



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 07:47 PM UTC

PDB ID : 8QEG / pdb_00008qeg
Title : Crystal structure of the G11 protein heterotrimer bound to YM-254890 inhibitor
Authors : Muehle, J.; Rodrigues, M.J.; Guixa-Gonzalez, R.; Deupi, X.; Schertler, G.F.X.
Deposited on : 2023-08-31
Resolution : 1.70 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

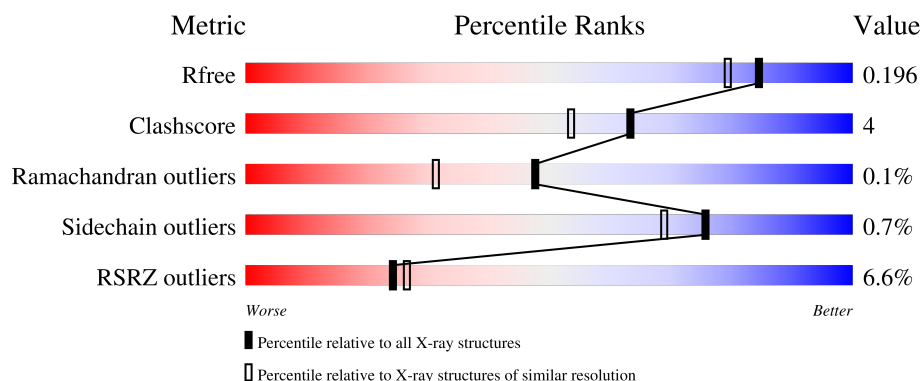
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	352	5% 87% 9% .
2	B	344	4% 87% 8% 5%
3	G	71	21% 75% 7% 18%

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 6952 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 Guanine nucleotide-binding protein subunit alpha-11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	340	Total	C	N	O	S	0	24	0
			2979	1897	514	556	12			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	8	GLY	-	expression tag	UNP P29992
A	9	CYS	-	expression tag	UNP P29992
A	10	THR	-	expression tag	UNP P29992
A	11	LEU	-	expression tag	UNP P29992
A	12	SER	-	expression tag	UNP P29992
A	13	ALA	-	expression tag	UNP P29992
A	14	GLU	-	expression tag	UNP P29992
A	15	ASP	-	expression tag	UNP P29992
A	16	LYS	-	expression tag	UNP P29992
A	17	ALA	-	expression tag	UNP P29992
A	18	ALA	-	expression tag	UNP P29992
A	19	VAL	-	expression tag	UNP P29992
A	20	GLU	-	expression tag	UNP P29992
A	21	ARG	-	expression tag	UNP P29992
A	22	SER	-	expression tag	UNP P29992
A	23	LYS	-	expression tag	UNP P29992
A	24	MET	-	expression tag	UNP P29992
A	25	ILE	-	expression tag	UNP P29992
A	26	ASP	-	expression tag	UNP P29992
A	27	ARG	-	expression tag	UNP P29992
A	28	ASN	-	expression tag	UNP P29992
A	29	LEU	-	expression tag	UNP P29992
A	30	ARG	-	expression tag	UNP P29992
A	31	GLU	-	expression tag	UNP P29992
A	32	ASP	-	expression tag	UNP P29992
A	33	GLY	-	expression tag	UNP P29992
A	34	GLU	-	expression tag	UNP P29992

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Chain	Residue	Modelled	Actual	Comment	Reference
A	35	LYS	-	expression tag	UNP P29992

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	328	Total	C	N	O	S	0	14	0
			2593	1600	466	503	24			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	PRO	-	expression tag	UNP P62873
B	-2	GLY	-	expression tag	UNP P62873
B	-1	SER	-	expression tag	UNP P62873
B	0	SER	-	expression tag	UNP P62873
B	1	GLY	-	expression tag	UNP P62873

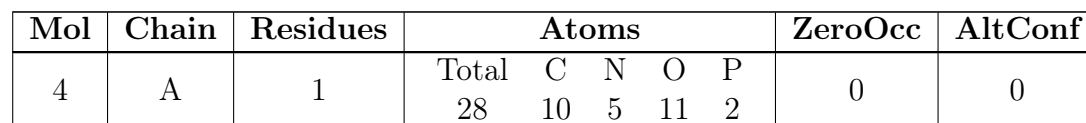
- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	58	Total	C	N	O	S	0	1	0
			442	282	73	84	3			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	69	SER	CYS	engineered mutation	UNP P59768

- Molecule 4 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



-
- EDO
- Chemical structure of EDO (Ethane-1,2-diol) showing a zigzag conformation. The carbon atoms are labeled C1 and C2 in green. The hydroxyl groups are labeled HO and OH in red, with their respective oxygen atoms labeled O1 and O2 in green.

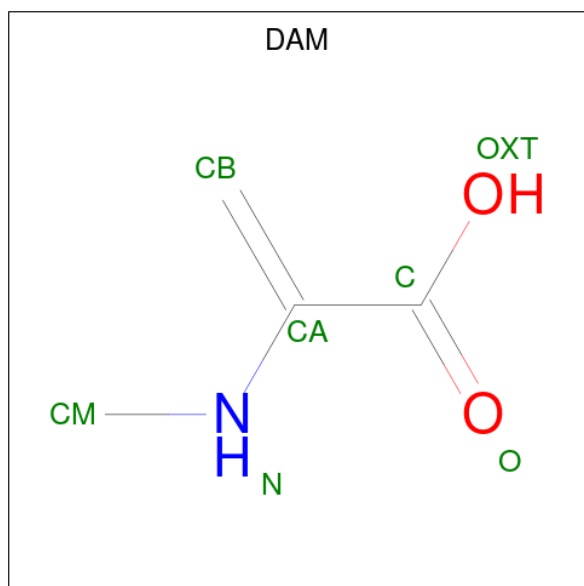
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0



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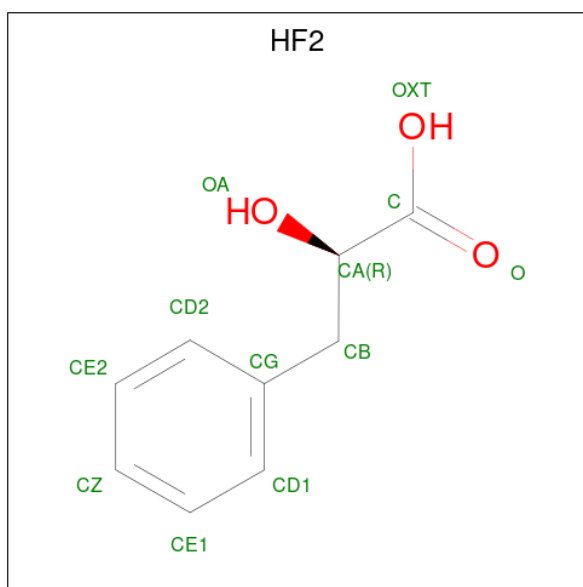
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is N-METHYL-ALPHA-BETA-DEHYDROALANINE (CCD ID: DAM) (formula: $C_4H_7NO_2$) (labeled as "Ligand of Interest" by depositor).



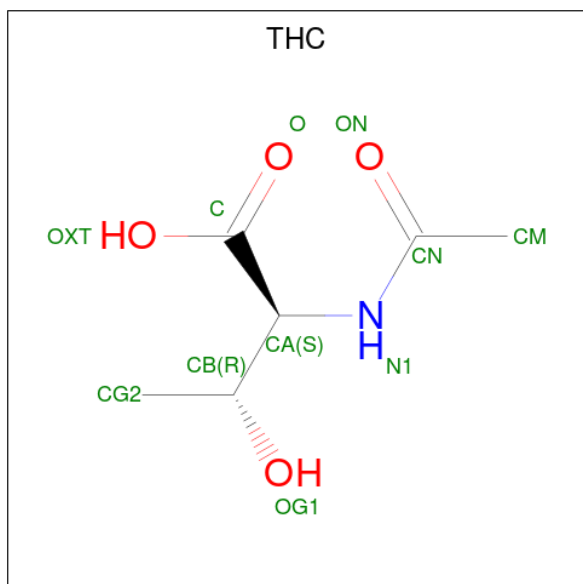
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			6	4	1	1		

- Molecule 7 is (2R)-2-hydroxy-3-phenylpropanoic acid (CCD ID: HF2) (formula: $C_9H_{10}O_3$) (labeled as "Ligand of Interest" by depositor).



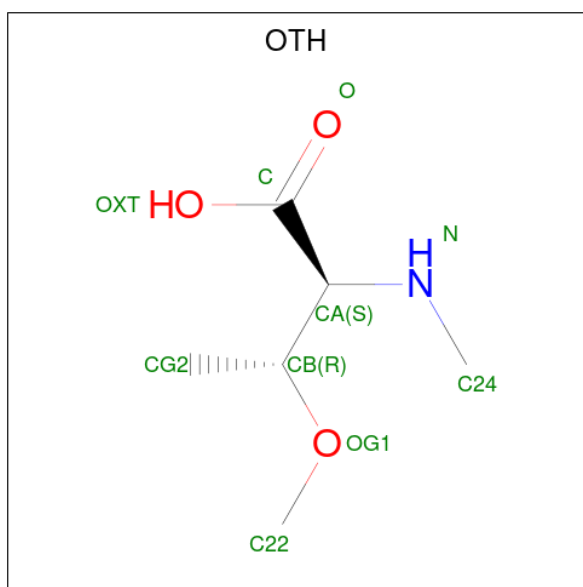
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			11	9	2		

- Molecule 8 is N-METHYLCARBONYLTHREONINE (CCD ID: THC) (formula: $C_6H_{11}NO_4$) (labeled as "Ligand of Interest" by depositor).



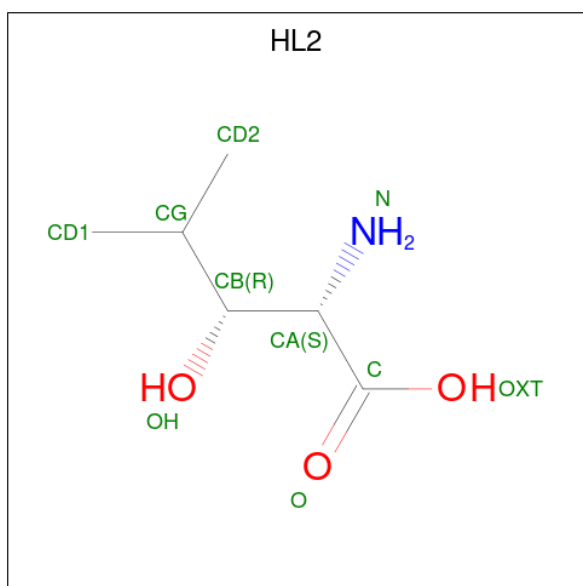
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	O	0	0
			10	6	1	3		

- Molecule 9 is N,O-dimethyl-L-threonine (CCD ID: OTH) (formula: $C_6H_{13}NO_3$) (labeled as "Ligand of Interest" by depositor).



