



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 08:47 AM UTC

PDB ID : 5ETZ / pdb_00005etz
Title : Structure of the all-trans isomer of pharaonis halorhodopsin in the absence of halide ions
Authors : Kouyama, T.
Deposited on : 2015-11-18
Resolution : 1.80 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

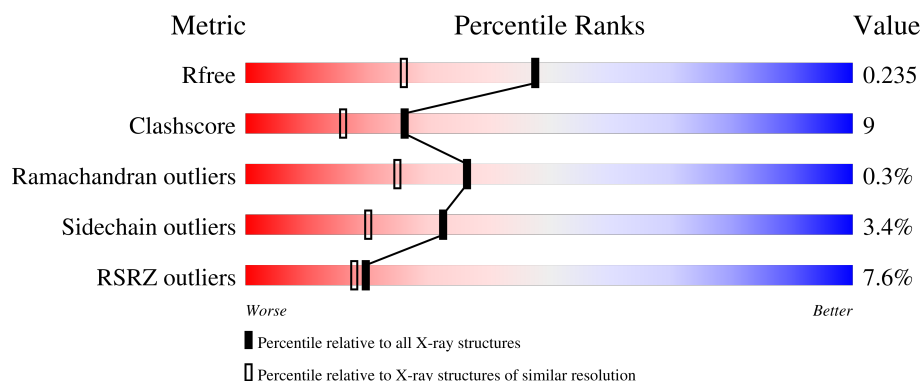
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	7662 (1.80-1.80)
Clashscore	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)
RSRZ outliers	180081	7663 (1.80-1.80)

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	291	6% 71% 17% • 10%
1	B	291	8% 73% 15% • 11%
1	D	291	6% 69% 19% • 11%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	22B	A	302	-	X	-	-
4	L3P	A	303	-	-	-	X
4	L3P	A	304	-	-	-	X
4	L3P	B	302	-	-	-	X
4	L3P	B	303	-	-	-	X
4	L3P	D	302	-	-	-	X
4	L3P	D	303	-	-	-	X
5	BNG	A	305	-	-	-	X
5	BNG	A	306	-	-	-	X

2 Entry composition [i](#)

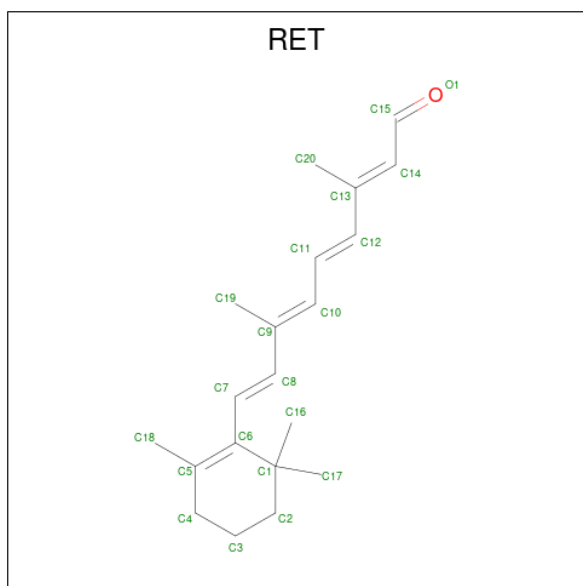
There are 6 unique types of molecules in this entry. The entry contains 6467 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Halorhodopsin.

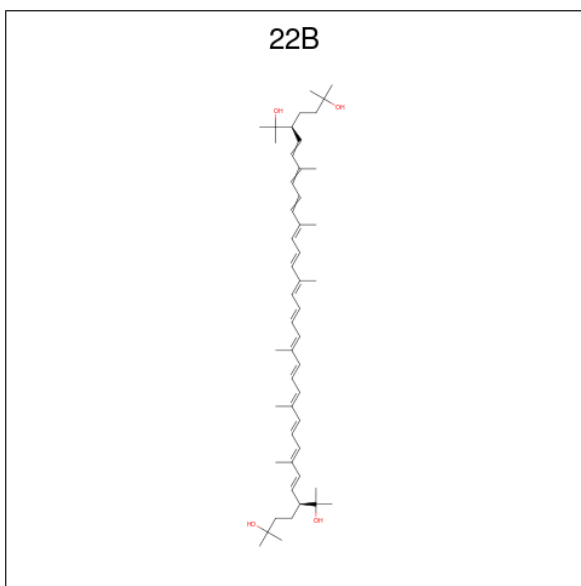
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	261	Total	C	N	O	S	0	0	0
			1971	1308	300	352	11			
1	B	260	Total	C	N	O	S	0	0	0
			1963	1302	299	351	11			
1	D	260	Total	C	N	O	S	0	0	0
			1963	1302	299	351	11			

- Molecule 2 is RETINAL (CCD ID: RET) (formula: $C_{20}H_{28}O$).



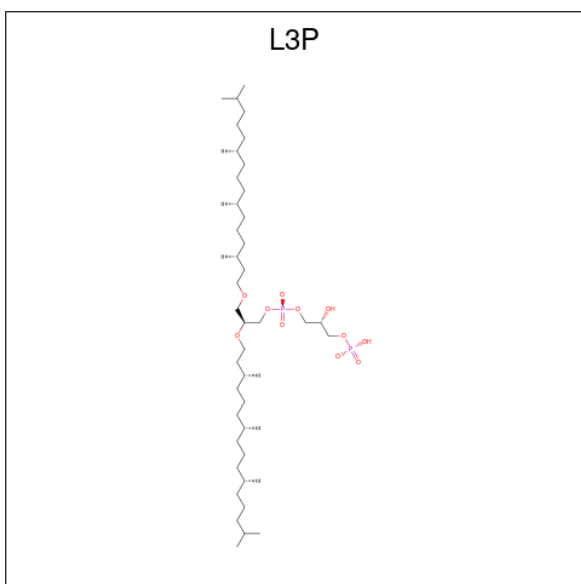
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	C	0	0
			20	20		
2	B	1	Total	C	0	0
			20	20		
2	D	1	Total	C	0	0
			20	20		

- Molecule 3 is BACTERIORUBERIN (CCD ID: 22B) (formula: $C_{50}H_{76}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			37	35	2		

- Molecule 4 is 2,3-DI-O-PHYTANLY-3-SN-GLYCERO-1-PHOSPHORYL-3'-SN-GLYCEROL-1'-PHOSPHATE (CCD ID: L3P) (formula: $C_{46}H_{94}O_{11}P_2$).



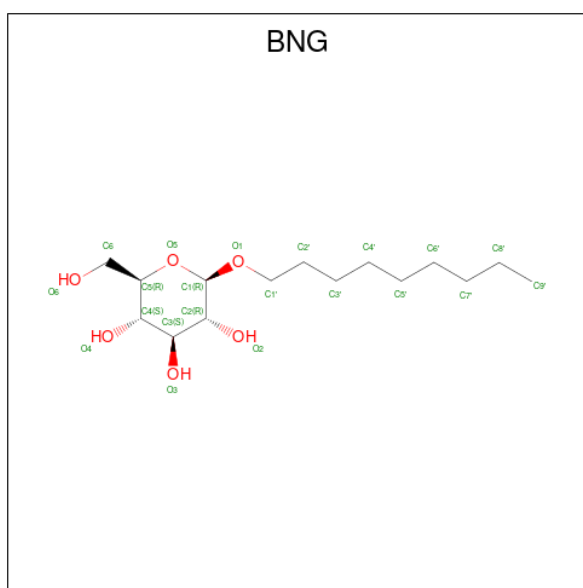
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	C	0	0
			20	20		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C 20 20	0	0
4	B	1	Total C 20 20	0	0
4	B	1	Total C 20 20	0	0
4	D	1	Total C 20 20	0	0
4	D	1	Total C 20 20	0	0

