



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 04:48 PM UTC

PDB ID : 6H6M / pdb_00006h6m
Title : CR10 murine norovirus protruding domain in complex with the CD300lf receptor and glycochenodeoxycholate (GCDCA)
Authors : Kilic, T.; Hansman, G.S.
Deposited on : 2018-07-27
Resolution : 2.38 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

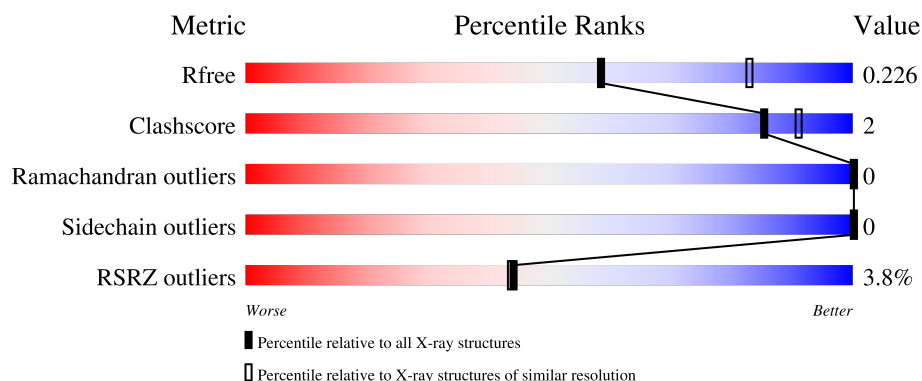
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.38 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	7164 (2.40-2.36)
Clashscore	190562	7722 (2.40-2.36)
Ramachandran outliers	187476	7626 (2.40-2.36)
Sidechain outliers	187428	7627 (2.40-2.36)
RSRZ outliers	180081	7170 (2.40-2.36)

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	303	3% 97% .
1	B	303	4% 95% 5%
1	C	303	4% 94% 6%
1	D	303	6% 94% 6%
2	E	111	3% 90% 10%

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Mol	Chain	Length	Quality of chain
2	F	111	 92%8%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 11579 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.

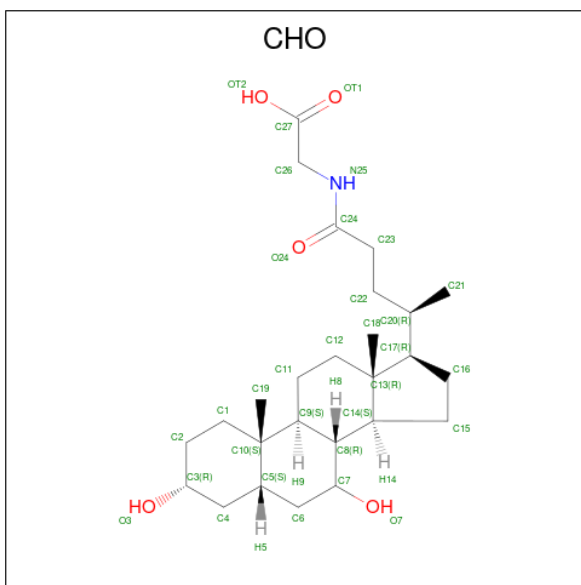
- Molecule 1 is a protein called Capsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	303	Total	C	N	O	S	0	0	0
			2284	1475	373	429	7			
1	B	303	Total	C	N	O	S	0	0	0
			2298	1485	374	432	7			
1	C	303	Total	C	N	O	S	0	1	0
			2304	1487	374	436	7			
1	D	303	Total	C	N	O	S	0	0	0
			2262	1461	371	423	7			

- Molecule 2 is a protein called CMRF35-like molecule 1.

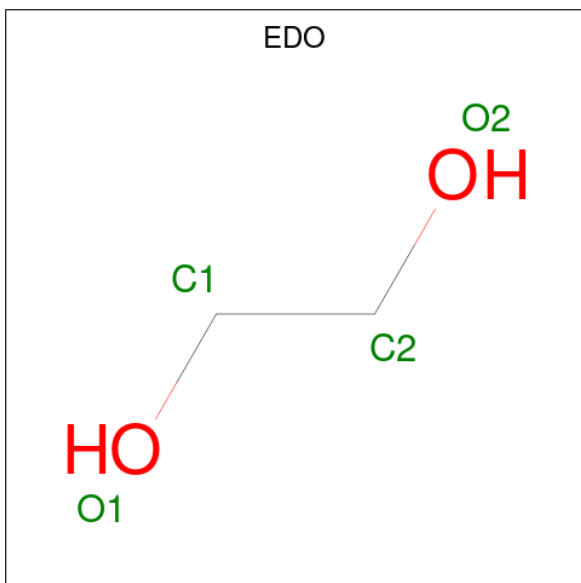
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	111	Total	C	N	O	S	0	0	0
			841	530	138	166	7			
2	F	111	Total	C	N	O	S	0	1	0
			870	547	144	171	8			

- Molecule 3 is GLYCOCHENODEOXYCHOLIC ACID (CCD ID: CHO) (formula: C₂₆H₄₃NO₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			32	26	1	5		
3	B	1	Total	C	N	O	0	0
			32	26	1	5		
3	C	1	Total	C	N	O	0	0
			32	26	1	5		
3	D	1	Total	C	N	O	0	0
			32	26	1	5		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).