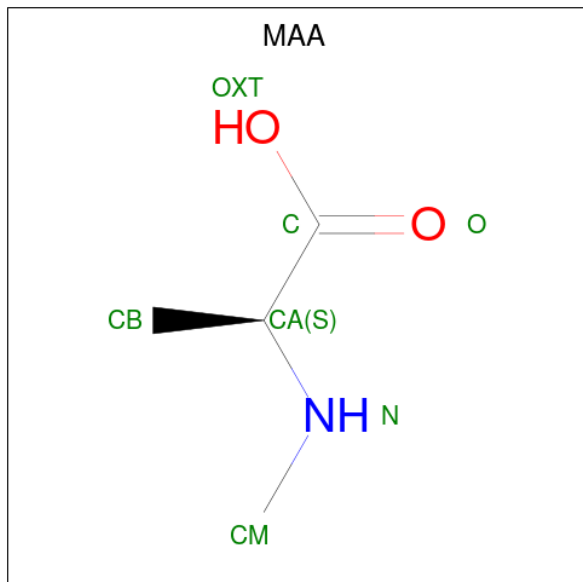
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	N	O	0	0
			9	6	1	2		

- Molecule 10 is (2S,3R)-2-amino-3-hydroxy-4-methylpentanoic acid (CCD ID: HL2) (formula: $C_6H_{13}NO_3$) (labeled as "Ligand of Interest" by depositor).



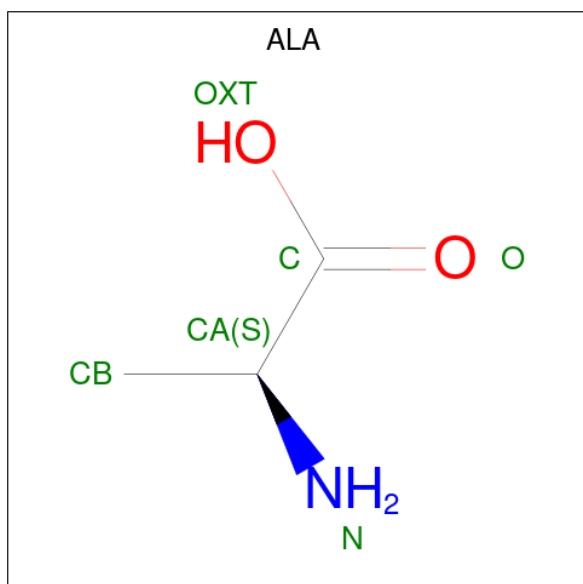
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	A	1	Total	C	N	O	0	0
			9	6	1	2		
10	A	1	Total	C	N	O	0	1
			15	11	1	3		

- Molecule 11 is N-methyl-L-alanine (CCD ID: MAA) (formula: $C_4H_9NO_2$) (labeled as "Ligand of Interest" by depositor).



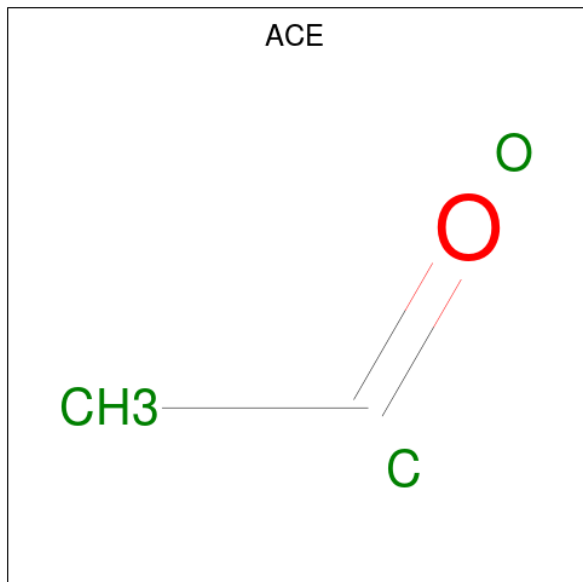
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	B	1	Total	C	N	O	0	0
			6	4	1	1		

- Molecule 12 is ALANINE (CCD ID: ALA) (formula: $C_3H_7NO_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
12	B	1	Total	C	N	O	0	0
			5	3	1	1		

- Molecule 13 is ACETYL GROUP (CCD ID: ACE) (formula: C_2H_4O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
13	B	1	Total	C	O	0	0
			3	2	1		

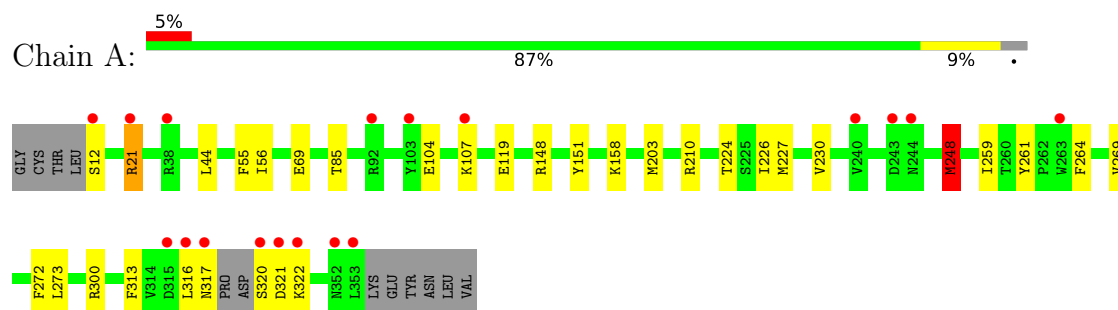
- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	438	Total	O	0	5
			438	438		
14	B	328	Total	O	0	5
			330	330		
14	G	36	Total	O	0	0
			36	36		

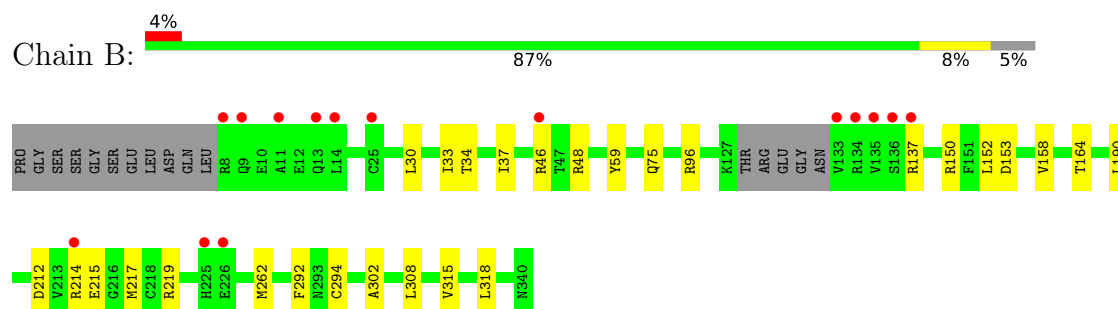
3 Residue-property plots [i](#)

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.

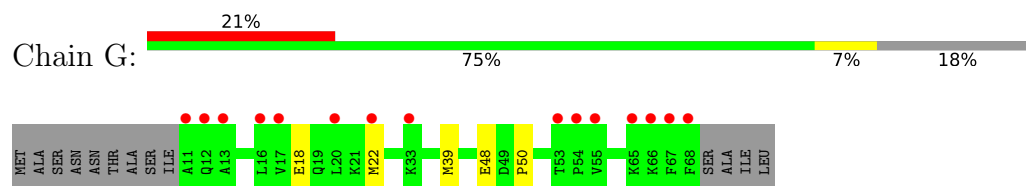
- Molecule 1: Guanine nucleotide-binding protein subunit alpha-11



- Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1



- Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.60Å 102.53Å 154.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	59.25 – 1.70 59.25 – 1.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (59.25-1.70) 100.0 (59.25-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.01 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.8.0403	Depositor
R, R_{free}	0.160 , 0.188 0.172 , 0.196	Depositor DCC
R_{free} test set	6216 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	29.3	Xtriage
Anisotropy	0.077	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 50.8	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	0.97	EDS
Total number of atoms	6952	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.45% 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: MAA, THC, HL2, OTH, ACE, GDP, EDO, HF2, DAM

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	0.66	1/3038 (0.0%)	0.96	2/4093 (0.0%)
2	B	0.69	0/2639	0.99	2/3579 (0.1%)
3	G	0.57	0/450	0.93	0/610
All	All	0.67	1/6127 (0.0%)	0.97	4/8282 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
2	B	0	2
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	224	THR	C-O	5.45	1.30	1.24

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	104	GLU	CB-CG-CD	5.77	122.41	112.60
2	B	292	PHE	CA-CB-CG	5.50	119.30	113.80
1	A	248	MET	CG-SD-CE	-5.17	89.54	100.90
2	B	164	THR	CA-CB-OG1	5.02	117.13	109.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	210	ARG	Sidechain
2	B	137	ARG	Sidechain
2	B	150	ARG	Sidechain

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	2979	0	2961	25	0
2	B	2593	0	2468	20	0
3	G	442	0	418	5	0
4	A	28	0	12	0	0
5	A	20	0	30	1	0
5	B	12	0	18	1	0
6	A	6	0	5	1	0
7	A	11	0	8	0	0
8	A	10	0	4	0	0
9	A	9	0	11	0	0
10	A	24	0	29	1	0
11	B	6	0	7	1	0
12	B	5	0	4	1	0
13	B	3	0	3	0	0
14	A	438	0	0	6	0
14	B	330	0	0	3	0
14	G	36	0	0	0	0
All	All	6952	0	5978	49	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.

The worst 5 of 49 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:212:ASP:OD2	2:B:219[B]:ARG:NH2	2.17	0.76
2:B:33:ILE:HG22	3:G:39:MET:CE	2.16	0.75
1:A:259:ILE:HD11	1:A:316:LEU:HD13	1.67	0.75
2:B:215:GLU:OE1	2:B:217:MET:CB	2.37	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:33:ILE:HG22	3:G:39:MET:HE1	1.73	0.70

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	360/352 (102%)	354 (98%)	5 (1%)	1 (0%)	36	22
2	B	338/344 (98%)	325 (96%)	13 (4%)	0	100	100
3	G	57/71 (80%)	57 (100%)	0	0	100	100
All	All	755/767 (98%)	736 (98%)	18 (2%)	1 (0%)	48	31

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	321	ASP

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	322/317 (102%)	317 (98%)	5 (2%)	55	41
2	B	278/285 (98%)	278 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	G	42/58 (72%)	42 (100%)	0	100	100
All	All	642/660 (97%)	637 (99%)	5 (1%)	76	65

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	SER
1	A	21[A]	ARG
1	A	21[B]	ARG
1	A	119	GLU
1	A	248	MET

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

Mol	Chain	Res	Type
1	A	350	GLN
2	B	44	GLN
2	B	155	ASN
3	G	25	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](#)