- Molecule 5 is nonyl beta-D-glucopyranoside (CCD ID: BNG) (formula: C₁₅H₃₀O₆).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 21 15 6	0	0
5	A	1	Total C O 21 15 6	0	0
5	A	1	Total C O 21 15 6	0	0
5	B	1	Total C O 21 15 6	0	0
5	B	1	Total C O 21 15 6	0	0
5	D	1	Total C O 21 15 6	0	0

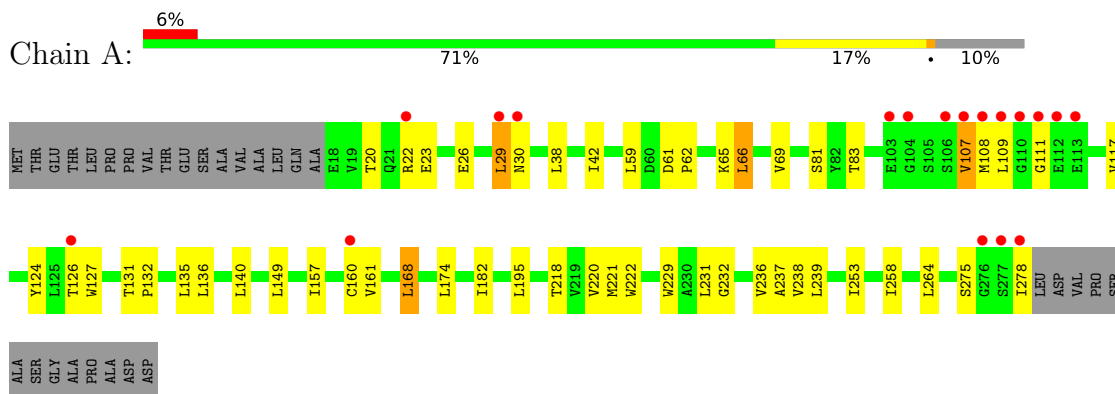
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	76	Total 76	O 76	0	0
6	B	76	Total 76	O 76	0	0
6	D	75	Total 75	O 75	0	0

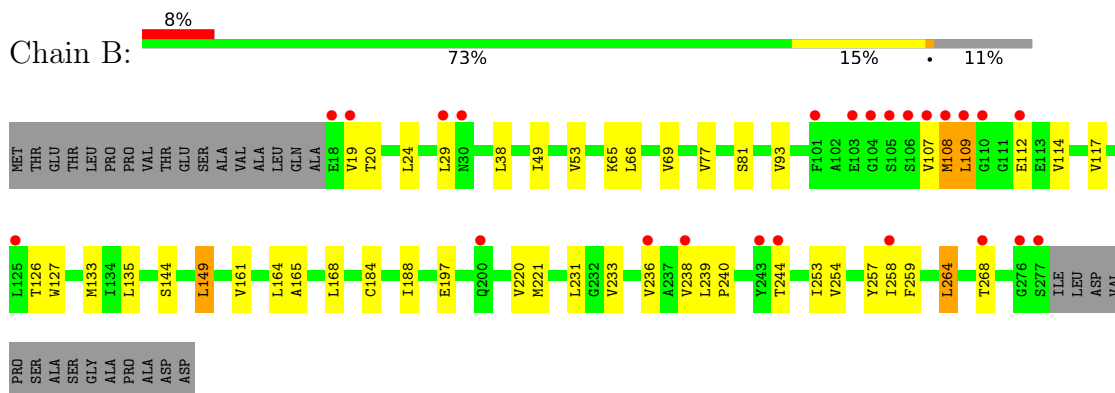
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

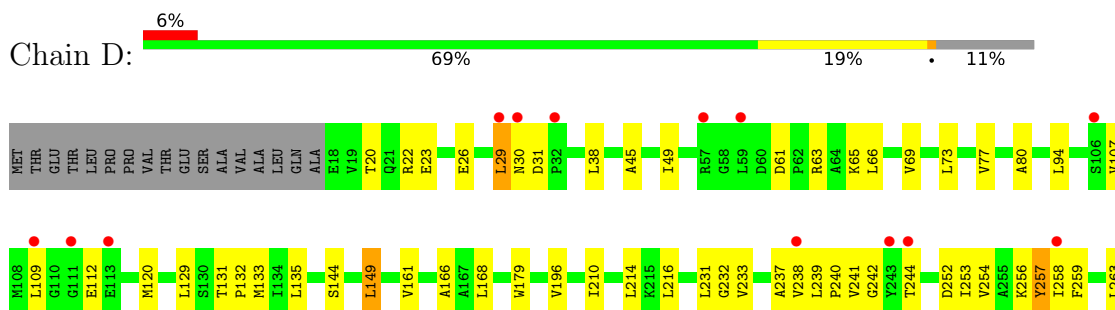
• Molecule 1: Halorhodopsin

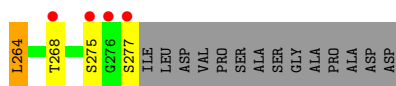


• Molecule 1: Halorhodopsin



• Molecule 1: Halorhodopsin





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	154.40Å 97.77Å 101.62Å 90.00° 128.81° 90.00°	Depositor
Resolution (Å)	15.00 – 1.80 15.00 – 1.80	Depositor EDS
% Data completeness (in resolution range)	91.2 (15.00-1.80) 91.0 (15.00-1.80)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.23 (at 1.79Å)	Xtriage
Refinement program	CNS 1.21	Depositor
R, R_{free}	0.218 , 0.236 0.219 , 0.235	Depositor DCC
R_{free} test set	5001 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	19.5	Xtriage
Anisotropy	0.086	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 61.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.014 for -h+k-l,-l,-k 0.000 for -h-k-l,l,k 0.019 for -h-2*l,-k,l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6467	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.60% 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: 22B, BNG, L3P, RET

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	0.42	0/2017	0.91	6/2762 (0.2%)
1	B	0.38	0/2009	0.85	2/2751 (0.1%)
1	D	0.38	0/2009	0.87	6/2751 (0.2%)
All	All	0.39	0/6035	0.88	14/8264 (0.2%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	29	LEU	N-CA-C	-8.39	99.46	110.53
1	B	29	LEU	N-CA-C	-7.92	100.67	110.41
1	D	237	ALA	N-CA-C	6.59	120.64	111.74
1	B	197	GLU	N-CA-C	6.54	118.29	111.03
1	D	257	TYR	N-CA-C	5.92	117.54	111.14
1	A	42	ILE	N-CA-C	-5.91	104.75	110.72
1	D	31	ASP	CA-C-N	5.54	126.77	119.84
1	D	31	ASP	C-N-CA	5.54	126.77	119.84
1	D	196	VAL	N-CA-C	5.46	116.61	111.48
1	A	107	VAL	N-CA-C	5.40	118.84	113.71
1	D	29	LEU	N-CA-C	-5.32	103.50	110.53
1	A	195	LEU	N-CA-C	5.14	118.70	112.23
1	A	237	ALA	N-CA-C	5.04	118.54	111.74
1	A	83	THR	N-CA-C	-5.01	106.00	111.82

