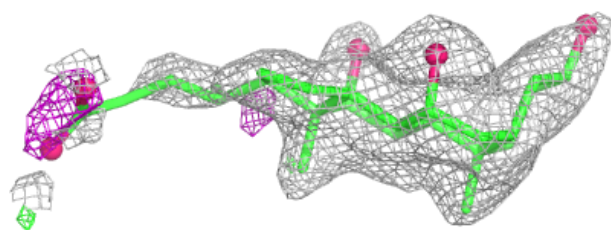
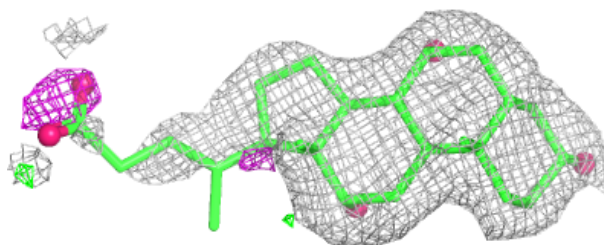
**Electron density around CHD B 506:**

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

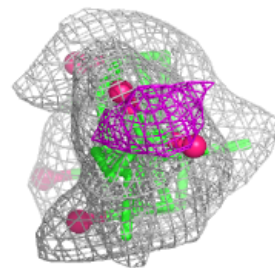
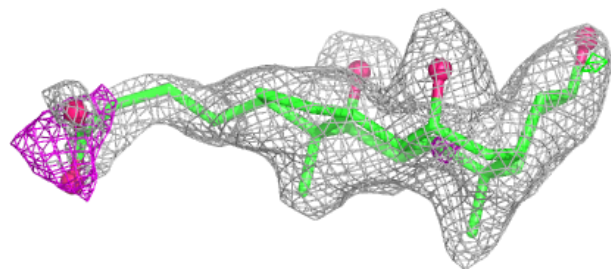
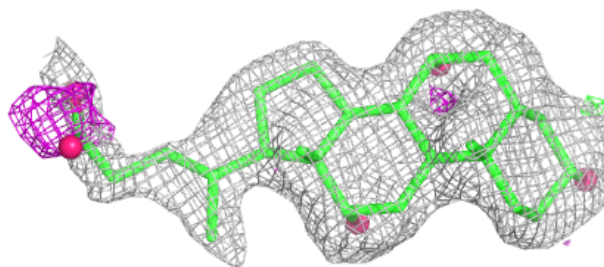


Electron density around CHD B 503:

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

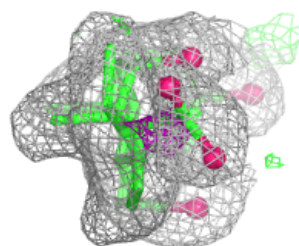
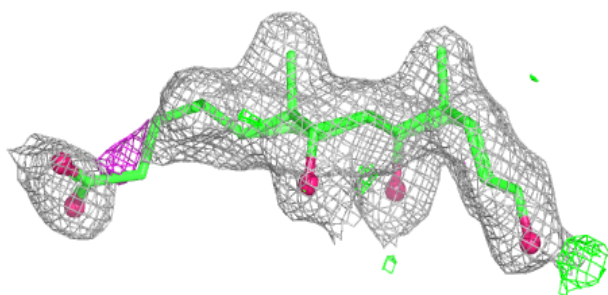
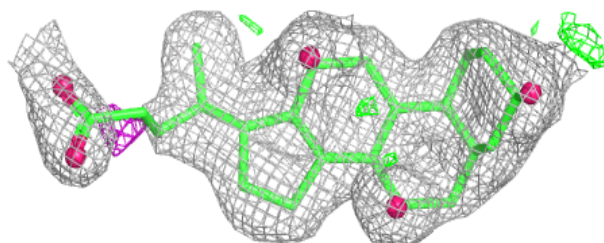
**Electron density around CHD A 1504:**