19 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
13	ACE	B	406	10	1,2,2	0.16	0	0,1,1	-	-
5	EDO	A	404	-	3,3,3	0.27	0	2,2,2	0.13	0
5	EDO	A	402	-	3,3,3	0.09	0	2,2,2	0.72	0
4	GDP	A	401	-	29,30,30	0.66	0	45,47,47	0.61	0
9	OTH	A	410	10,8	7,8,9	0.87	0	5,9,11	0.88	0
11	MAA	B	404	10,12	4,5,6	0.90	0	2,5,7	0.16	0
7	HF2	A	408	6,8	10,11,12	0.63	0	11,13,15	0.48	0
5	EDO	B	402	-	3,3,3	0.42	0	2,2,2	0.40	0
5	EDO	B	401	-	3,3,3	0.33	0	2,2,2	0.23	0
5	EDO	A	406	-	3,3,3	0.29	0	2,2,2	0.24	0
6	DAM	A	407	7,12	4,5,6	2.41	2 (50%)	3,5,7	2.11	2 (66%)
5	EDO	A	403	-	3,3,3	0.36	0	2,2,2	0.47	0
10	HL2	A	412[A]	-	7,8,9	0.84	0	7,10,12	0.80	0
5	EDO	B	403	-	3,3,3	0.34	0	2,2,2	0.29	0
5	EDO	A	405	-	3,3,3	0.09	0	2,2,2	0.23	0
10	HL2	A	411	9,11,10	7,8,9	0.49	0	7,10,12	1.06	1 (14%)
8	THC	A	409	9,7	8,9,10	0.49	0	10,11,13	1.55	2 (20%)
12	ALA	B	405	6,11	3,4,5	0.72	0	2,4,6	1.18	0
10	HL2	A	412[B]	-	7,8,9	0.83	0	7,10,12	1.03	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
5	EDO	A	404	-	-	0/1/1/1	-
5	EDO	A	402	-	-	1/1/1/1	-
5	EDO	B	401	-	-	1/1/1/1	-
5	EDO	A	405	-	-	0/1/1/1	-
5	EDO	B	402	-	-	1/1/1/1	-
5	EDO	B	403	-	-	0/1/1/1	-
4	GDP	A	401	-	-	2/16/32/32	0/3/3/3
9	OTH	A	410	10,8	-	5/8/10/12	-
11	MAA	B	404	10,12	-	1/2/4/6	-
7	HF2	A	408	6,8	-	0/5/6/8	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	HL2	A	411	9,11,10	-	0/9/10/12	-
8	THC	A	409	9,7	-	0/9/10/12	-
12	ALA	B	405	6,11	-	0/1/2/4	-
5	EDO	A	406	-	-	1/1/1/1	-
6	DAM	A	407	7,12	-	0/0/4/6	-
10	HL2	A	412[A]	-	-	1/9/10/12	-
10	HL2	A	412[B]	-	-	5/9/10/12	-
5	EDO	A	403	-	-	1/1/1/1	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	407	DAM	O-C	3.54	1.29	1.22
6	A	407	DAM	C-CA	-3.25	1.39	1.45

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	409	THC	C-CA-N1	3.67	115.59	109.80
6	A	407	DAM	O-C-CA	2.53	128.62	125.33
10	A	411	HL2	O-C-CA	-2.45	118.47	124.77
8	A	409	THC	CB-CA-C	-2.44	107.50	111.55
6	A	407	DAM	CB-CA-N	2.25	131.38	125.84

There are no chirality outliers.

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	A	410	OTH	CB-CA-N-C24
9	A	410	OTH	N-CA-CB-OG1
9	A	410	OTH	C-CA-CB-CG2
10	A	412[B]	HL2	O-C-CA-CB
10	A	412[B]	HL2	OH-CB-CG-CD2

There are no ring outliers.

6 monomers are involved in 5 short contacts:

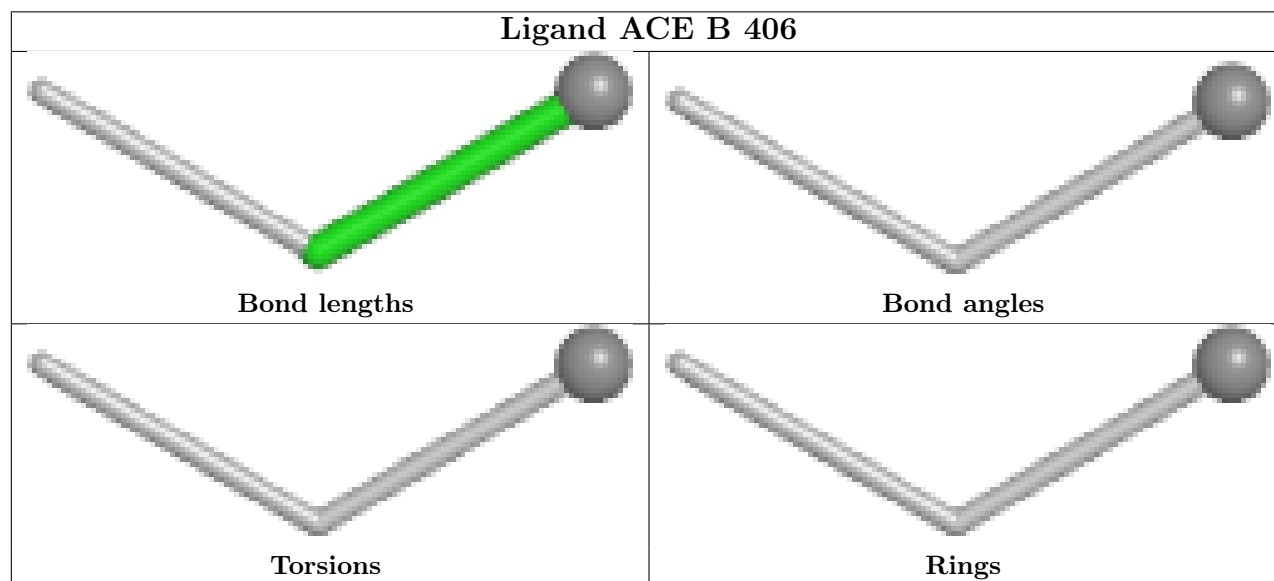
Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	B	404	MAA	1	0
6	A	407	DAM	1	0
10	A	412[A]	HL2	1	0