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	1971	0	2025	40	0
1	B	1963	0	2014	36	0
1	D	1963	0	2014	41	0
2	A	20	0	27	1	0
2	B	20	0	27	2	0
2	D	20	0	27	0	0
3	A	37	0	49	6	0
4	A	40	0	78	2	0
4	B	40	0	78	2	0
4	D	40	0	78	8	0
5	A	63	0	90	0	0
5	B	42	0	60	1	0
5	D	21	0	30	0	0
6	A	76	0	0	2	1
6	B	76	0	0	4	0
6	D	75	0	0	3	0
All	All	6467	0	6597	120	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (120) 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:D:254:VAL:HG13	1:D:258:ILE:HD11	1.63	0.81
3:A:302:22B:H15	3:A:302:22B:H42	1.62	0.80
1:D:210:ILE:HA	6:D:467:HOH:O	1.86	0.75
1:B:254:VAL:HG13	1:B:258:ILE:HD11	1.70	0.73
1:D:20:THR:OG1	1:D:22:ARG:HG2	1.89	0.72
1:D:240:PRO:O	1:D:244:THR:HG23	1.93	0.69
1:B:19:VAL:HG11	1:B:109:LEU:HD13	1.74	0.69
1:A:22:ARG:HD2	6:A:440:HOH:O	1.93	0.69
1:B:108:MET:HA	1:B:112:GLU:O	1.93	0.68
1:A:253:ILE:O	1:A:258:ILE:HD13	1.95	0.67
1:D:129:LEU:HD13	4:D:302:L3P:H23	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:VAL:HG23	1:A:239:LEU:HD13	1.76	0.66
1:D:254:VAL:HG13	1:D:258:ILE:CD1	2.25	0.66
1:D:233:VAL:H	1:D:244:THR:HG21	1.62	0.65
1:A:220:VAL:HG12	1:A:221:MET:HE2	1.78	0.64
1:B:254:VAL:HG13	1:B:258:ILE:CD1	2.27	0.64
1:B:240:PRO:O	1:B:244:THR:HG23	1.99	0.63
1:D:120:MET:HG2	6:D:434:HOH:O	1.97	0.62
1:A:81:SER:HB3	1:A:126:THR:OG1	1.99	0.62
1:A:107:VAL:HG23	1:A:109:LEU:HD13	1.81	0.62
1:B:236:VAL:HG13	1:B:238:VAL:HG13	1.82	0.62
1:B:109:LEU:HD12	1:B:114:VAL:HB	1.83	0.61
1:D:254:VAL:HA	1:D:258:ILE:HG12	1.83	0.61
1:B:254:VAL:HA	1:B:258:ILE:HG12	1.82	0.60
1:A:29:LEU:O	1:A:30:ASN:HB2	2.02	0.60
1:A:231:LEU:O	1:A:238:VAL:HG22	2.02	0.60
1:A:182:ILE:HG23	3:A:302:22B:H14	1.85	0.58
1:D:80:ALA:HB3	4:D:302:L3P:H241	1.85	0.58
1:B:184:CYS:O	1:B:188:ILE:HD13	2.04	0.58
1:B:258:ILE:HG13	1:B:259:PHE:N	2.19	0.57
1:D:77:VAL:HG13	4:D:302:L3P:H243	1.86	0.57
1:A:161:VAL:HG11	4:B:303:L3P:H222	1.85	0.57
1:A:174:LEU:HD23	5:B:304:BNG:H4'1	1.87	0.56
1:D:20:THR:OG1	1:D:23:GLU:HG3	2.06	0.56
1:B:49:ILE:O	1:B:53:VAL:HG23	2.05	0.56
1:B:164:LEU:O	1:B:168:LEU:HD13	2.06	0.56
1:B:161:VAL:HG11	4:D:302:L3P:H221	1.87	0.55
1:A:69:VAL:HG22	6:D:463:HOH:O	2.07	0.55
1:D:264:LEU:O	1:D:268:THR:HG22	2.07	0.55
1:B:233:VAL:H	1:B:244:THR:HG21	1.71	0.55
6:B:407:HOH:O	1:D:65:LYS:HE2	2.07	0.55
1:D:94:LEU:HD21	4:D:303:L3P:H192	1.89	0.54
1:A:66:LEU:HD13	1:A:140:LEU:HD11	1.89	0.54
1:B:20:THR:O	1:B:24:LEU:HD23	2.08	0.53
1:B:264:LEU:O	1:B:268:THR:HG22	2.09	0.53
1:A:65:LYS:O	1:A:69:VAL:HG23	2.09	0.53
1:A:22:ARG:O	1:A:26:GLU:HG3	2.09	0.53
1:A:61:ASP:O	1:A:65:LYS:HG3	2.09	0.53
1:A:168:LEU:HD21	4:A:303:L3P:H242	1.91	0.52
1:D:65:LYS:O	1:D:69:VAL:HG23	2.09	0.52
1:D:238:VAL:HG23	1:D:239:LEU:CD1	2.40	0.51
1:A:26:GLU:O	1:A:29:LEU:O	2.29	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:ILE:O	1:A:160:CYS:SG	2.60	0.51
1:B:117:VAL:HG21	6:B:420:HOH:O	2.10	0.51
4:A:304:L3P:H201	1:D:161:VAL:HG12	1.91	0.50
1:D:29:LEU:O	1:D:30:ASN:HB2	2.11	0.50
1:B:93:VAL:HG21	1:B:109:LEU:HD11	1.94	0.50
1:B:107:VAL:O	1:B:108:MET:HB3	2.11	0.50
1:A:232:GLY:HA2	1:A:239:LEU:HB2	1.93	0.50
1:D:61:ASP:OD2	1:D:275:SER:HA	2.11	0.50
1:D:258:ILE:HG13	1:D:259:PHE:N	2.27	0.49
1:A:107:VAL:CG2	1:A:109:LEU:HD13	2.43	0.49
1:A:236:VAL:HG22	1:A:236:VAL:O	2.12	0.49
1:D:63:ARG:HD2	1:D:277:SER:O	2.11	0.49
1:D:216:LEU:C	1:D:216:LEU:HD13	2.38	0.49
1:A:124:TYR:HH	1:A:229:TRP:CD1	2.31	0.49
1:B:165:ALA:HB2	4:D:302:L3P:H172	1.94	0.49
1:A:108:MET:O	1:A:109:LEU:HD12	2.14	0.48
1:B:144:SER:OG	1:B:149:LEU:HD22	2.14	0.48
1:A:20:THR:OG1	1:A:23:GLU:HG3	2.14	0.47
1:B:109:LEU:HA	6:B:466:HOH:O	2.14	0.47
1:A:22:ARG:HB3	1:A:22:ARG:NH1	2.28	0.47
1:B:65:LYS:O	1:B:69:VAL:HG23	2.14	0.47
1:A:182:ILE:HA	3:A:302:22B:H14	1.96	0.47
1:B:220:VAL:HG12	1:B:221:MET:HE2	1.96	0.47
1:B:231:LEU:O	1:B:238:VAL:HG22	2.15	0.47
1:D:107:VAL:HG22	1:D:109:LEU:HD13	1.97	0.47
1:B:81:SER:HB2	1:B:126:THR:OG1	2.16	0.46
1:A:117:VAL:HG21	6:A:425:HOH:O	2.15	0.46
1:B:253:ILE:HA	1:B:257:TYR:CD2	2.50	0.46
1:A:258:ILE:HD12	1:A:258:ILE:N	2.30	0.46
1:B:127:TRP:CD1	2:B:301:RET:H14	2.51	0.45
1:D:131:THR:OG1	1:D:132:PRO:HD3	2.16	0.45
1:D:232:GLY:HA2	1:D:239:LEU:HB2	1.99	0.45
3:A:302:22B:C12	3:A:302:22B:H191	2.46	0.45
1:D:238:VAL:HG23	1:D:239:LEU:HD13	1.99	0.45
1:A:29:LEU:O	1:A:30:ASN:CB	2.65	0.45
1:B:161:VAL:CG1	4:D:302:L3P:H221	2.47	0.44
1:D:73:LEU:HD13	1:D:133:MET:HE3	1.99	0.44
1:D:214:LEU:CD1	1:D:263:LEU:HD13	2.48	0.44
1:A:236:VAL:HG13	1:A:238:VAL:HG13	1.99	0.44
1:B:238:VAL:HG23	1:B:239:LEU:CD1	2.48	0.44
1:B:238:VAL:HG23	1:B:239:LEU:HD13	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:PRO:HB2	1:A:278:ILE:HD11	1.98	0.43
1:D:253:ILE:HA	1:D:257:TYR:CD2	2.54	0.43
1:B:77:VAL:HG22	4:B:303:L3P:H262	2.00	0.43
1:D:45:ALA:O	1:D:49:ILE:HG13	2.19	0.43
1:B:254:VAL:O	1:B:258:ILE:HG12	2.19	0.42
2:B:301:RET:H7	2:B:301:RET:H181	1.84	0.42
1:A:258:ILE:N	1:A:258:ILE:CD1	2.82	0.42
1:D:129:LEU:CD1	4:D:302:L3P:H23	2.45	0.42
1:A:66:LEU:HD13	1:A:140:LEU:CD1	2.50	0.42
1:D:166:ALA:HB2	1:D:179:TRP:HB3	2.01	0.42
1:A:127:TRP:CD1	2:A:301:RET:H14	2.55	0.42
1:D:20:THR:HG1	1:D:23:GLU:HG3	1.85	0.41
1:A:182:ILE:HG23	3:A:302:22B:C14	2.50	0.41
1:A:218:THR:HG23	1:A:222:TRP:NE1	2.35	0.41
1:B:133:MET:HA	1:B:133:MET:HE2	2.02	0.41
1:A:61:ASP:OD2	1:A:275:SER:HA	2.20	0.41
1:D:61:ASP:O	1:D:65:LYS:HG3	2.20	0.41
1:A:157:ILE:HA	1:A:160:CYS:SG	2.60	0.41
1:B:109:LEU:HG	6:B:466:HOH:O	2.20	0.41
1:D:252:ASP:O	1:D:256:LYS:HB2	2.20	0.41
1:D:144:SER:OG	1:D:149:LEU:HD22	2.21	0.41
3:A:302:22B:H202	1:B:49:ILE:HD13	2.03	0.41
1:D:131:THR:N	1:D:132:PRO:CD	2.83	0.41
1:D:241:VAL:HG13	1:D:242:GLY:N	2.35	0.41
1:D:22:ARG:O	1:D:26:GLU:HG3	2.21	0.40
1:D:231:LEU:O	1:D:238:VAL:HG22	2.22	0.40
1:A:131:THR:N	1:A:132:PRO:CD	2.84	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:418:HOH:O	6:A:418:HOH:O[2_656]	0.94	1.26