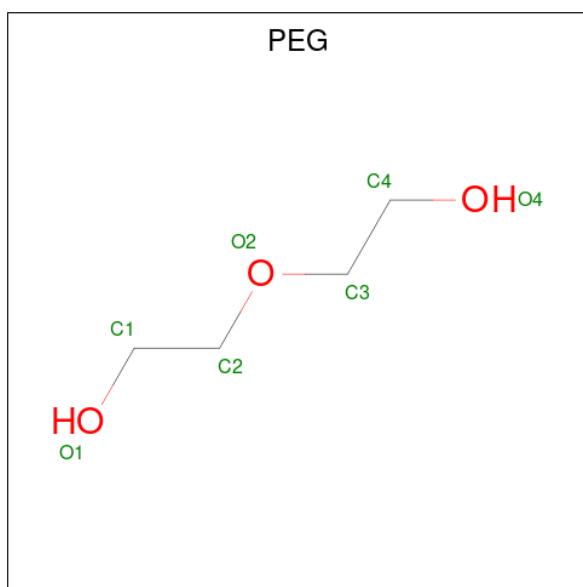


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0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

- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

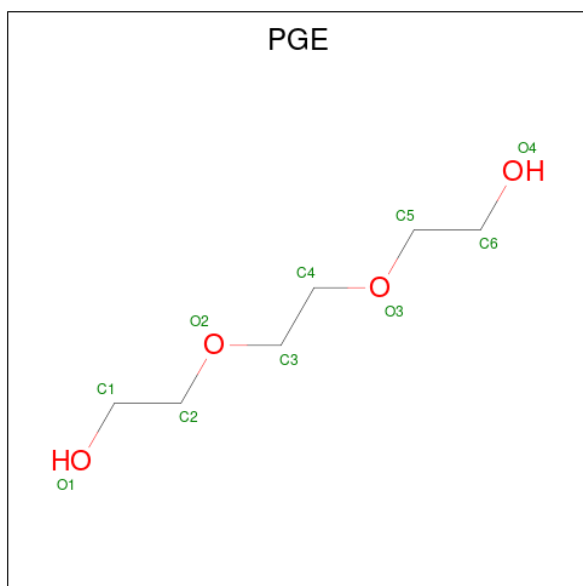
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Na 1 1	0	0
5	B	1	Total Na 1 1	0	0
5	C	1	Total Na 1 1	0	0
5	D	1	Total Na 1 1	0	0

- Molecule 6 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	E	1	Total	C	O	0	0
			7	4	3		

- Molecule 7 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	F	1	Total	C	O	0	0
			10	6	4		

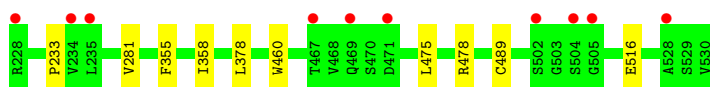
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	98	Total 98	O 98	0	0
8	B	119	Total 119	O 119	0	0
8	C	128	Total 128	O 128	0	0
8	D	97	Total 97	O 97	0	0
8	E	28	Total 28	O 28	0	0
8	F	41	Total 41	O 41	0	0

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.

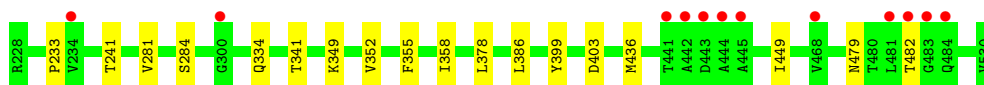
- Molecule 1: Capsid protein



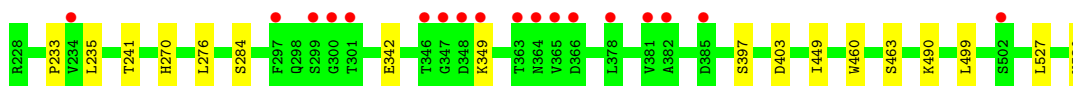
- Molecule 1: Capsid protein



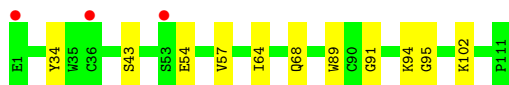
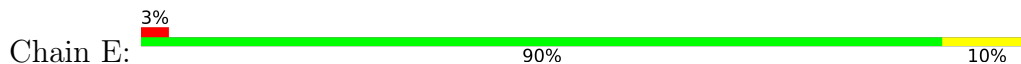
- Molecule 1: Capsid protein



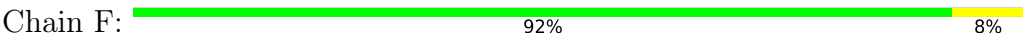
- Molecule 1: Capsid protein



- Molecule 2: CMRF35-like molecule 1



- Molecule 2: CMRF35-like molecule 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	75.94Å 137.55Å 93.80Å 90.00° 95.84° 90.00°	Depositor
Resolution (Å)	46.66 – 2.38 46.66 – 2.38	Depositor EDS
% Data completeness (in resolution range)	98.0 (46.66-2.38) 97.9 (46.66-2.38)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.04 (at 2.39Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.186 , 0.225 0.188 , 0.226	Depositor DCC
R_{free} test set	3751 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	31.8	Xtriage
Anisotropy	0.706	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 38.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11579	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.64% 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, PEG, EDO, CHO, PGE

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	0.16	0/2348	0.36	0/3224
1	B	0.15	0/2362	0.36	0/3240
1	C	0.15	0/2371	0.38	0/3252
1	D	0.14	0/2325	0.35	0/3193
2	E	0.15	0/859	0.41	0/1170
2	F	0.14	0/891	0.42	0/1207
All	All	0.15	0/11156	0.37	0/15286