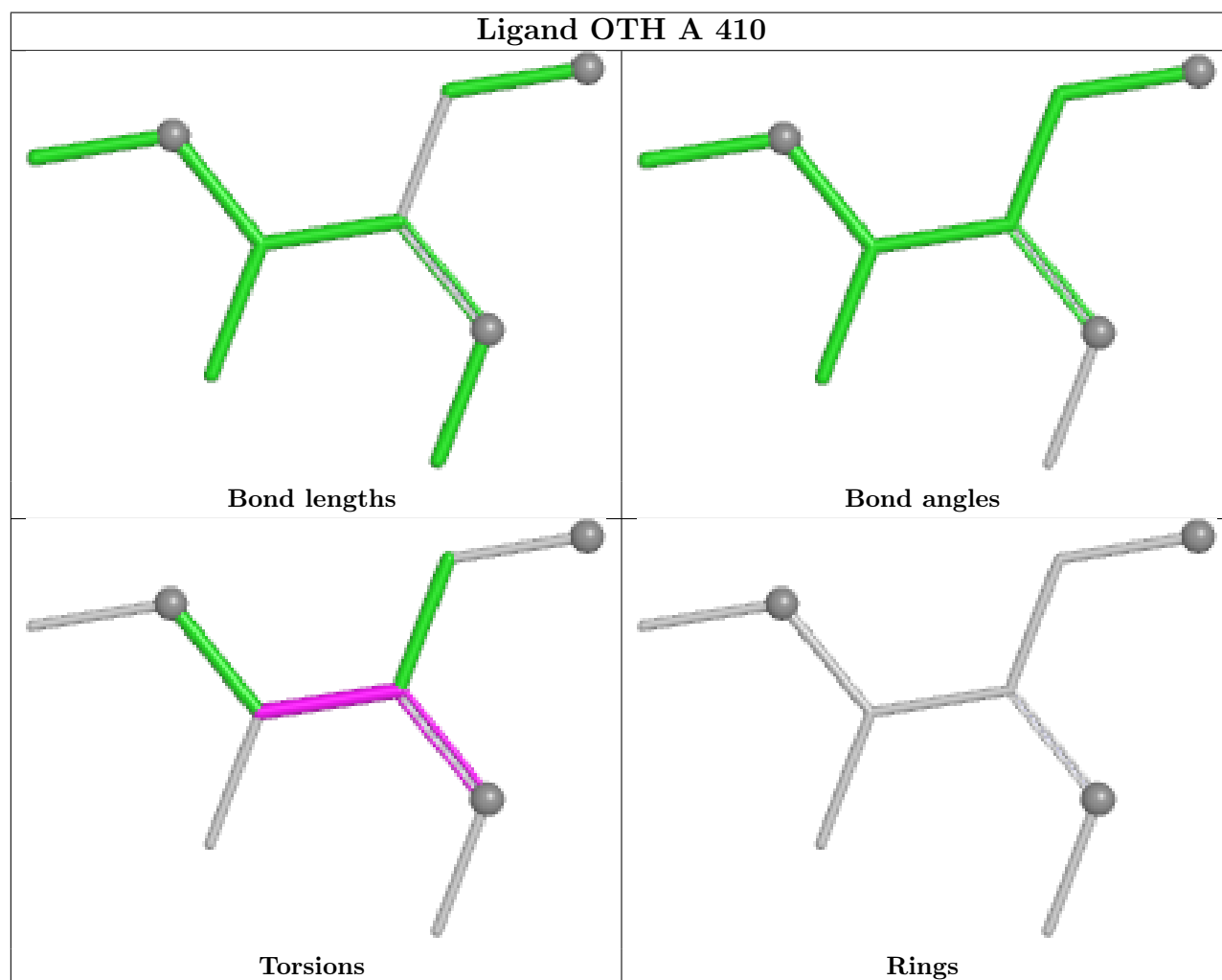
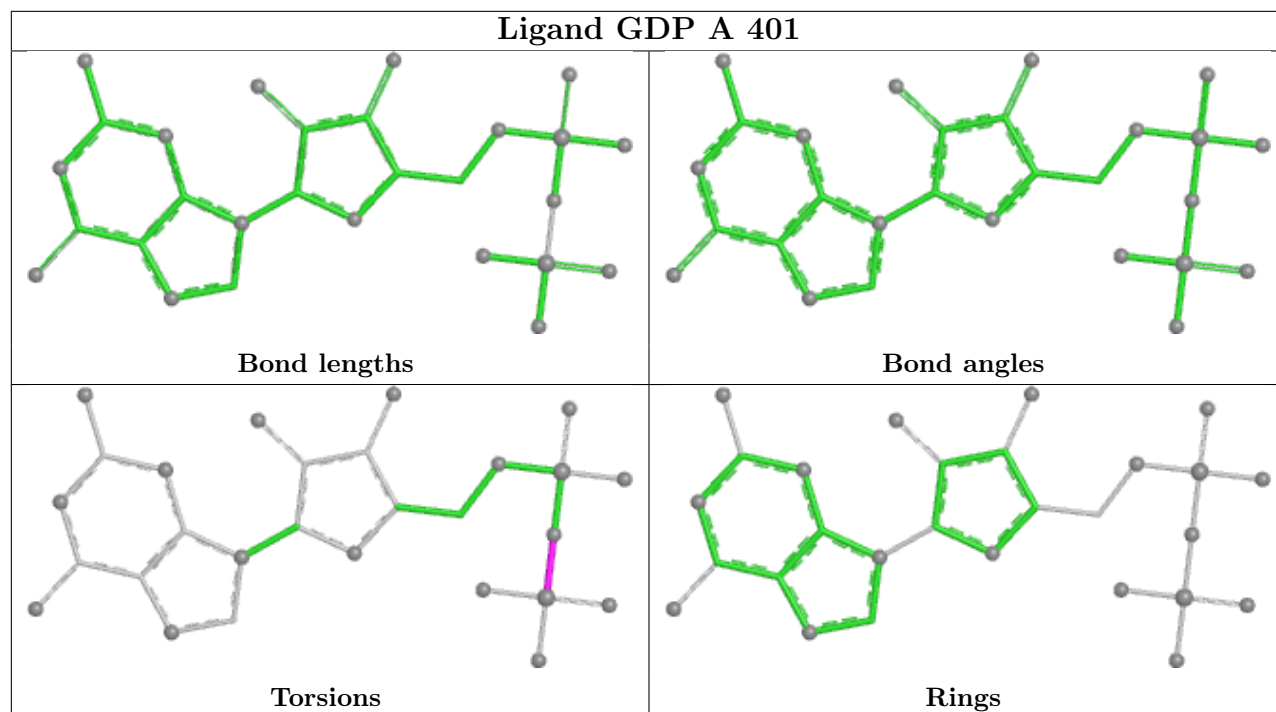
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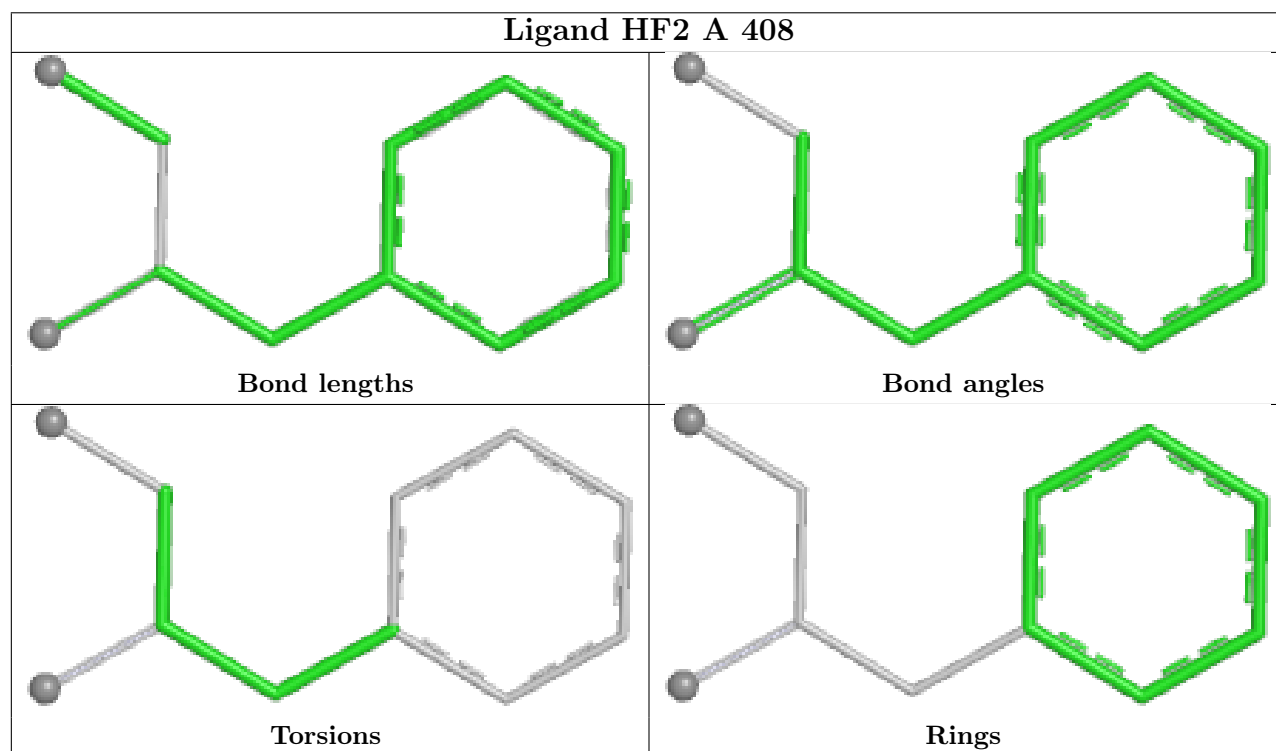
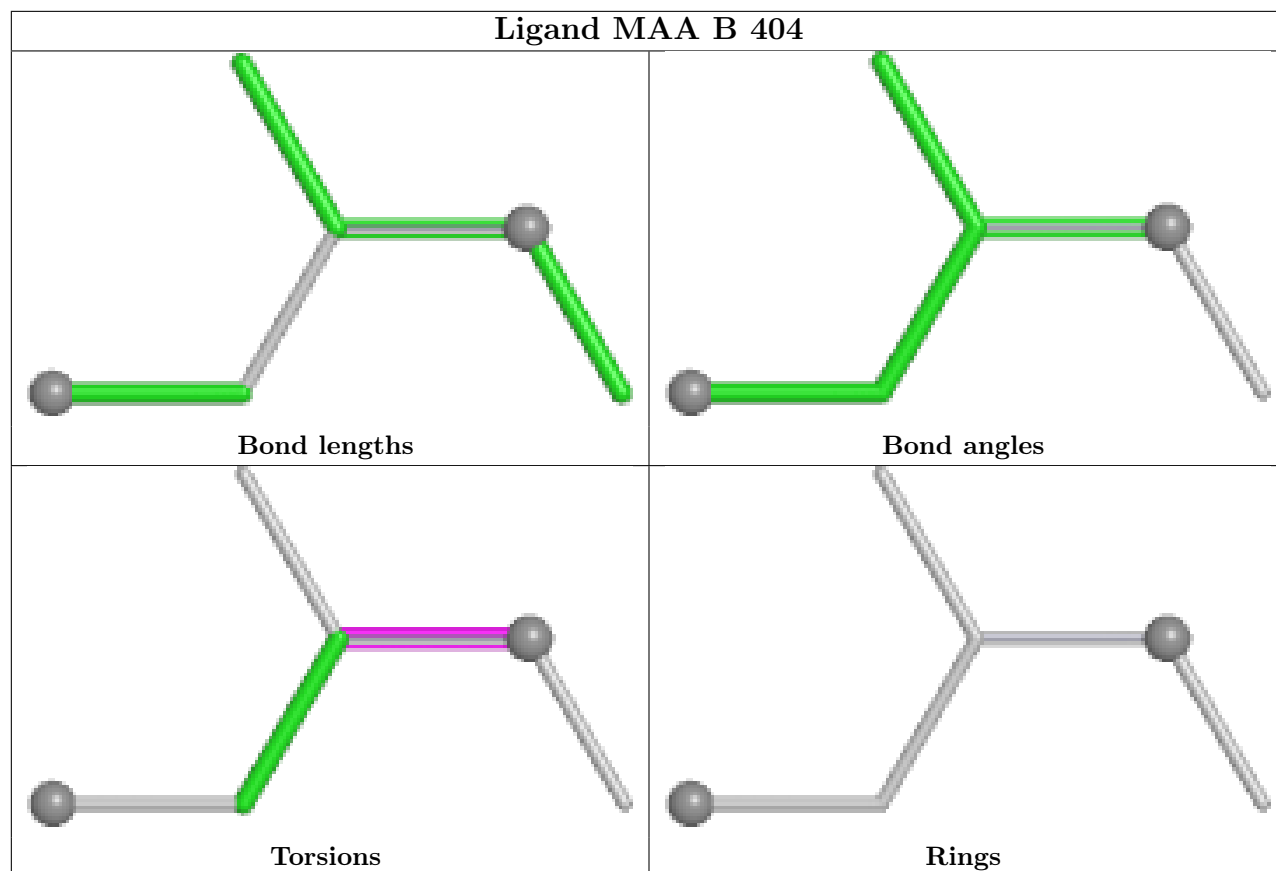
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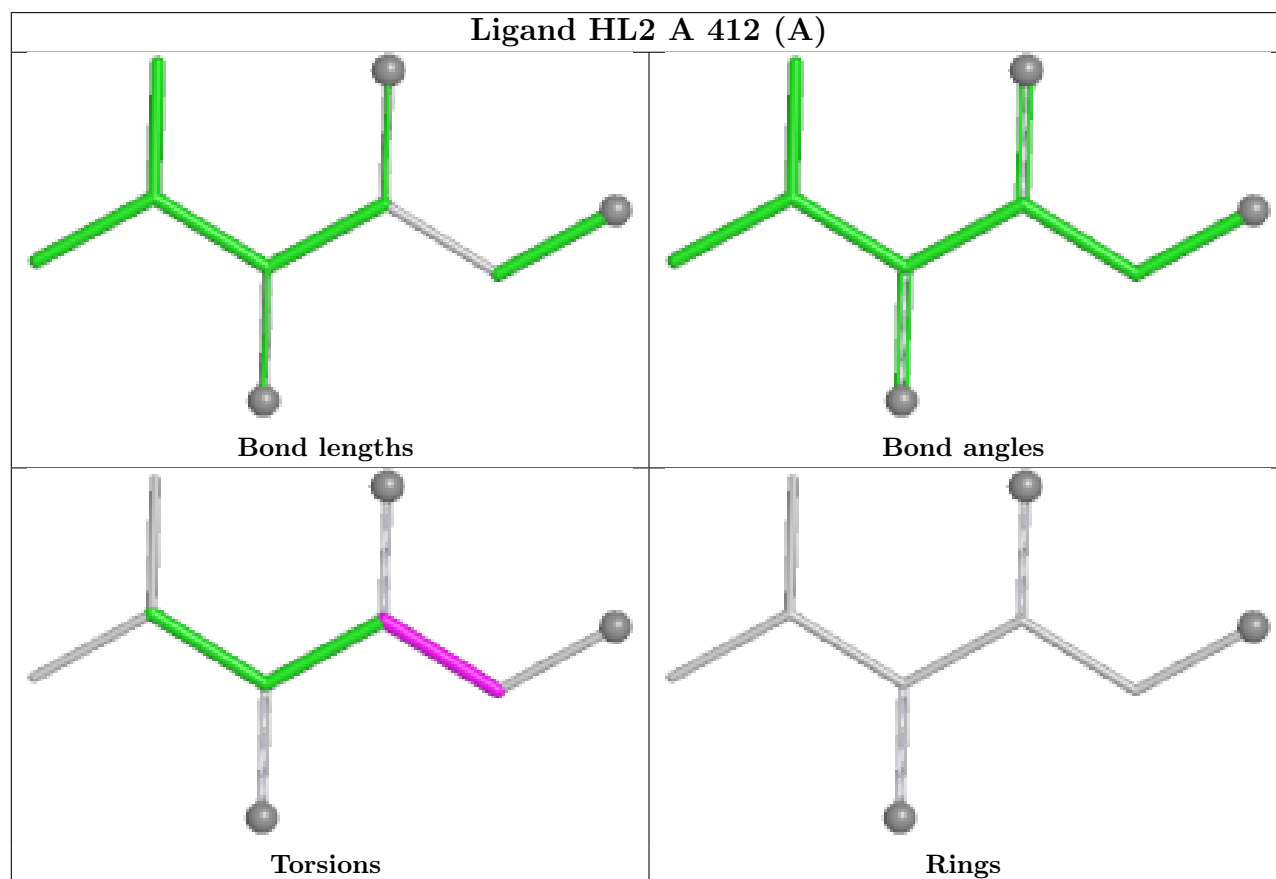
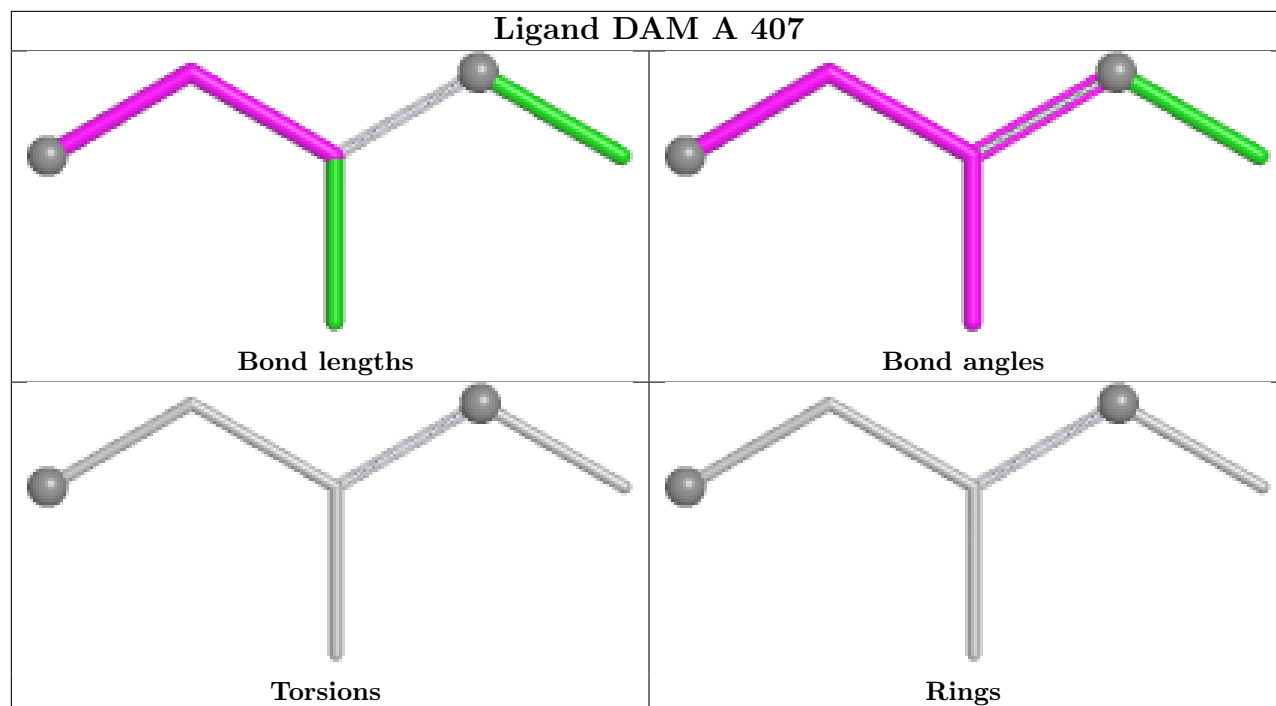
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	403	EDO	1	0
5	A	405	EDO	1	0
12	B	405	ALA	1	0