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	259/291 (89%)	251 (97%)	7 (3%)	1 (0%)	30	19
1	B	258/291 (89%)	253 (98%)	4 (2%)	1 (0%)	30	19
1	D	258/291 (89%)	255 (99%)	3 (1%)	0	100	100
All	All	775/873 (89%)	759 (98%)	14 (2%)	2 (0%)	36	25

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	108	MET
1	A	111	GLY

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	209/233 (90%)	201 (96%)	8 (4%)	29	17
1	B	208/233 (89%)	202 (97%)	6 (3%)	37	25
1	D	208/233 (89%)	201 (97%)	7 (3%)	32	20
All	All	625/699 (89%)	604 (97%)	21 (3%)	32	20

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	LEU
1	A	59	LEU
1	A	66	LEU
1	A	135	LEU
1	A	136	LEU
1	A	149	LEU
1	A	168	LEU

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Mol	Chain	Res	Type
1	A	264	LEU
1	B	38	LEU
1	B	66	LEU
1	B	109	LEU
1	B	135	LEU
1	B	149	LEU
1	B	264	LEU
1	D	38	LEU
1	D	66	LEU
1	D	112	GLU
1	D	135	LEU
1	D	149	LEU
1	D	168	LEU
1	D	264	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	265	ASN
1	B	41	ASN
1	B	265	ASN
1	D	41	ASN
1	D	265	ASN

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

16 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
5	BNG	B	305	-	21,21,21	1.73	6 (28%)	26,26,26	0.70	0
5	BNG	D	304	-	21,21,21	1.72	5 (23%)	26,26,26	0.71	0
4	L3P	B	302	-	19,19,58	2.02	8 (42%)	22,22,73	1.23	3 (13%)
5	BNG	A	306	-	21,21,21	1.68	6 (28%)	26,26,26	0.72	0
4	L3P	B	303	-	19,19,58	2.00	8 (42%)	22,22,73	1.22	3 (13%)
2	RET	D	301	1	20,20,21	2.26	6 (30%)	27,27,28	1.57	5 (18%)
3	22B	A	302	-	36,36,53	3.38	25 (69%)	43,47,72	1.52	9 (20%)
4	L3P	D	303	-	19,19,58	2.00	8 (42%)	22,22,73	1.19	2 (9%)
5	BNG	B	304	-	21,21,21	1.59	5 (23%)	26,26,26	0.71	0
5	BNG	A	305	-	21,21,21	1.68	6 (28%)	26,26,26	0.70	0
4	L3P	A	304	-	19,19,58	2.00	8 (42%)	22,22,73	1.21	3 (13%)
4	L3P	D	302	-	19,19,58	1.99	8 (42%)	22,22,73	1.15	2 (9%)
2	RET	A	301	1	20,20,21	2.28	6 (30%)	27,27,28	1.57	7 (25%)
4	L3P	A	303	-	19,19,58	2.00	8 (42%)	22,22,73	1.17	1 (4%)
2	RET	B	301	1	20,20,21	2.31	6 (30%)	27,27,28	1.75	8 (29%)
5	BNG	A	307	-	21,21,21	1.69	5 (23%)	26,26,26	0.73	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	BNG	B	305	-	-	6/12/32/32	0/1/1/1
5	BNG	D	304	-	-	3/12/32/32	0/1/1/1
4	L3P	B	302	-	-	7/20/20/67	-
5	BNG	A	306	-	-	1/12/32/32	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	L3P	B	303	-	-	5/20/20/67	-
2	RET	D	301	1	-	0/13/30/31	0/1/1/1
3	22B	A	302	-	-	18/42/42/65	-
4	L3P	D	303	-	-	8/20/20/67	-
5	BNG	B	304	-	-	2/12/32/32	0/1/1/1
5	BNG	A	305	-	-	2/12/32/32	0/1/1/1
4	L3P	A	304	-	-	4/20/20/67	-
4	L3P	D	302	-	-	11/20/20/67	-
2	RET	A	301	1	-	0/13/30/31	0/1/1/1
4	L3P	A	303	-	-	6/20/20/67	-
2	RET	B	301	1	-	0/13/30/31	0/1/1/1
5	BNG	A	307	-	-	4/12/32/32	0/1/1/1