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

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	2284	0	2169	6	0
1	B	2298	0	2212	11	0
1	C	2304	0	2217	13	0
1	D	2262	0	2148	12	0
2	E	841	0	786	6	0
2	F	870	0	844	5	0
3	A	32	0	42	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	32	0	42	0	0
3	C	32	0	42	1	0
3	D	32	0	42	0	0
4	A	16	0	24	0	0
4	B	16	0	24	1	0
4	C	12	0	18	1	0
4	D	8	0	12	2	0
4	E	4	0	6	0	0
4	F	4	0	6	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	E	7	0	10	0	0
7	F	10	0	14	0	0
8	A	98	0	0	0	0
8	B	119	0	0	0	0
8	C	128	0	0	0	0
8	D	97	0	0	0	0
8	E	28	0	0	0	0
8	F	41	0	0	0	0
All	All	11579	0	10658	47	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 2.

All (47) 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:B:449:ILE:HA	4:B:602:EDO:H12	1.68	0.74
1:D:449:ILE:HA	4:D:603:EDO:H21	1.73	0.69
1:A:281:VAL:HG11	1:B:235:LEU:HD21	1.83	0.61
2:E:54:GLU:HG2	2:E:68:GLN:HG3	1.86	0.57
1:B:355:PHE:CD2	1:B:378:LEU:HD23	2.39	0.57
1:C:479:ASN:OD1	1:C:482:THR:N	2.34	0.56
2:E:57:VAL:HB	2:E:64:ILE:HG22	1.91	0.52
3:A:601:CHO:H21	1:B:390:ARG:HB3	1.91	0.52
1:A:355:PHE:CE2	1:A:378:LEU:HD23	2.46	0.51
1:A:358:ILE:HD11	2:E:43:SER:HB3	1.93	0.51
1:B:233:PRO:HD3	1:B:460:TRP:CE2	2.46	0.50
2:F:23:ARG:HG2	2:F:72:ILE:HG12	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:355:PHE:CE2	1:C:378:LEU:HD23	2.49	0.48
1:C:403:ASP:HB2	4:C:603:EDO:H22	1.95	0.48
1:D:499:LEU:HD23	1:D:530:VAL:HG11	1.95	0.48
1:D:270:HIS:CD2	1:D:276:LEU:HD11	2.49	0.47
1:D:403:ASP:O	4:D:602:EDO:H22	2.13	0.47
1:C:352:VAL:HG21	1:D:397:SER:HB3	1.97	0.47
2:E:34:TYR:CZ	2:E:91:GLY:HA3	2.50	0.46
1:C:281:VAL:HG11	1:D:235:LEU:HD22	1.98	0.46
3:C:601:CHO:H222	3:C:601:CHO:H162	1.66	0.45
1:C:349:LYS:HA	1:C:349:LYS:HD3	1.82	0.44
1:C:284:SER:HB3	1:D:241:THR:HG23	1.99	0.43
2:E:89:TRP:CZ3	2:E:102:LYS:HB2	2.54	0.43
1:B:256:PRO:HG2	1:B:503:GLY:O	2.18	0.43
1:C:233:PRO:HB3	1:D:463:SER:HB3	2.00	0.43
1:C:334:GLN:HB3	1:C:399:TYR:HB3	2.01	0.43
1:C:241:THR:HG23	1:D:284:SER:HB3	2.01	0.43
3:A:601:CHO:H222	3:A:601:CHO:H162	1.83	0.42
1:D:233:PRO:HG3	1:D:460:TRP:CE3	2.54	0.42
2:F:34:TYR:CZ	2:F:91:GLY:HA3	2.54	0.42
1:A:475:LEU:HB2	1:A:489:CYS:SG	2.60	0.42
1:B:436:MET:HE2	1:B:449:ILE:HB	2.01	0.42
1:D:342:GLU:HA	1:D:349:LYS:O	2.19	0.41
2:F:89:TRP:CZ3	2:F:102:LYS:HB2	2.55	0.41
1:C:436:MET:HE2	1:C:449:ILE:HB	2.02	0.41
1:D:490:LYS:HG3	1:D:527:LEU:HD21	2.02	0.41
1:A:233:PRO:HD3	1:A:460:TRP:CE2	2.55	0.41
1:B:230:VAL:HG22	1:B:466:PHE:CB	2.51	0.41
2:F:39:VAL:HA	2:F:40:PRO:C	2.44	0.41
1:C:341:THR:HB	1:C:386:LEU:HD22	2.01	0.41
1:A:478:ARG:HE	1:A:516:GLU:CD	2.29	0.41
2:E:94:LYS:HG2	2:E:95:GLY:N	2.35	0.41
1:B:344:THR:OG1	1:B:385:ASP:HB3	2.21	0.41
1:C:358:ILE:HD11	2:F:43:SER:HB3	2.03	0.41
1:B:230:VAL:HG22	1:B:466:PHE:HB3	2.03	0.40
1:B:269:VAL:O	1:B:495:GLY:HA3	2.21	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	301/303 (99%)	290 (96%)	11 (4%)	0	100	100
1	B	301/303 (99%)	287 (95%)	14 (5%)	0	100	100
1	C	302/303 (100%)	290 (96%)	12 (4%)	0	100	100
1	D	301/303 (99%)	288 (96%)	13 (4%)	0	100	100
2	E	109/111 (98%)	106 (97%)	3 (3%)	0	100	100