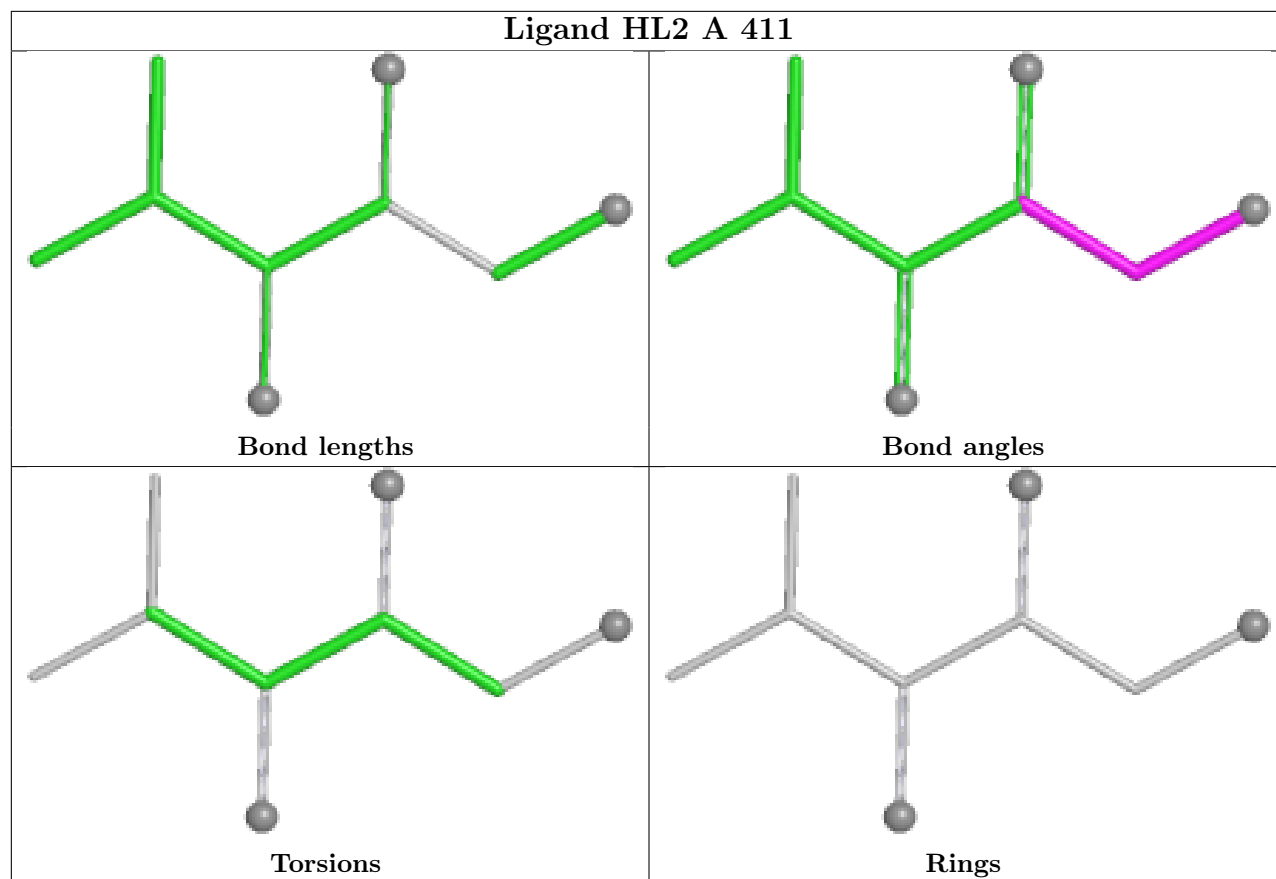
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