All (124) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	302	22B	C4-C3	10.61	1.56	1.32
2	A	301	RET	C1-C6	6.67	1.62	1.53
2	B	301	RET	C1-C6	6.47	1.62	1.53
2	D	301	RET	C1-C6	6.18	1.61	1.53
3	A	302	22B	C16-C1	5.28	1.61	1.52
3	A	302	22B	C4-C5	5.02	1.56	1.46
3	A	302	22B	C19-C9	4.80	1.60	1.50
2	A	301	RET	C5-C6	4.47	1.42	1.34
2	B	301	RET	C5-C6	4.39	1.41	1.34
3	A	302	22B	C22-C21	4.34	1.64	1.53
2	D	301	RET	C5-C6	4.32	1.41	1.34
5	B	305	BNG	O1-C1	4.30	1.47	1.40
5	D	304	BNG	O1-C1	4.29	1.47	1.40
3	A	302	22B	C10-C9	4.26	1.45	1.35
2	D	301	RET	C14-C13	4.21	1.36	1.33
3	A	302	22B	C2-C3	4.20	1.56	1.49
5	A	307	BNG	O1-C1	4.16	1.47	1.40
5	A	305	BNG	O1-C1	4.16	1.47	1.40
3	A	302	22B	O27-C23	4.14	1.54	1.44
5	A	306	BNG	O1-C1	4.12	1.47	1.40
5	D	304	BNG	O5-C1	4.04	1.52	1.41
5	B	305	BNG	O5-C1	4.02	1.52	1.41
5	A	306	BNG	O5-C1	4.00	1.52	1.41
5	A	307	BNG	O5-C1	3.96	1.52	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	RET	C14-C13	3.91	1.36	1.33
5	A	305	BNG	O5-C1	3.90	1.51	1.41
5	B	304	BNG	O1-C1	3.88	1.46	1.40
3	A	302	22B	C17-C1	3.85	1.58	1.52
3	A	302	22B	C42-C43	3.78	1.54	1.46
3	A	302	22B	C50-C43	3.75	1.58	1.50
5	B	304	BNG	O5-C1	3.70	1.51	1.41
3	A	302	22B	C20-C13	3.53	1.58	1.50
3	A	302	22B	C18-C5	3.34	1.57	1.50
2	A	301	RET	C14-C13	3.16	1.35	1.33
4	D	302	L3P	C15-C13	3.11	1.67	1.52
3	A	302	22B	C38-C39	3.10	1.58	1.50
4	A	304	L3P	C15-C13	3.10	1.67	1.52
4	B	302	L3P	C15-C13	3.10	1.67	1.52
3	A	302	22B	C11-C10	3.10	1.52	1.43
4	D	303	L3P	C15-C13	3.09	1.67	1.52
3	A	302	22B	C45-C44	3.08	1.52	1.43
4	B	303	L3P	C15-C13	3.08	1.67	1.52
4	A	303	L3P	C15-C13	3.08	1.67	1.52
2	B	301	RET	C7-C6	2.96	1.55	1.45
2	A	301	RET	C7-C6	2.90	1.55	1.45
2	D	301	RET	C7-C6	2.90	1.55	1.45
4	D	302	L3P	C25-C23	2.83	1.66	1.52
5	D	304	BNG	C4-C5	2.83	1.59	1.53
2	B	301	RET	C2-C3	-2.82	1.45	1.52
4	B	302	L3P	C25-C23	2.82	1.66	1.52
3	A	302	22B	C44-C43	2.81	1.42	1.35
4	B	303	L3P	C25-C23	2.79	1.66	1.52
4	A	303	L3P	C25-C23	2.78	1.66	1.52
5	B	304	BNG	C4-C5	2.78	1.58	1.53
5	A	307	BNG	C4-C5	2.77	1.58	1.53
5	B	305	BNG	C4-C5	2.76	1.58	1.53
4	D	303	L3P	C25-C23	2.76	1.66	1.52
3	A	302	22B	C21-C2	2.76	1.57	1.53
4	A	304	L3P	C25-C23	2.75	1.66	1.52
4	B	302	L3P	C26-C27	2.75	1.63	1.52
2	D	301	RET	C2-C3	-2.72	1.46	1.52
4	A	303	L3P	C26-C27	2.70	1.63	1.52
4	D	302	L3P	C17-C18	2.70	1.65	1.52
4	B	302	L3P	C17-C18	2.69	1.65	1.52
4	A	304	L3P	C17-C18	2.69	1.65	1.52
4	D	303	L3P	C26-C27	2.69	1.63	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	303	L3P	C26-C27	2.67	1.63	1.52
4	B	303	L3P	C17-C18	2.67	1.65	1.52
5	A	306	BNG	C4-C5	2.66	1.58	1.53
5	A	305	BNG	C4-C5	2.65	1.58	1.53
4	D	303	L3P	C17-C18	2.65	1.65	1.52
4	A	304	L3P	C26-C27	2.64	1.63	1.52
4	B	302	L3P	C19-C18	2.64	1.61	1.52
4	A	303	L3P	C17-C18	2.64	1.65	1.52
4	D	302	L3P	C26-C27	2.63	1.63	1.52
2	A	301	RET	C2-C3	-2.60	1.46	1.52
4	A	304	L3P	C14-C13	2.59	1.61	1.52
4	A	304	L3P	C19-C18	2.59	1.61	1.52
4	D	302	L3P	C14-C13	2.59	1.60	1.52
4	A	303	L3P	C14-C13	2.59	1.60	1.52
4	D	303	L3P	C14-C13	2.58	1.60	1.52
4	B	302	L3P	C14-C13	2.58	1.60	1.52
4	B	303	L3P	C14-C13	2.58	1.60	1.52
4	D	303	L3P	C19-C18	2.56	1.60	1.52
4	A	303	L3P	C19-C18	2.54	1.60	1.52
4	B	303	L3P	C19-C18	2.51	1.60	1.52
4	D	302	L3P	C19-C18	2.49	1.60	1.52
4	D	302	L3P	C26-C25	2.45	1.62	1.52
4	A	303	L3P	C26-C25	2.45	1.62	1.52
4	B	302	L3P	C26-C25	2.45	1.62	1.52
4	D	303	L3P	C26-C25	2.39	1.62	1.52
4	A	304	L3P	C26-C25	2.39	1.62	1.52
3	A	302	22B	C8-C9	2.39	1.51	1.46
4	B	303	L3P	C26-C25	2.38	1.62	1.52
5	B	305	BNG	O5-C5	2.33	1.50	1.44
5	D	304	BNG	O5-C5	2.32	1.50	1.44
3	A	302	22B	C22-C23	2.31	1.60	1.53
5	A	306	BNG	O5-C5	2.25	1.49	1.44
5	A	305	BNG	C1-C2	2.25	1.59	1.52
5	A	307	BNG	O5-C5	2.25	1.49	1.44
5	B	305	BNG	C1-C2	2.23	1.59	1.52
3	A	302	22B	C12-C13	2.22	1.50	1.46
3	A	302	22B	C15-C14	2.21	1.50	1.43
5	A	307	BNG	C1-C2	2.18	1.58	1.52
3	A	302	22B	C40-C39	2.18	1.40	1.34
5	A	306	BNG	C1-C2	2.17	1.58	1.52
5	A	305	BNG	O5-C5	2.17	1.49	1.44
5	D	304	BNG	C1-C2	2.14	1.58	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	303	L3P	C16-C15	2.13	1.61	1.52
4	A	303	L3P	C16-C15	2.13	1.61	1.52
4	D	303	L3P	C16-C15	2.12	1.61	1.52
4	D	302	L3P	C16-C15	2.12	1.61	1.52
4	B	302	L3P	C16-C15	2.12	1.61	1.52
2	A	301	RET	C2-C1	2.12	1.58	1.54
2	D	301	RET	C2-C1	2.08	1.58	1.54
4	A	304	L3P	C16-C15	2.07	1.60	1.52
5	B	304	BNG	O5-C5	2.06	1.49	1.44
5	A	305	BNG	C3-C2	2.06	1.57	1.52
5	B	305	BNG	C3-C2	2.05	1.57	1.52
3	A	302	22B	C41-C40	2.05	1.49	1.43
2	B	301	RET	C2-C1	2.04	1.58	1.54
3	A	302	22B	C1-C2	2.02	1.57	1.55
5	A	306	BNG	C3-C2	2.01	1.57	1.52
5	B	304	BNG	C1-C2	2.00	1.58	1.52