2	F	110/111 (99%)	107 (97%)	3 (3%)	0	100	100
All	All	1424/1434 (99%)	1368 (96%)	56 (4%)	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	232/252 (92%)	232 (100%)	0	100	100
1	B	239/252 (95%)	239 (100%)	0	100	100
1	C	241/252 (96%)	241 (100%)	0	100	100
1	D	228/252 (90%)	228 (100%)	0	100	100
2	E	90/99 (91%)	90 (100%)	0	100	100
2	F	98/99 (99%)	98 (100%)	0	100	100
All	All	1128/1206 (94%)	1128 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	236	GLN
1	A	464	ASN
1	B	236	GLN
1	B	266	ASN
1	B	371	GLN
1	B	438	GLN
1	C	364	ASN
1	D	261	ASN
2	E	68	GLN
2	E	106	ASN
2	F	21	GLN
2	F	55	GLN
2	F	106	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 25 ligands modelled in this entry, 4 are 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
4	EDO	C	603	-	3,3,3	0.44	0	2,2,2	0.22	0
4	EDO	F	201	-	3,3,3	0.47	0	2,2,2	0.38	0
4	EDO	A	603	-	3,3,3	0.43	0	2,2,2	0.29	0
4	EDO	A	604	-	3,3,3	0.46	0	2,2,2	0.32	0
7	PGE	F	202	-	9,9,9	0.53	0	8,8,8	0.18	0
4	EDO	C	604	-	3,3,3	0.43	0	2,2,2	0.28	0
4	EDO	C	602	-	3,3,3	0.45	0	2,2,2	0.50	0
4	EDO	B	605	-	3,3,3	0.44	0	2,2,2	0.26	0
6	PEG	E	202	-	6,6,6	0.50	0	5,5,5	0.26	0
3	CHO	A	601	-	35,35,35	0.48	0	54,54,54	0.68	0
3	CHO	D	600	-	35,35,35	0.45	0	54,54,54	0.66	0
4	EDO	B	603	-	3,3,3	0.43	0	2,2,2	0.38	0
4	EDO	A	605	-	3,3,3	0.42	0	2,2,2	0.33	0
4	EDO	A	602	-	3,3,3	0.45	0	2,2,2	0.33	0
4	EDO	B	604	-	3,3,3	0.42	0	2,2,2	0.44	0
4	EDO	D	603	-	3,3,3	0.46	0	2,2,2	0.16	0
3	CHO	C	601	-	35,35,35	0.47	0	54,54,54	0.60	0
4	EDO	B	602	-	3,3,3	0.45	0	2,2,2	0.30	0
3	CHO	B	600	-	35,35,35	0.50	0	54,54,54	0.70	0
4	EDO	D	602	-	3,3,3	0.42	0	2,2,2	0.45	0
4	EDO	E	201	-	3,3,3	0.44	0	2,2,2	0.34	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
4	EDO	C	603	-	-	1/1/1/1	-
4	EDO	F	201	-	-	0/1/1/1	-
4	EDO	A	603	-	-	1/1/1/1	-
4	EDO	A	604	-	-	1/1/1/1	-
7	PGE	F	202	-	-	2/7/7/7	-
4	EDO	C	604	-	-	1/1/1/1	-
4	EDO	C	602	-	-	0/1/1/1	-
4	EDO	B	605	-	-	0/1/1/1	-
6	PEG	E	202	-	-	2/4/4/4	-
3	CHO	A	601	-	-	4/14/75/75	0/4/4/4
3	CHO	D	600	-	-	4/14/75/75	0/4/4/4
4	EDO	B	603	-	-	1/1/1/1	-
4	EDO	A	605	-	-	0/1/1/1	-
4	EDO	A	602	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	B	604	-	-	0/1/1/1	-
4	EDO	D	603	-	-	1/1/1/1	-
3	CHO	C	601	-	-	5/14/75/75	0/4/4/4
4	EDO	B	602	-	-	1/1/1/1	-
3	CHO	B	600	-	-	4/14/75/75	0/4/4/4
4	EDO	D	602	-	-	1/1/1/1	-
4	EDO	E	201	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	CHO	C16-C17-C20-C21
3	D	600	CHO	C16-C17-C20-C21
3	A	601	CHO	C13-C17-C20-C21
3	C	601	CHO	C13-C17-C20-C21
3	D	600	CHO	C13-C17-C20-C21
3	C	601	CHO	C16-C17-C20-C21
3	A	601	CHO	C13-C17-C20-C22
3	C	601	CHO	C13-C17-C20-C22
3	D	600	CHO	C13-C17-C20-C22
3	B	600	CHO	C13-C17-C20-C21
3	A	601	CHO	C16-C17-C20-C22
3	B	600	CHO	C13-C17-C20-C22
3	B	600	CHO	C16-C17-C20-C21
3	D	600	CHO	C16-C17-C20-C22
3	C	601	CHO	C16-C17-C20-C22
6	E	202	PEG	O1-C1-C2-O2
6	E	202	PEG	O2-C3-C4-O4
4	A	603	EDO	O1-C1-C2-O2
4	B	602	EDO	O1-C1-C2-O2
4	C	603	EDO	O1-C1-C2-O2
4	D	602	EDO	O1-C1-C2-O2
3	B	600	CHO	C16-C17-C20-C22
7	F	202	PGE	C6-C5-O3-C4
4	A	604	EDO	O1-C1-C2-O2
4	C	604	EDO	O1-C1-C2-O2
4	D	603	EDO	O1-C1-C2-O2