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

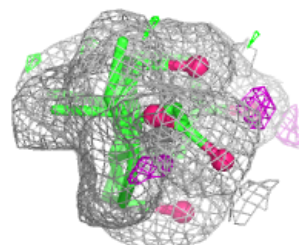
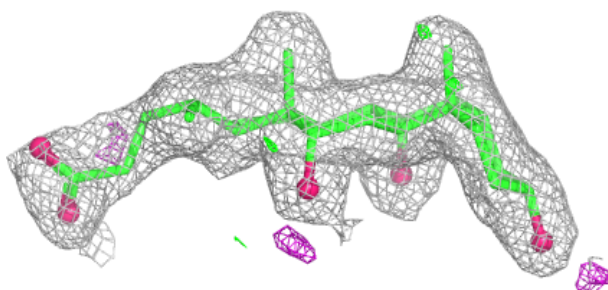
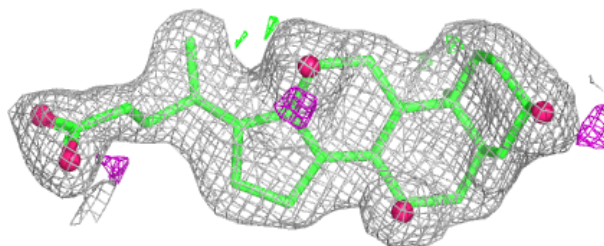


Electron density around CHD B 502:

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

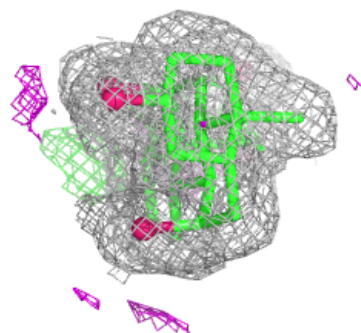
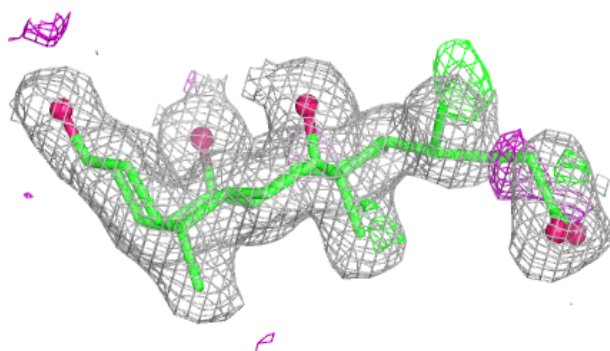
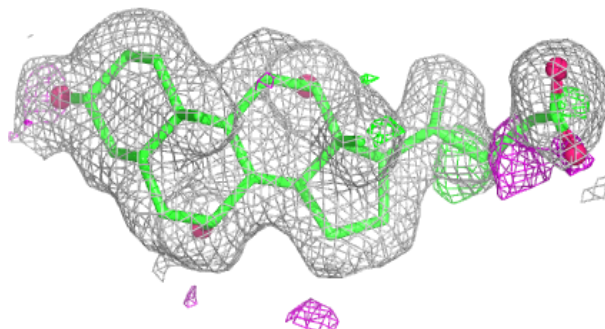
**Electron density around CHD A 1503:**

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

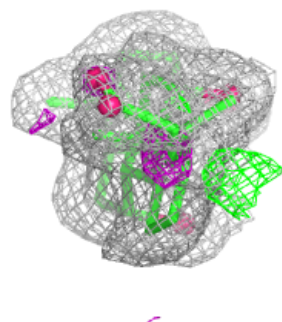
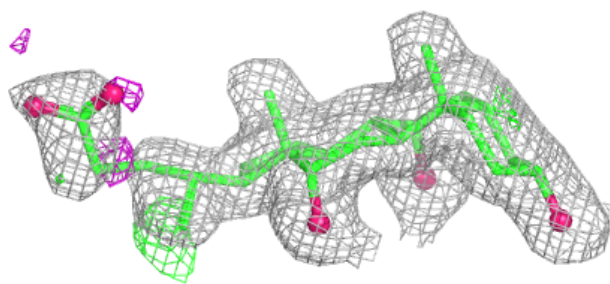
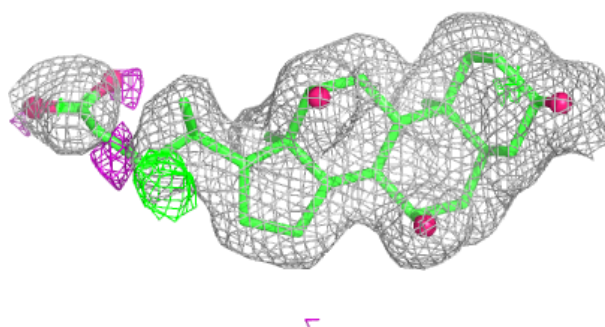


Electron density around CHD B 504:

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

**Electron density around CHD A 1502:**

$2mF_o-DF_c$ (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.