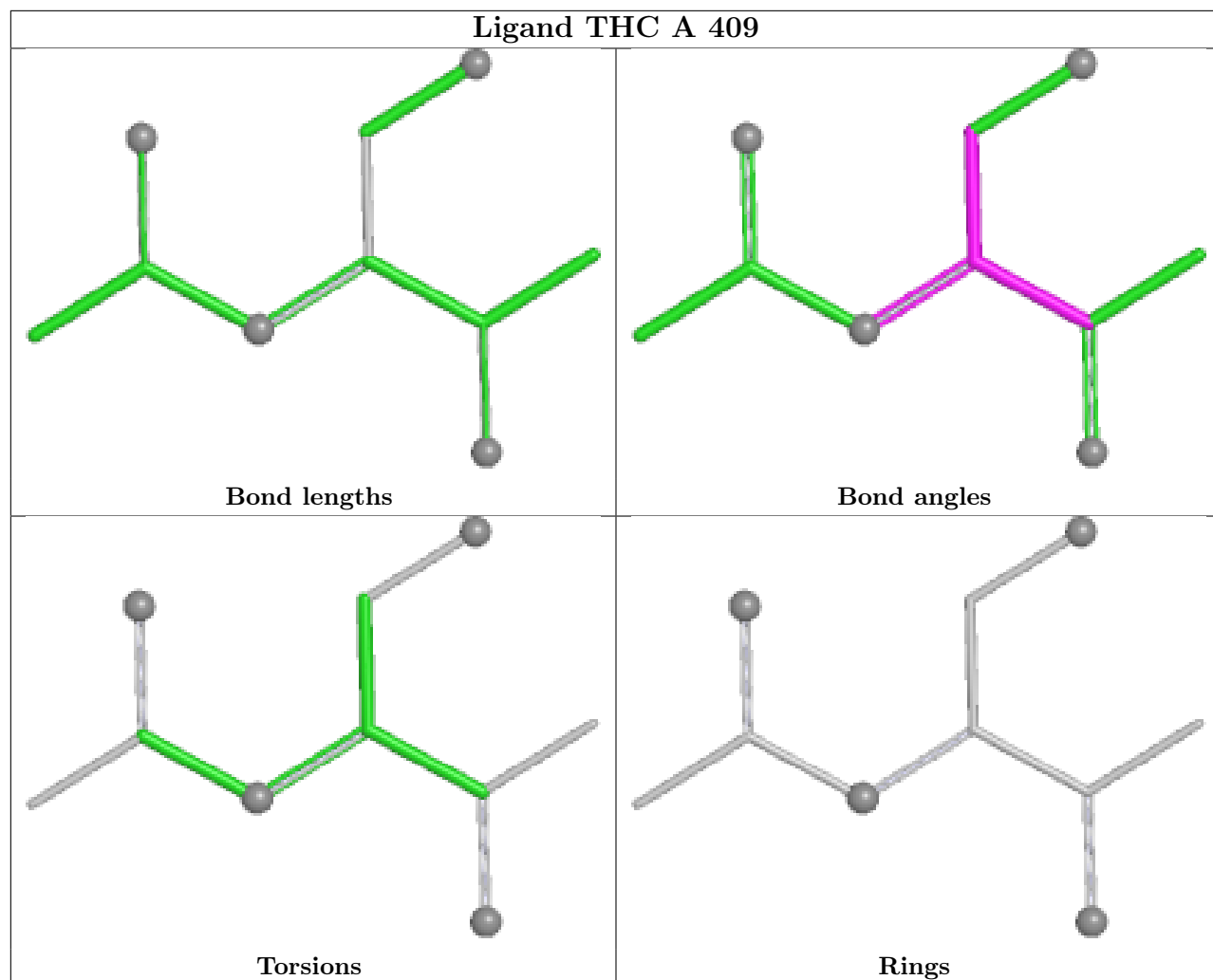




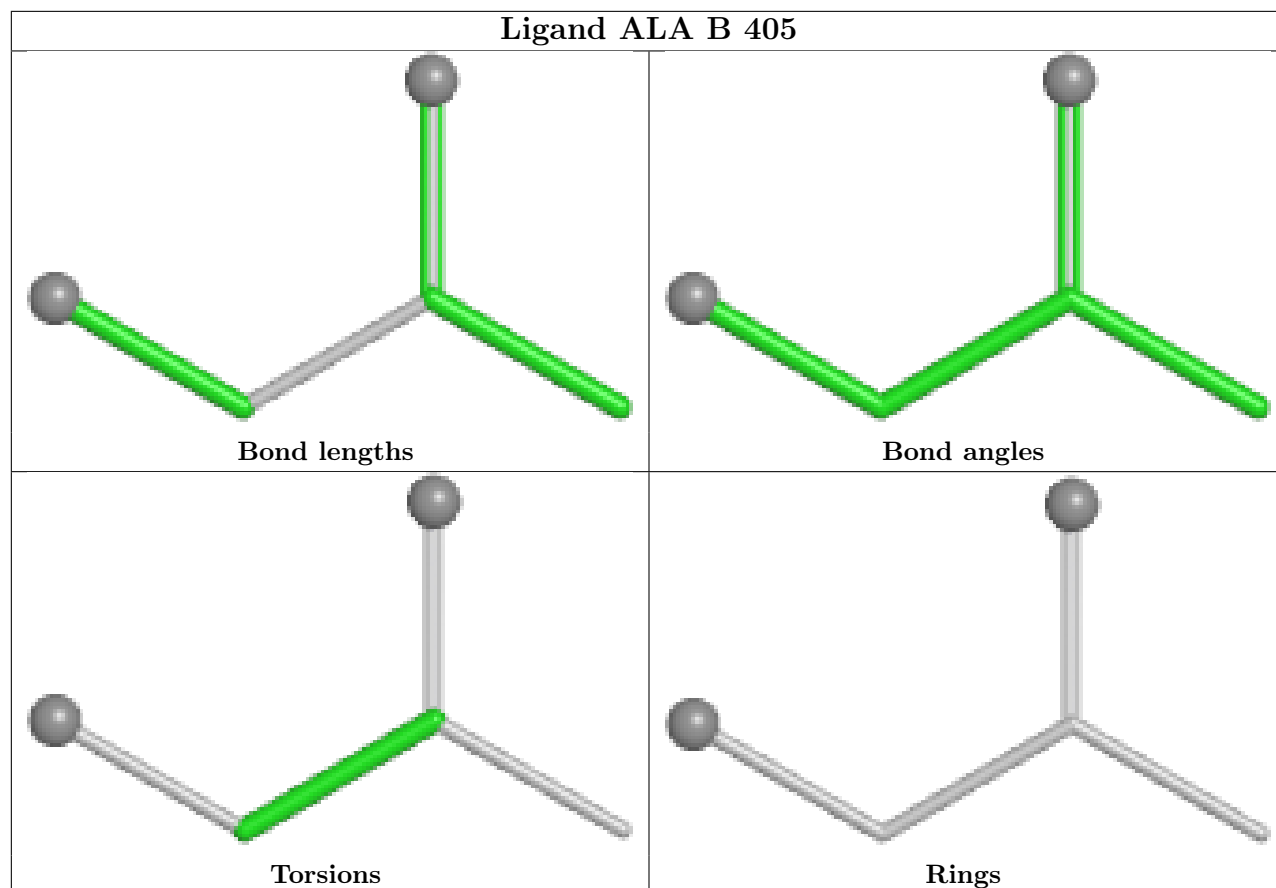




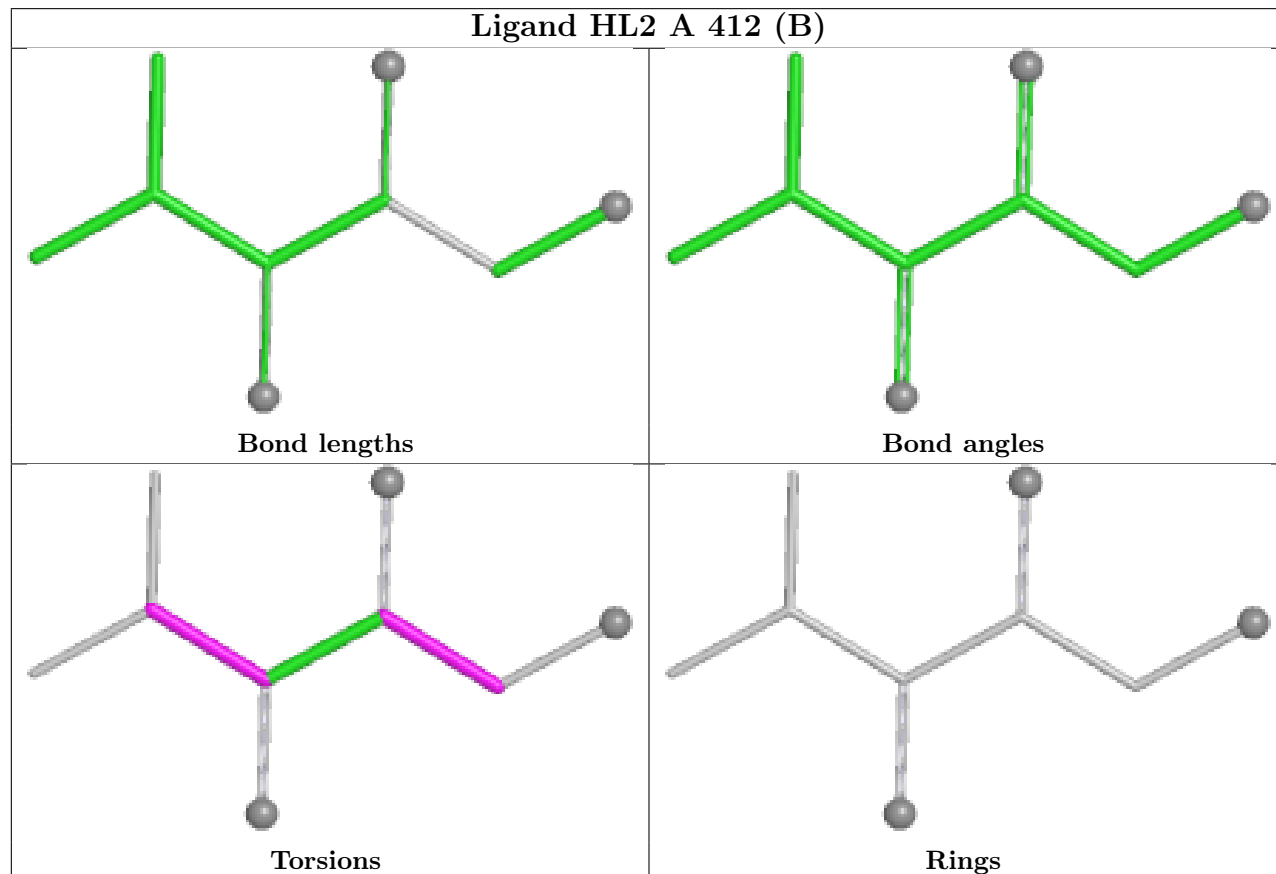




Ligand ALA B 405



Ligand HL2 A 412 (B)



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	340/352 (96%)	0.24	18 (5%) 32 35	12, 31, 54, 86	24 (7%)
2	B	328/344 (95%)	0.09	15 (4%) 37 41	12, 31, 65, 123	14 (4%)
3	G	58/71 (81%)	1.22	15 (25%) 1 1	29, 58, 96, 111	1 (1%)
All	All	726/767 (94%)	0.25	48 (6%) 24 26	12, 32, 68, 123	39 (5%)

The worst 5 of 48 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	353	LEU	7.1
3	G	11	ALA	6.7
1	A	317	ASN	4.9
2	B	8	ARG	4.8
3	G	68	PHE	4.3

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

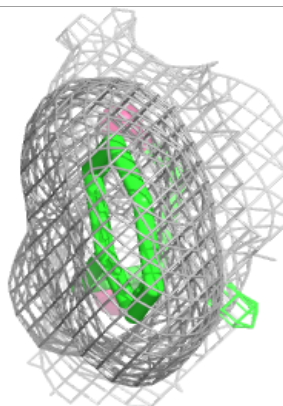
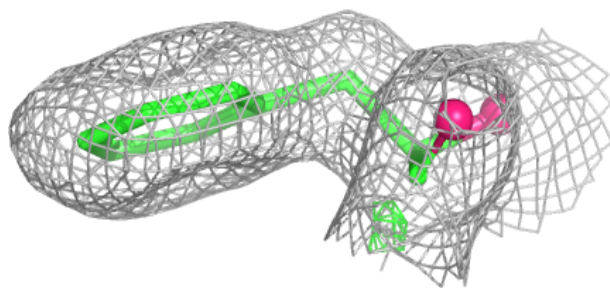
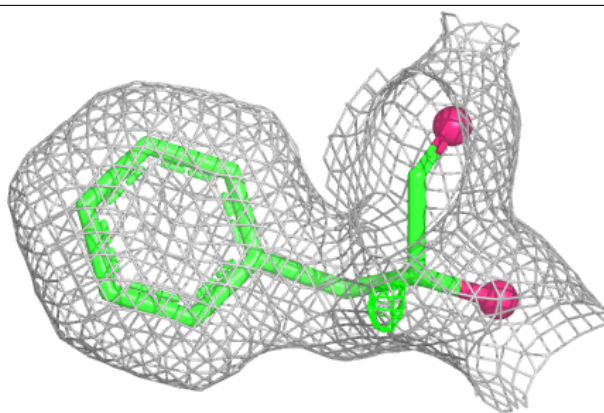
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	EDO	A	406	4/4	0.81	0.23	53,65,71,72	0
5	EDO	A	405	4/4	0.83	0.20	66,66,67,69	0
5	EDO	A	403	4/4	0.83	0.15	33,39,42,51	0
5	EDO	B	402	4/4	0.88	0.15	50,56,57,59	0
5	EDO	B	401	4/4	0.90	0.17	49,52,53,68	0
5	EDO	A	404	4/4	0.91	0.17	55,59,61,64	0
5	EDO	B	403	4/4	0.91	0.14	33,47,51,53	0
5	EDO	A	402	4/4	0.97	0.08	27,29,33,34	0
7	HF2	A	408	11/12	0.97	0.05	23,24,27,29	0
6	DAM	A	407	6/7	0.98	0.06	25,25,26,27	0
8	THC	A	409	10/11	0.98	0.05	29,31,34,36	0
9	OTH	A	410	9/10	0.98	0.06	25,30,32,33	0
10	HL2	A	411	9/10	0.98	0.05	24,26,26,28	0
10	HL2	A	412[A]	9/10	0.98	0.05	24,27,28,28	6
10	HL2	A	412[B]	9/10	0.98	0.05	24,27,29,29	6
11	MAA	B	404	6/7	0.98	0.05	28,29,30,30	0
12	ALA	B	405	5/6	0.98	0.05	25,25,27,28	0
13	ACE	B	406	3/3	0.98	0.05	33,33,33,34	0
4	GDP	A	401	28/28	0.99	0.03	20,22,23,25	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.