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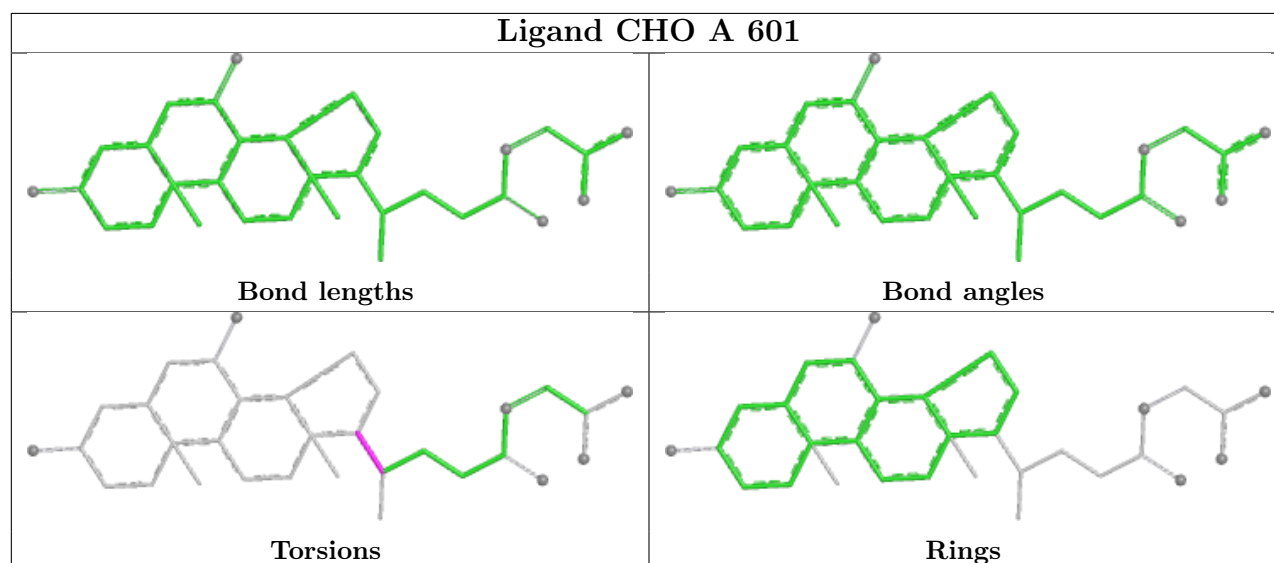
Mol	Chain	Res	Type	Atoms
3	C	601	CHO	C17-C20-C22-C23
7	F	202	PGE	C3-C4-O3-C5
4	B	603	EDO	O1-C1-C2-O2