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	302	22B	C50-C43-C44	-3.90	116.49	122.82
4	B	302	L3P	C26-C25-C23	3.53	127.69	115.97
2	B	301	RET	C1-C6-C7	3.47	125.06	115.65
4	B	303	L3P	C26-C25-C23	3.47	127.49	115.97
4	D	303	L3P	C26-C25-C23	3.45	127.43	115.97
4	A	303	L3P	C26-C25-C23	3.37	127.17	115.97
2	B	301	RET	C1-C6-C5	-3.27	118.17	122.64
2	D	301	RET	C1-C6-C5	-3.25	118.19	122.64
3	A	302	22B	C42-C43-C44	3.22	124.07	119.01
4	A	304	L3P	C26-C25-C23	3.20	126.61	115.97
2	A	301	RET	C17-C1-C6	3.17	115.22	110.24
2	D	301	RET	C1-C6-C7	3.08	124.02	115.65
4	D	302	L3P	C26-C25-C23	3.05	126.09	115.97
3	A	302	22B	C41-C40-C39	-3.03	122.85	127.48
3	A	302	22B	C7-C6-C5	-3.02	123.04	127.28
2	A	301	RET	C1-C6-C7	2.95	123.65	115.65
2	B	301	RET	C17-C1-C6	2.78	114.61	110.24
2	A	301	RET	C1-C6-C5	-2.77	118.85	122.64
3	A	302	22B	C3-C4-C5	-2.73	120.44	126.32
2	D	301	RET	C17-C1-C6	2.60	114.32	110.24
2	B	301	RET	C2-C1-C6	2.55	114.14	110.44
2	A	301	RET	C20-C13-C12	2.51	121.92	118.09

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	301	RET	C19-C9-C8	2.44	121.82	118.09
2	D	301	RET	C2-C1-C6	2.41	113.94	110.44
2	B	301	RET	C20-C13-C12	2.41	121.77	118.09
3	A	302	22B	C20-C13-C14	-2.35	119.00	122.82
2	D	301	RET	C20-C13-C12	2.32	121.63	118.09
2	B	301	RET	C8-C9-C10	-2.29	115.40	119.01
4	B	303	L3P	C21-C20-C18	2.27	123.50	115.97
4	A	304	L3P	C16-C17-C18	2.26	123.47	115.97
4	A	304	L3P	C21-C20-C18	2.20	123.29	115.97
4	B	302	L3P	C16-C17-C18	2.17	123.19	115.97
2	A	301	RET	C8-C9-C10	-2.15	115.63	119.01
4	D	302	L3P	C16-C17-C18	2.10	122.96	115.97
4	B	303	L3P	C16-C17-C18	2.09	122.91	115.97
3	A	302	22B	C20-C13-C12	2.09	121.28	118.09
2	B	301	RET	C7-C6-C5	-2.08	116.77	121.56
4	D	303	L3P	C21-C20-C18	2.06	122.80	115.97
3	A	302	22B	C26-C39-C38	2.06	119.32	114.59
4	B	302	L3P	C21-C20-C18	2.05	122.79	115.97
2	A	301	RET	C19-C9-C8	2.03	121.19	118.09
2	A	301	RET	C2-C1-C6	2.02	113.38	110.44
3	A	302	22B	C15-C14-C13	-2.01	124.47	127.28

There are no chirality outliers.

All (77) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	302	22B	C1-C2-C3-C4
3	A	302	22B	C2-C3-C4-C5
3	A	302	22B	C10-C11-C12-C13
3	A	302	22B	C12-C13-C14-C15
3	A	302	22B	C20-C13-C14-C15
3	A	302	22B	C13-C14-C15-C45
3	A	302	22B	C21-C22-C23-C24
3	A	302	22B	C21-C22-C23-O27
5	D	304	BNG	C2'-C1'-O1-C1
4	A	304	L3P	C15-C16-C17-C18
4	A	303	L3P	C15-C16-C17-C18
4	B	302	L3P	C15-C16-C17-C18
4	B	303	L3P	C15-C16-C17-C18
4	D	302	L3P	C15-C16-C17-C18
4	D	303	L3P	C15-C16-C17-C18
3	A	302	22B	C9-C10-C11-C12

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Mol	Chain	Res	Type	Atoms
3	A	302	22B	C43-C44-C45-C15
3	A	302	22B	C7-C8-C9-C19
3	A	302	22B	C7-C8-C9-C10
3	A	302	22B	C21-C22-C23-C25
4	A	303	L3P	C25-C26-C27-C28
4	A	304	L3P	C18-C20-C21-C22
4	B	303	L3P	C13-C15-C16-C17
4	B	303	L3P	C26-C27-C28-C29
4	B	302	L3P	C26-C27-C28-C29
4	B	302	L3P	C26-C27-C28-C30
4	D	302	L3P	C26-C27-C28-C30
4	D	302	L3P	C13-C15-C16-C17
4	D	302	L3P	C18-C20-C21-C22
5	B	305	BNG	C3'-C4'-C5'-C6'
5	D	304	BNG	C3'-C4'-C5'-C6'
4	B	303	L3P	C26-C27-C28-C30
5	A	305	BNG	C1'-C2'-C3'-C4'
4	D	302	L3P	C26-C27-C28-C29
5	A	307	BNG	C5'-C6'-C7'-C8'
5	A	307	BNG	C2'-C3'-C4'-C5'
4	B	303	L3P	C25-C26-C27-C28
4	A	303	L3P	C26-C27-C28-C29
4	A	303	L3P	C26-C27-C28-C30
5	A	307	BNG	C1'-C2'-C3'-C4'
3	A	302	22B	C21-C2-C3-C4
4	B	302	L3P	C24-C23-C25-C26
4	B	302	L3P	C25-C26-C27-C28
5	B	304	BNG	C5'-C6'-C7'-C8'
5	B	305	BNG	C2'-C1'-O1-C1
4	D	303	L3P	C26-C27-C28-C30
5	A	305	BNG	C6'-C7'-C8'-C9'
4	B	302	L3P	C22-C23-C25-C26
4	D	302	L3P	C16-C17-C18-C20
4	D	303	L3P	C22-C23-C25-C26
5	D	304	BNG	C6'-C7'-C8'-C9'
5	B	305	BNG	C5'-C6'-C7'-C8'
3	A	302	22B	C11-C10-C9-C19
4	A	304	L3P	C26-C27-C28-C30
4	A	303	L3P	C22-C23-C25-C26
4	D	302	L3P	C17-C18-C20-C21
4	D	302	L3P	C22-C23-C25-C26
5	A	307	BNG	C6'-C7'-C8'-C9'

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Mol	Chain	Res	Type	Atoms
5	A	306	BNG	C6'-C7'-C8'-C9'
4	A	303	L3P	C24-C23-C25-C26
4	D	303	L3P	C26-C27-C28-C29
5	B	305	BNG	C6'-C7'-C8'-C9'
4	D	303	L3P	C16-C17-C18-C20
4	D	302	L3P	C24-C23-C25-C26
5	B	305	BNG	C1'-C2'-C3'-C4'
4	A	304	L3P	C26-C27-C28-C29
4	B	302	L3P	C13-C15-C16-C17
4	D	302	L3P	C16-C17-C18-C19
4	D	302	L3P	C19-C18-C20-C21
4	D	303	L3P	C24-C23-C25-C26
4	D	303	L3P	C16-C17-C18-C19
4	D	303	L3P	C18-C20-C21-C22
3	A	302	22B	C50-C43-C44-C45
3	A	302	22B	C42-C43-C44-C45
5	B	305	BNG	C2'-C3'-C4'-C5'
5	B	304	BNG	C1'-C2'-C3'-C4'
3	A	302	22B	C11-C10-C9-C8