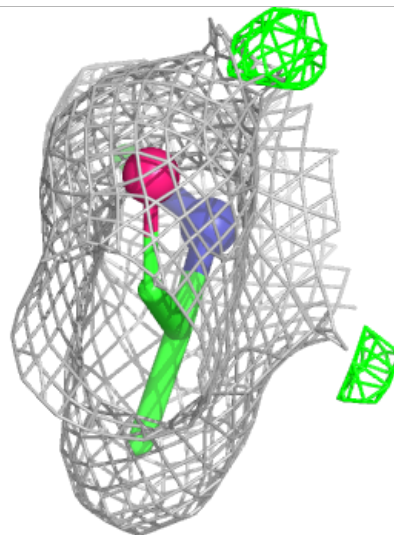
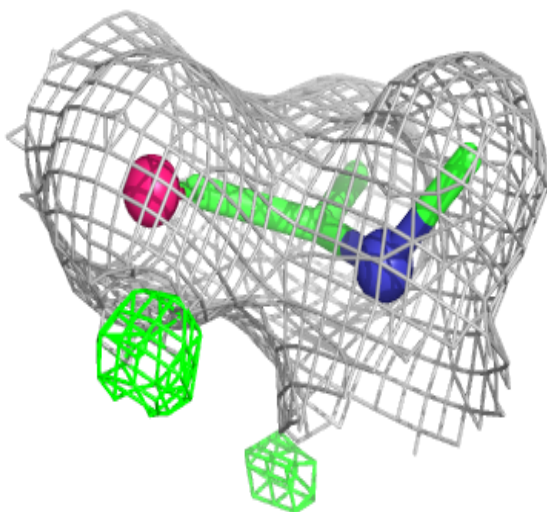
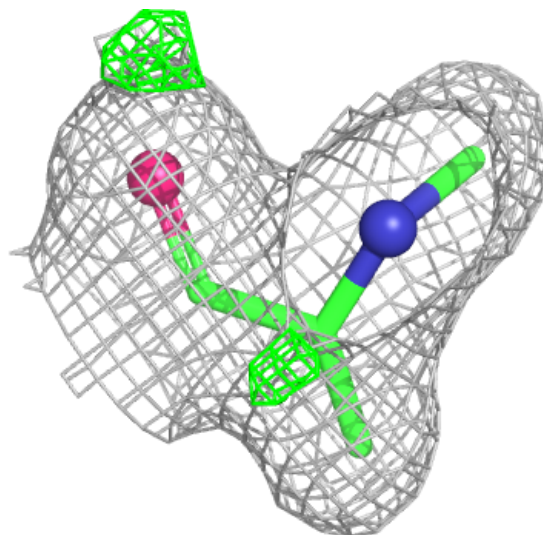
Electron density around HF2 A 408:

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



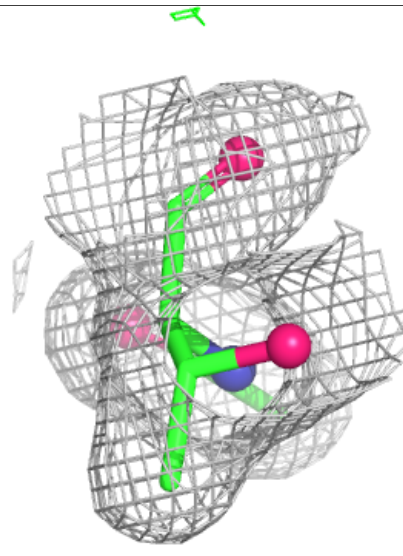
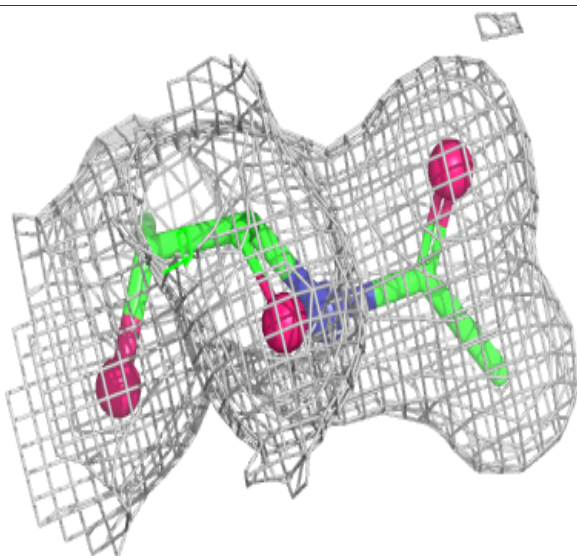
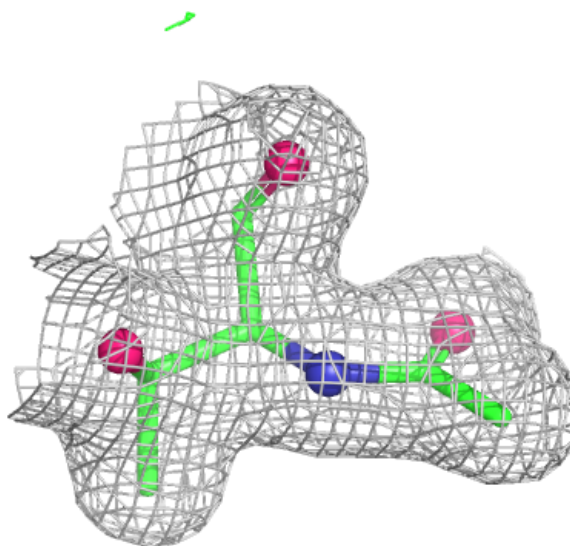
Electron density around DAM A 407:

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



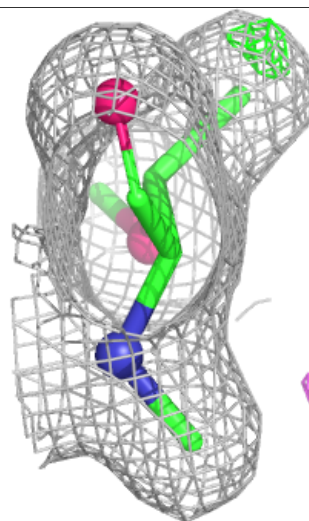
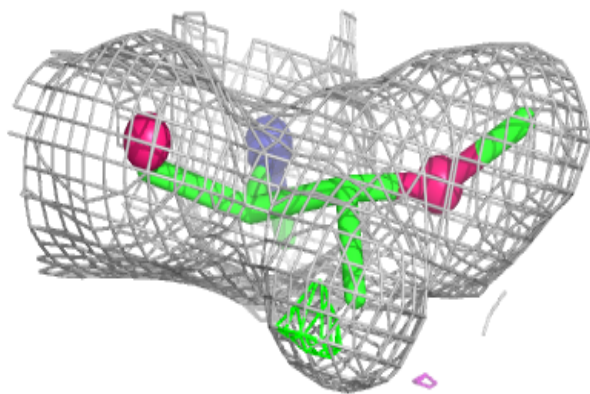
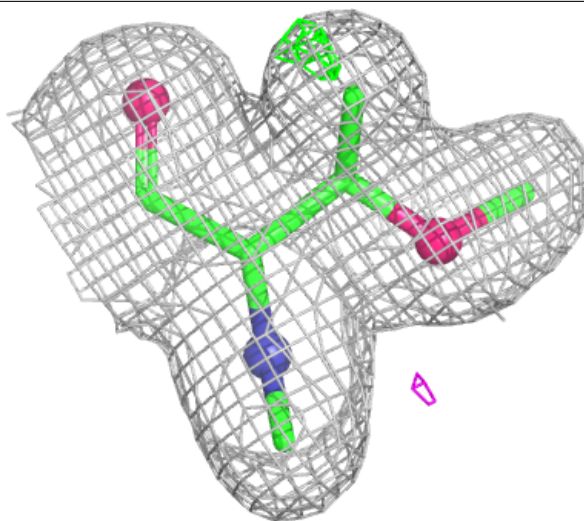
Electron density around THC A 409:

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



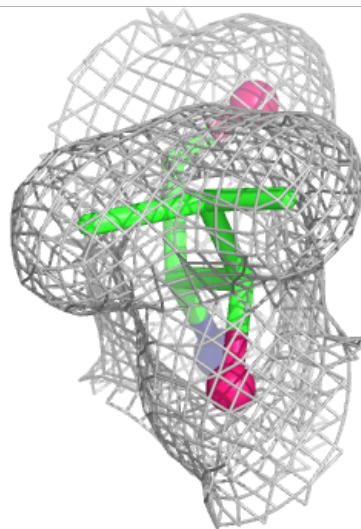
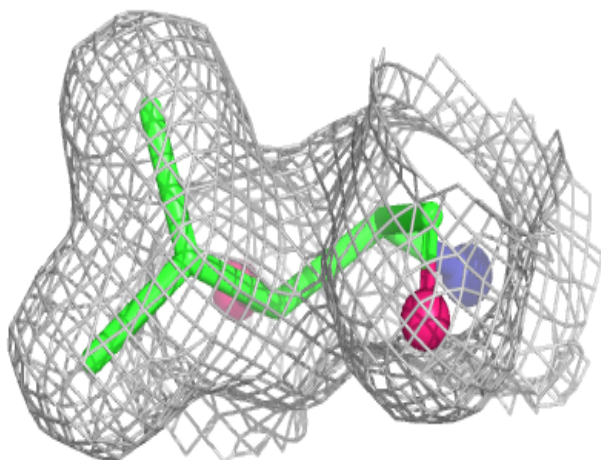
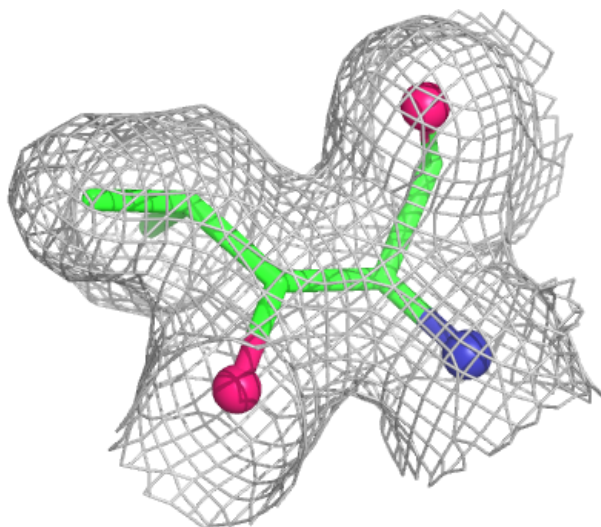
Electron density around OTH A 410:

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and green (positive)



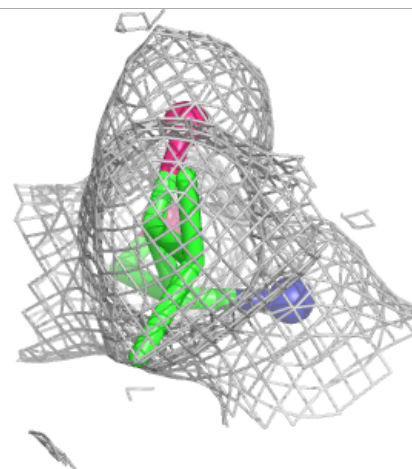
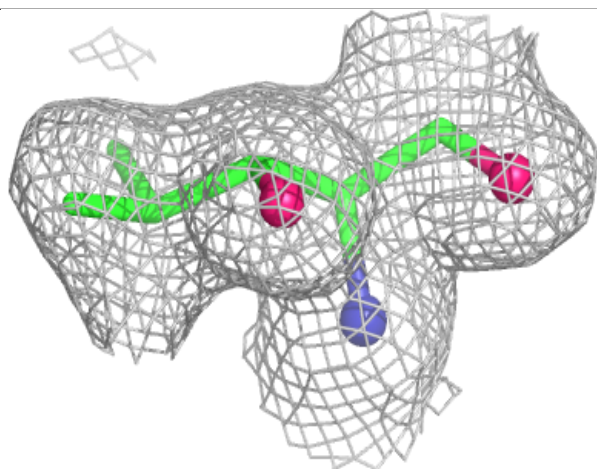
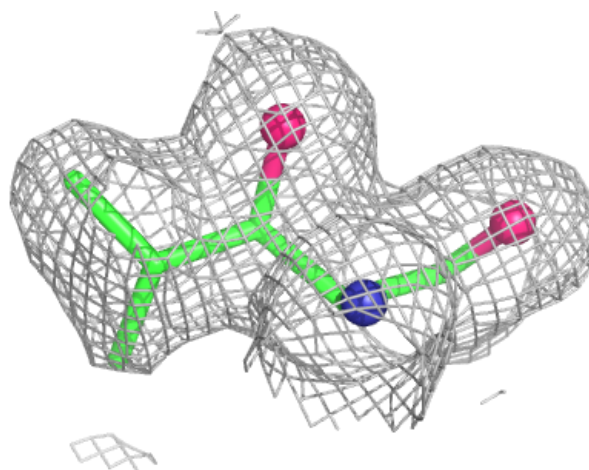
Electron density around HL2 A 411:

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



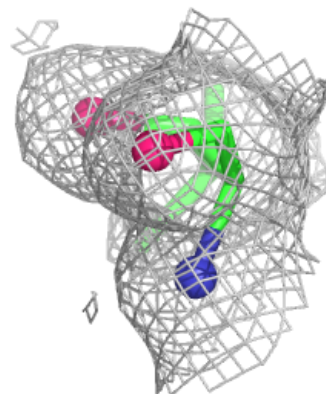
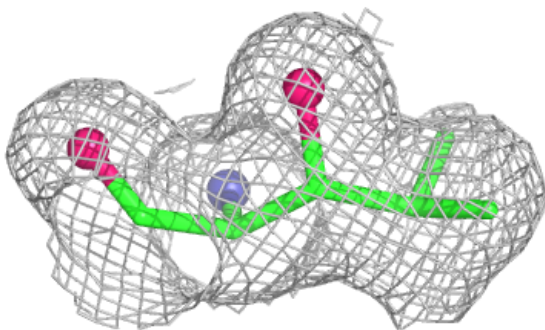
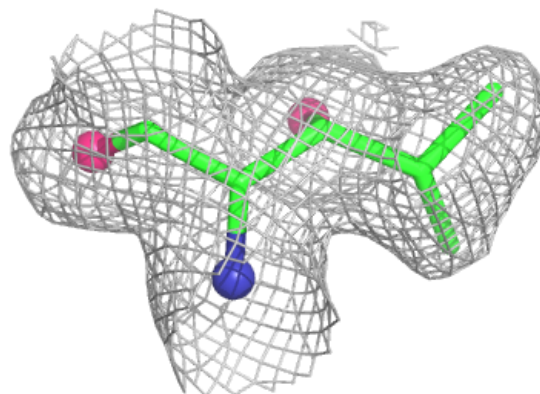
Electron density around HL2 A 412 (A):

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

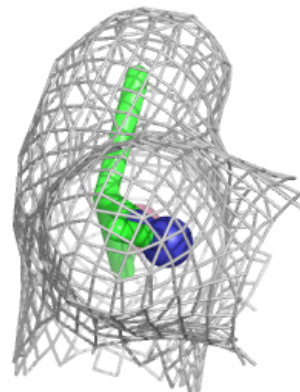
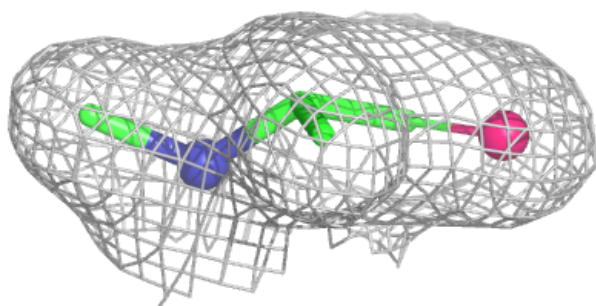
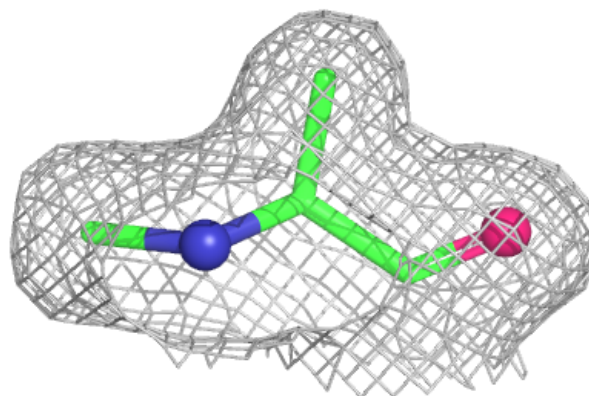


Electron density around HL2 A 412 (B):

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

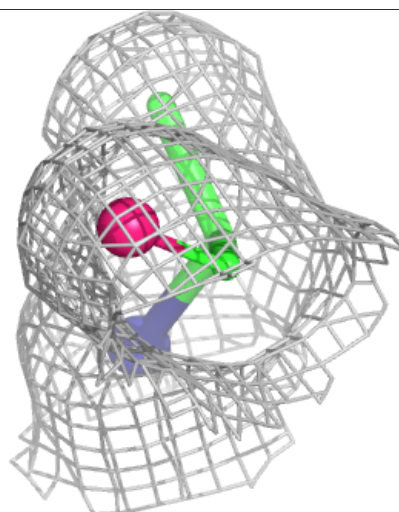
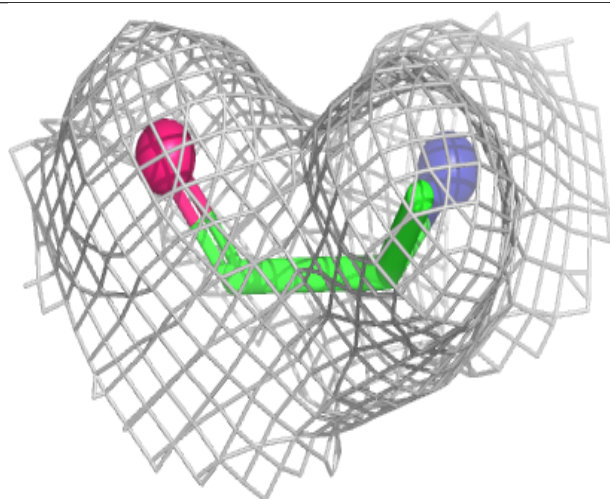
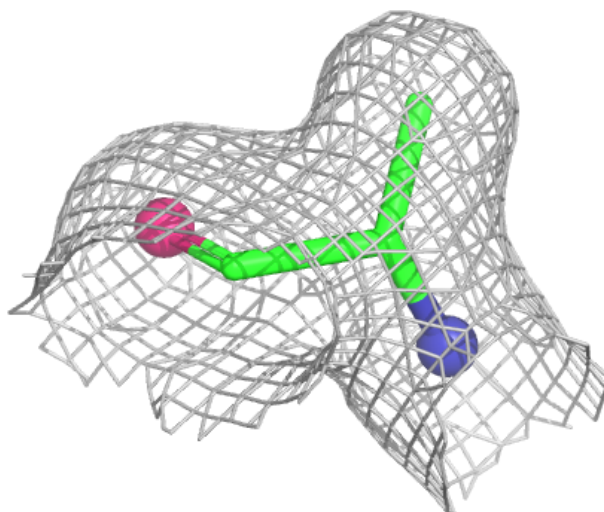
**Electron density around MAA B 404:**

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



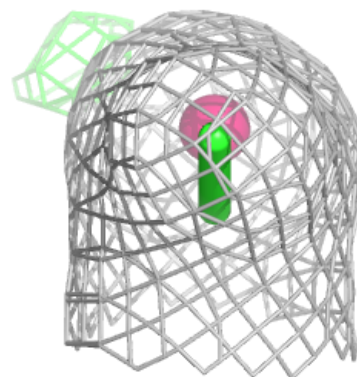
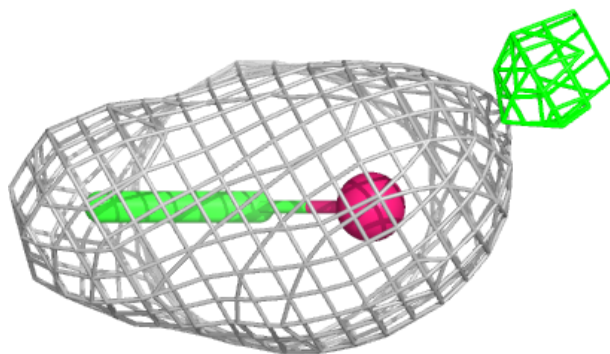
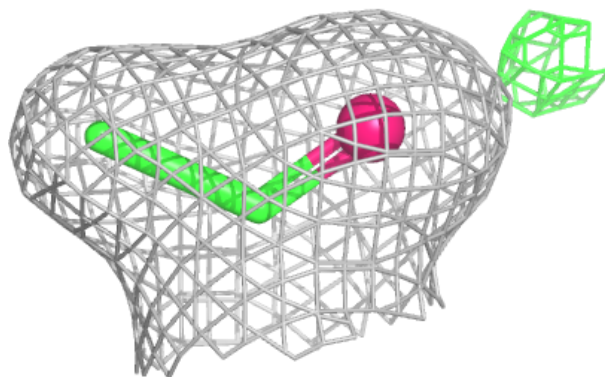
Electron density around ALA B 405:

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

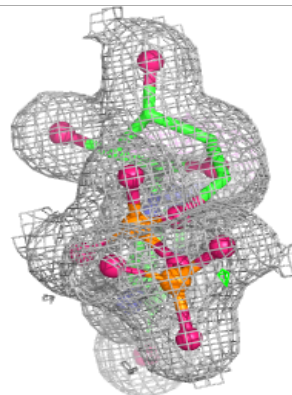
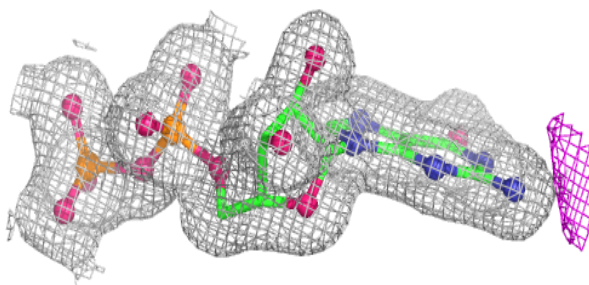
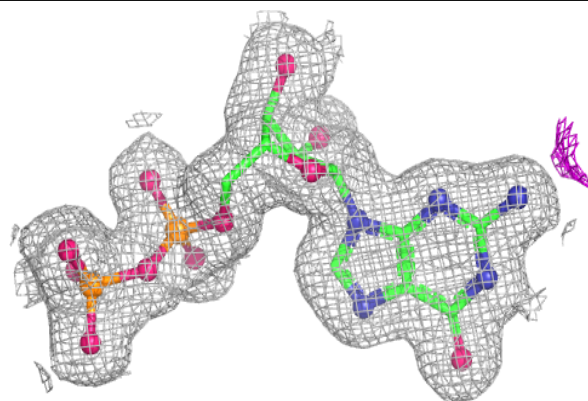


Electron density around ACE B 406:

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

**Electron density around GDP A 401:**

$2mF_o-DF_c$ (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.