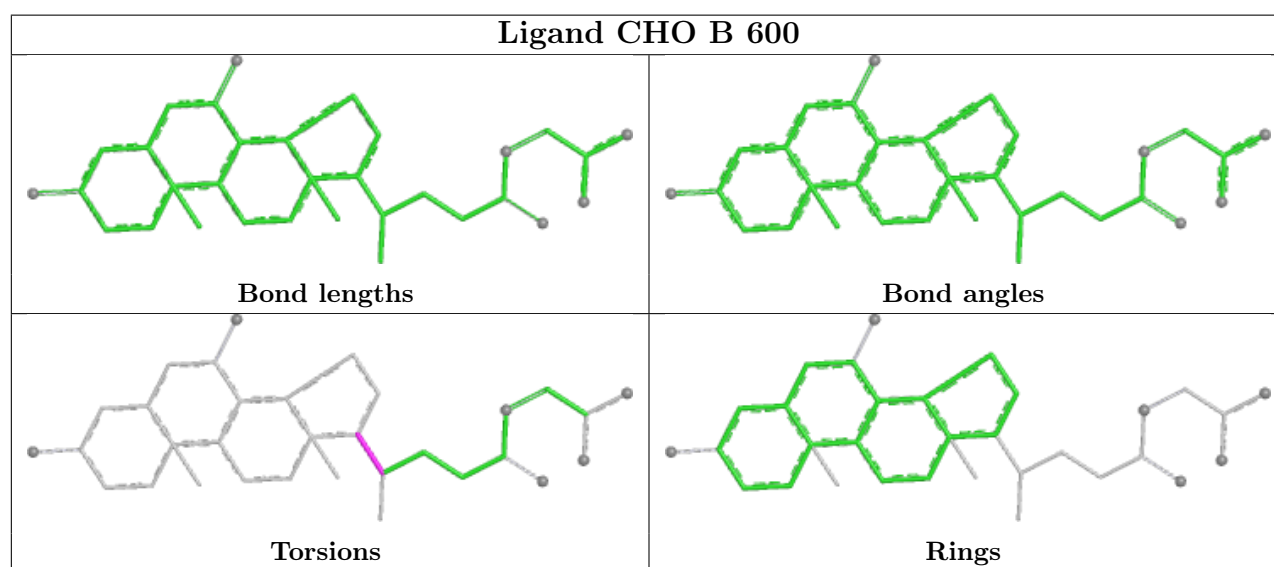
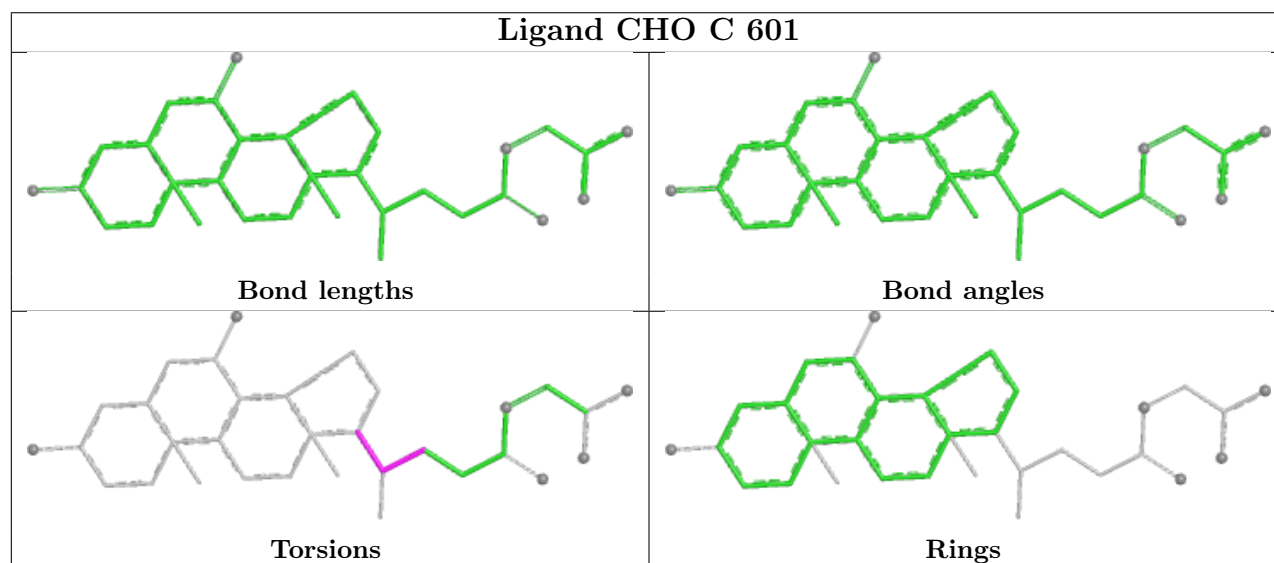
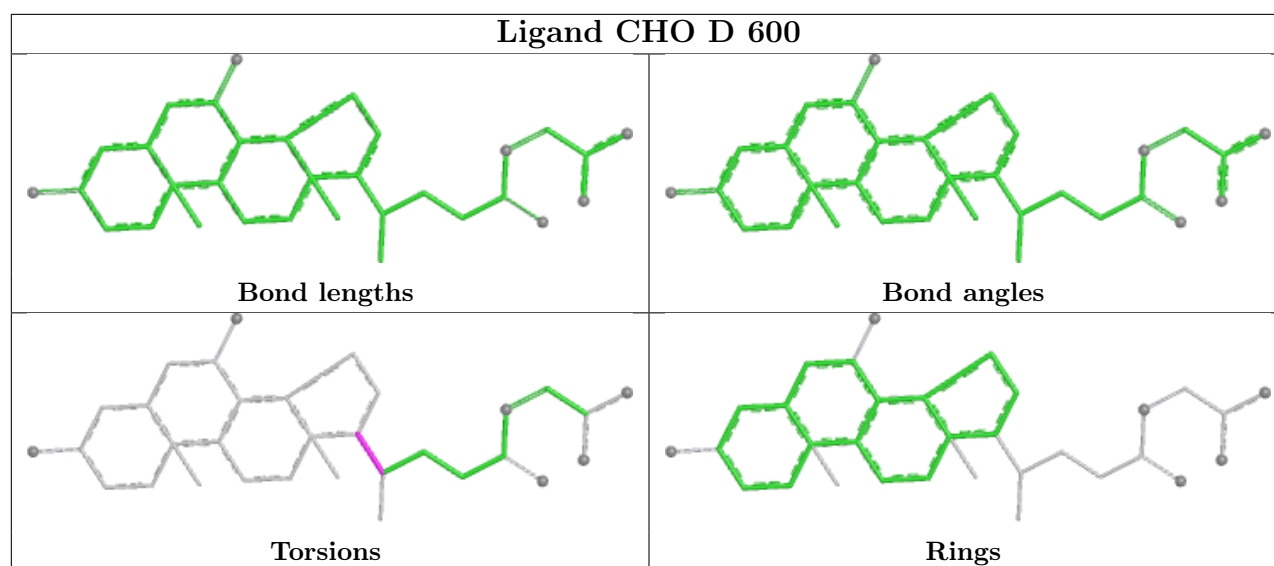
There are no ring outliers.

6 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	603	EDO	1	0
3	A	601	CHO	2	0
4	D	603	EDO	1	0
3	C	601	CHO	1	0
4	B	602	EDO	1	0
4	D	602	EDO	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2			OWAB(Å ²)	Q < 0.9
1	A	303/303 (100%)	0.20	10 (3%)	49	49	24, 38, 66, 79	0
1	B	303/303 (100%)	-0.02	11 (3%)	46	46	22, 31, 50, 75	0
1	C	303/303 (100%)	-0.00	12 (3%)	42	42	19, 32, 49, 72	1 (0%)
1	D	303/303 (100%)	0.20	18 (5%)	28	27	23, 36, 66, 83	0
2	E	111/111 (100%)	0.19	3 (2%)	56	56	27, 39, 56, 67	0
2	F	111/111 (100%)	-0.08	0	100	100	21, 35, 47, 64	1 (0%)
All	All	1434/1434 (100%)	0.09	54 (3%)	44	44	19, 34, 60, 83	2 (0%)

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	470	SER	5.1
1	B	348	ASP	5.0
1	C	482	THR	4.8
1	A	504	SER	4.5
1	D	348	ASP	4.5
2	E	1	GLU	4.3
1	A	228	ARG	4.3
1	D	364	ASN	4.3
1	A	502	SER	4.2
1	C	234	VAL	4.1
1	D	346	THR	4.1
1	B	471	ASP	3.9
1	A	234	VAL	3.6
1	B	347	GLY	3.5
1	C	441	THR	3.3
1	A	467	THR	3.3
1	C	443	ASP	3.2
1	D	300	GLY	3.1
1	D	297	PHE	3.0

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Mol	Chain	Res	Type	RSRZ
1	D	301	THR	3.0
1	D	363	THR	2.9
1	D	347	GLY	2.8
1	D	349	LYS	2.8
1	B	469	GLN	2.8
1	C	442	ALA	2.8
1	A	471	ASP	2.7
1	C	481	LEU	2.7
1	D	365	VAL	2.6
1	D	381	VAL	2.6
1	B	346	THR	2.6
1	C	444	ALA	2.3
1	A	528	ALA	2.3
1	B	413	LEU	2.3
1	D	385	ASP	2.3
1	A	505	GLY	2.3
1	C	300	GLY	2.3
1	A	469	GLN	2.3
1	B	235	LEU	2.2
1	D	502	SER	2.2
1	C	468	VAL	2.2
1	D	234	VAL	2.2
1	C	484	GLN	2.2
1	C	445	ALA	2.2
2	E	53	SER	2.2
1	D	378	LEU	2.1
1	C	483	GLY	2.1
1	A	235	LEU	2.1
2	E	36	CYS	2.1
1	B	467	THR	2.1
1	B	234	VAL	2.1
1	B	228	ARG	2.1
1	D	366	ASP	2.0
1	D	299	SER	2.0
1	D	382	ALA	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

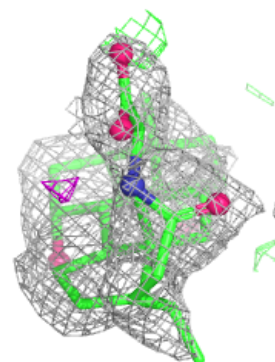
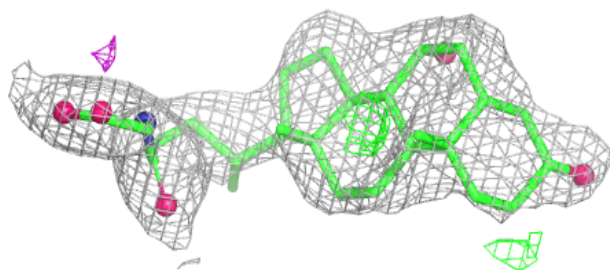
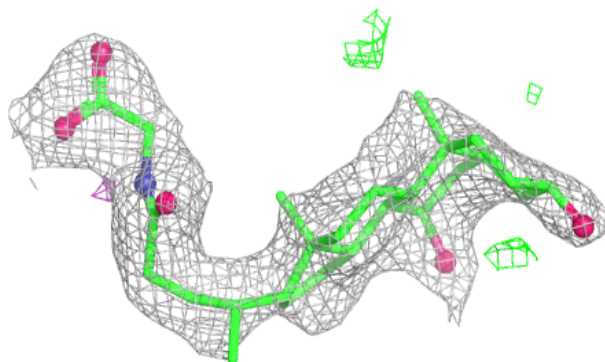
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	EDO	B	602	4/4	0.80	0.17	40,40,41,41	0
7	PGE	F	202	10/10	0.80	0.20	60,60,60,60	0
4	EDO	A	604	4/4	0.81	0.21	40,41,43,44	0
3	CHO	C	601	32/32	0.83	0.17	56,59,61,61	0
6	PEG	E	202	7/7	0.84	0.18	67,67,67,67	0
4	EDO	C	604	4/4	0.85	0.15	34,36,39,42	0
5	NA	B	601	1/1	0.85	0.08	45,45,45,45	0
4	EDO	A	602	4/4	0.86	0.16	44,44,44,45	0
4	EDO	F	201	4/4	0.88	0.14	34,34,35,36	0
4	EDO	D	602	4/4	0.90	0.15	34,34,35,35	0
3	CHO	A	601	32/32	0.91	0.10	37,38,41,42	0
4	EDO	A	603	4/4	0.92	0.09	45,45,45,45	0
4	EDO	C	603	4/4	0.93	0.13	43,44,45,45	0
4	EDO	D	603	4/4	0.93	0.12	41,43,43,44	0
3	CHO	D	600	32/32	0.93	0.09	32,35,37,37	0
3	CHO	B	600	32/32	0.95	0.08	28,30,34,35	0
4	EDO	B	603	4/4	0.95	0.08	36,36,37,38	0
5	NA	D	601	1/1	0.95	0.10	44,44,44,44	0
4	EDO	B	604	4/4	0.95	0.09	29,31,33,35	0
4	EDO	B	605	4/4	0.95	0.09	30,32,33,33	0
4	EDO	E	201	4/4	0.96	0.10	35,37,37,37	0
4	EDO	C	602	4/4	0.96	0.09	26,27,28,28	0
4	EDO	A	605	4/4	0.98	0.05	34,34,34,35	0
5	NA	C	605	1/1	0.99	0.04	42,42,42,42	0
5	NA	A	606	1/1	0.99	0.02	36,36,36,36	0

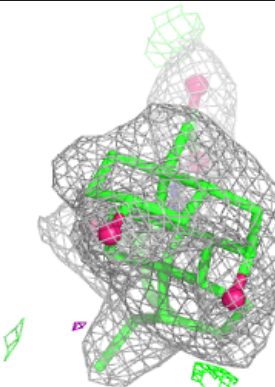
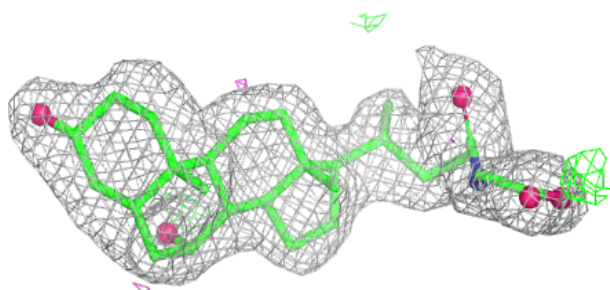
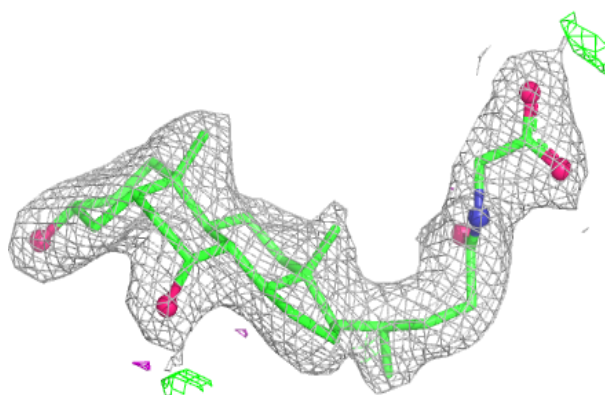
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around CHO C 601:

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

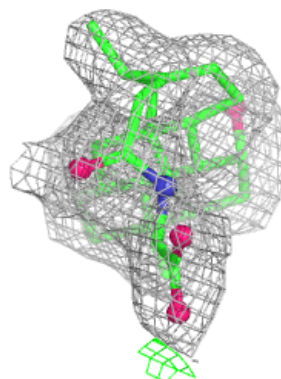
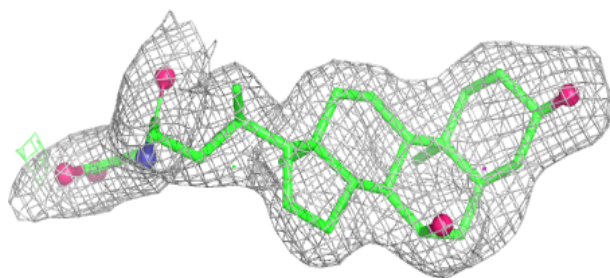
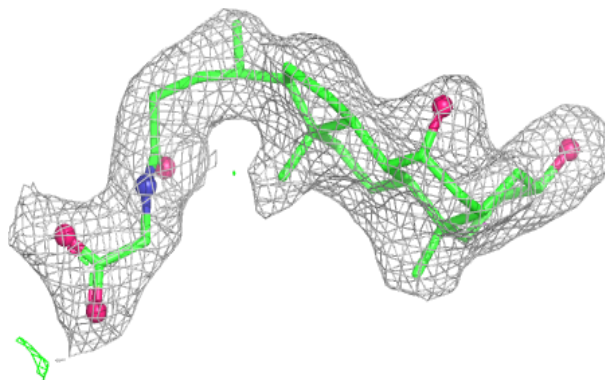
**Electron density around CHO A 601:**

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

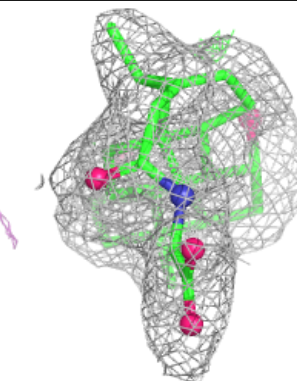
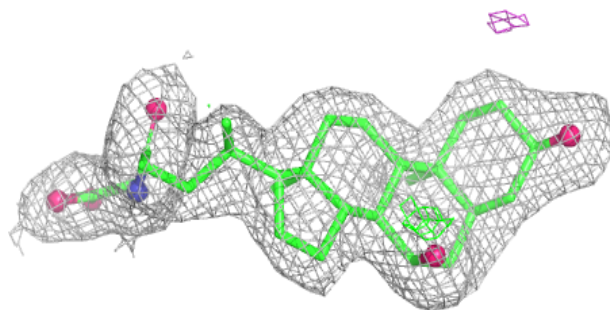
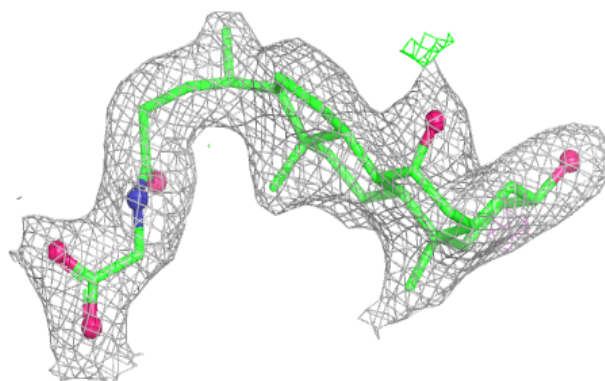


Electron density around CHO D 600:

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

**Electron density around CHO B 600:**

$2mF_o-DF_c$ (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.