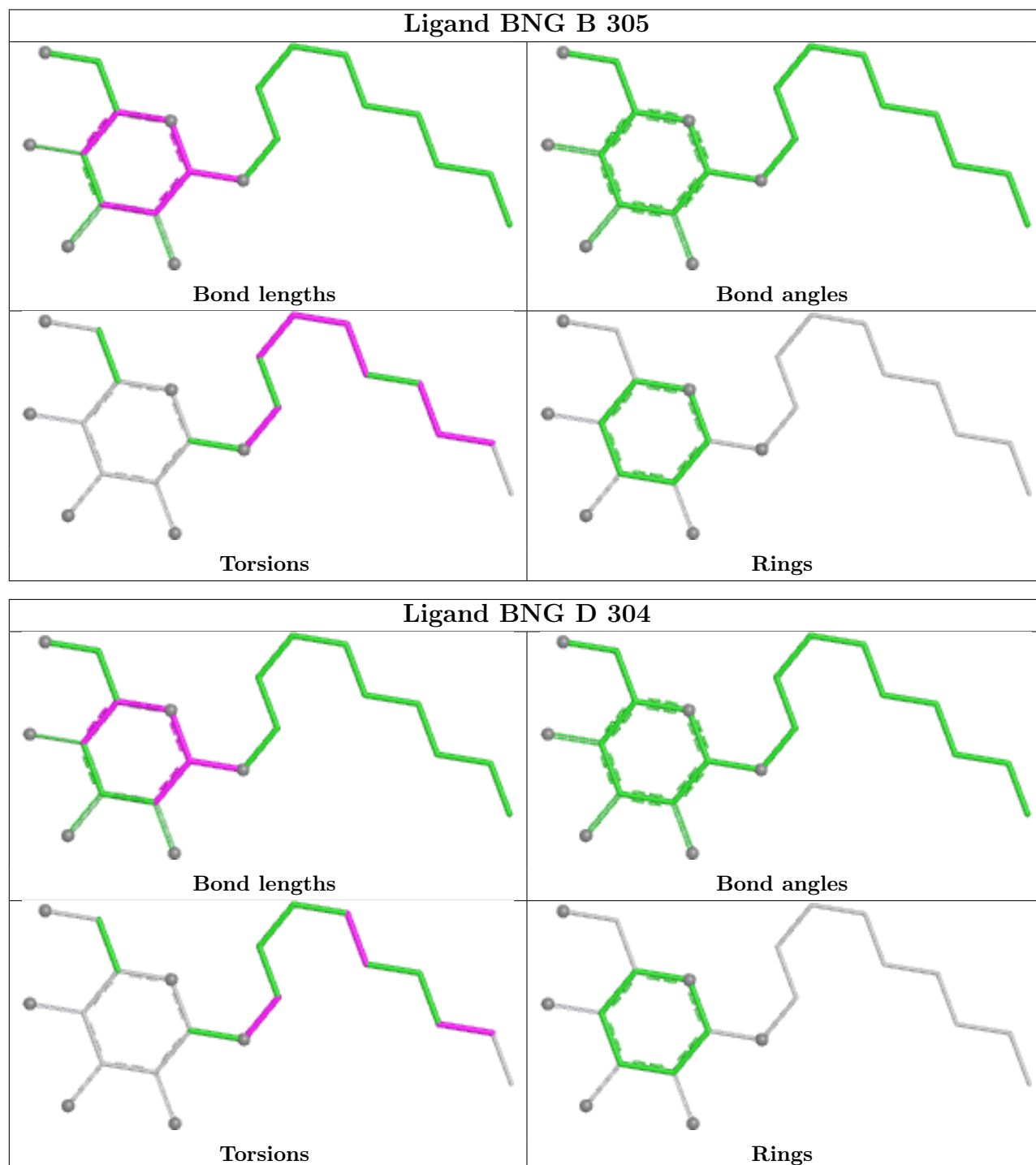
There are no ring outliers.

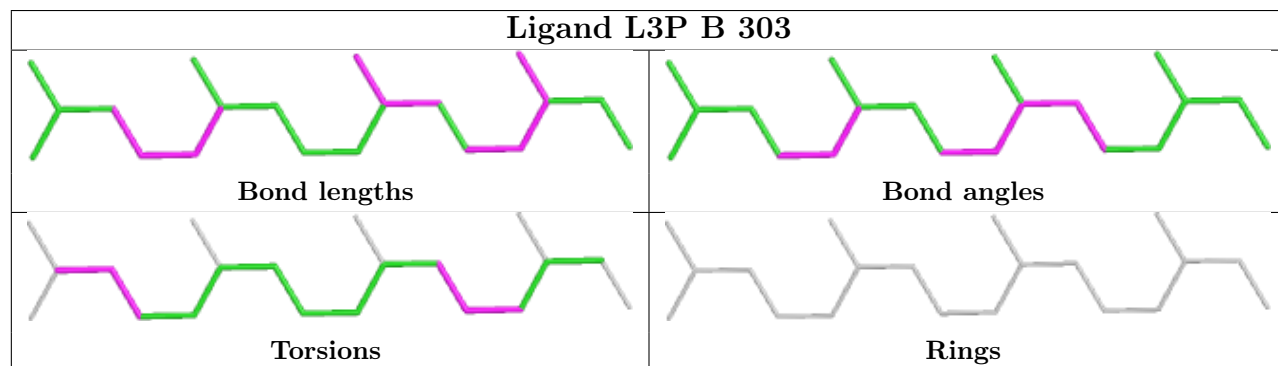
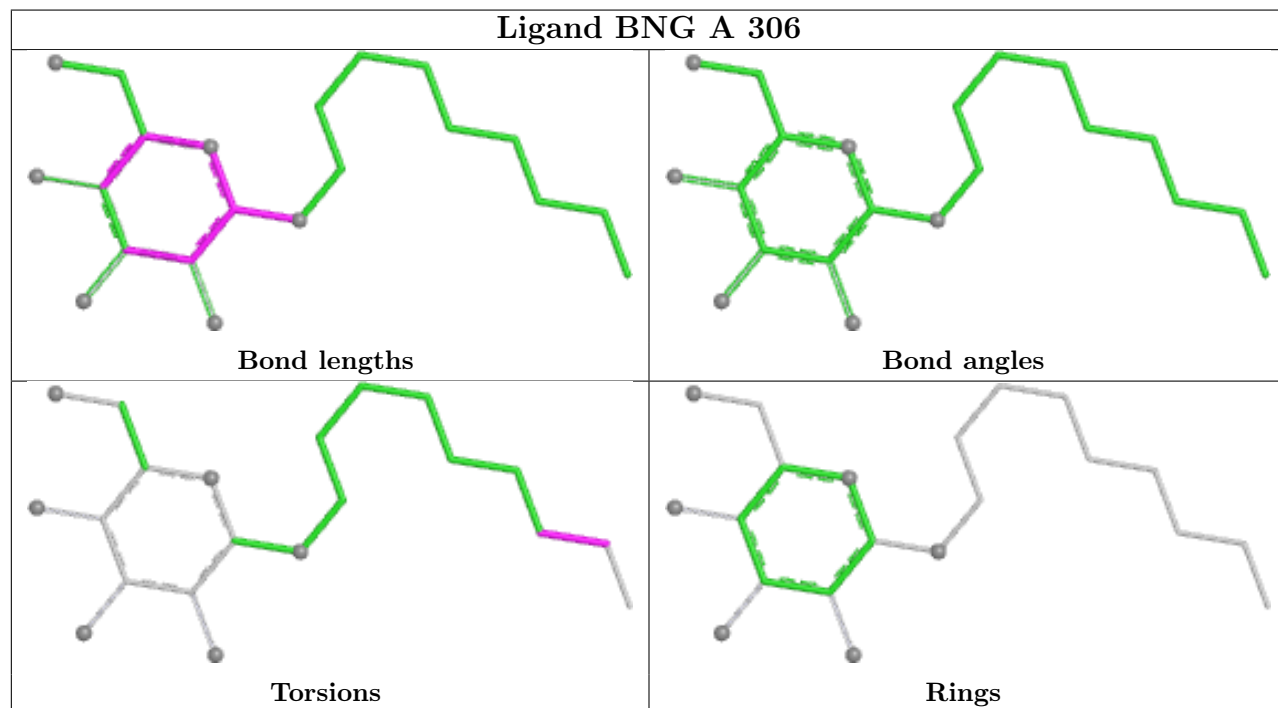
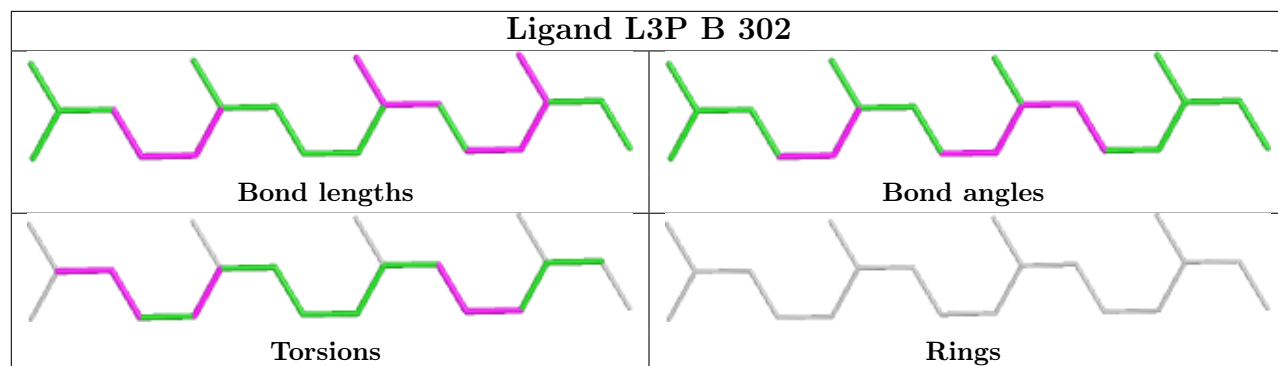
9 monomers are involved in 22 short contacts:

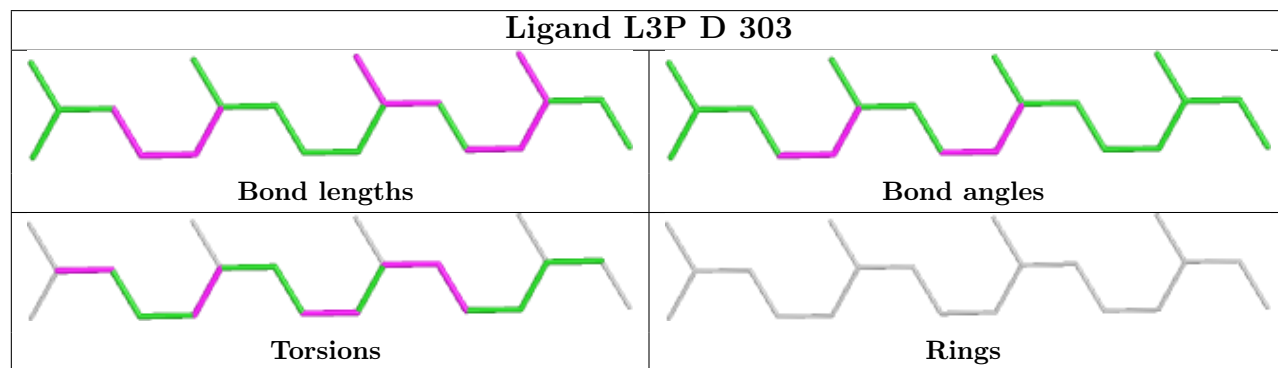
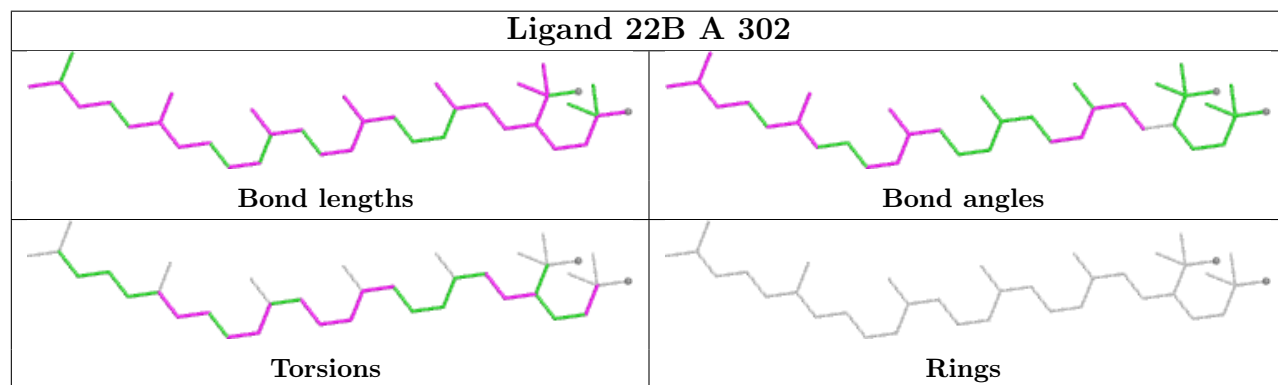
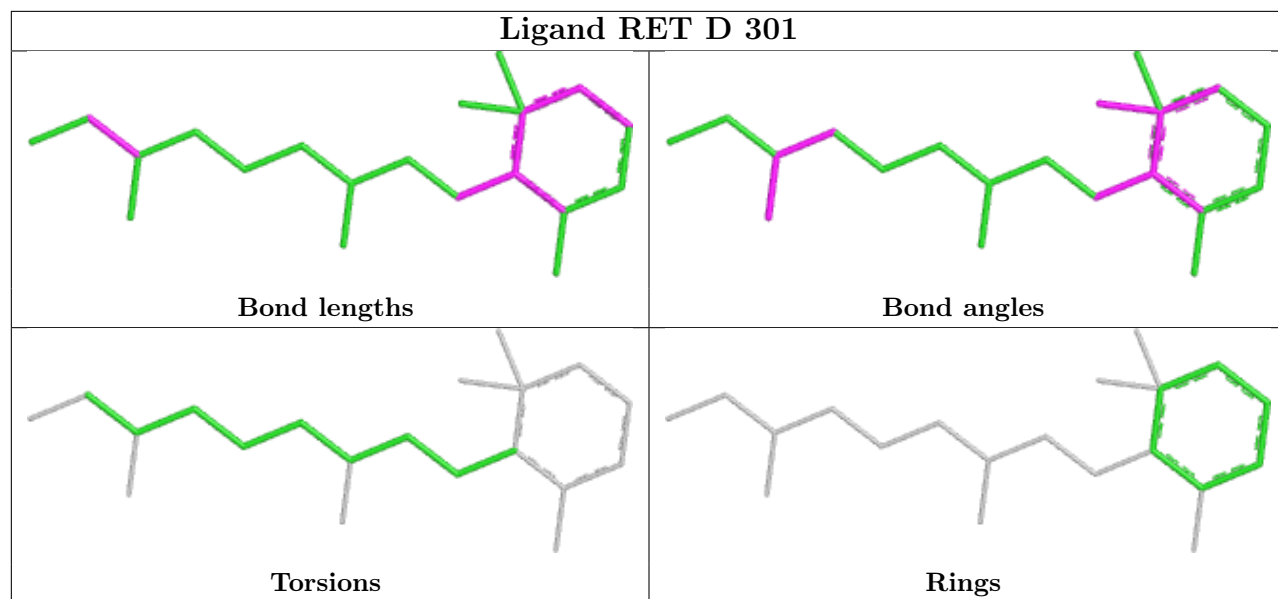
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	303	L3P	2	0
3	A	302	22B	6	0
4	D	303	L3P	1	0
5	B	304	BNG	1	0
4	A	304	L3P	1	0
4	D	302	L3P	7	0
2	A	301	RET	1	0
4	A	303	L3P	1	0
2	B	301	RET	2	0

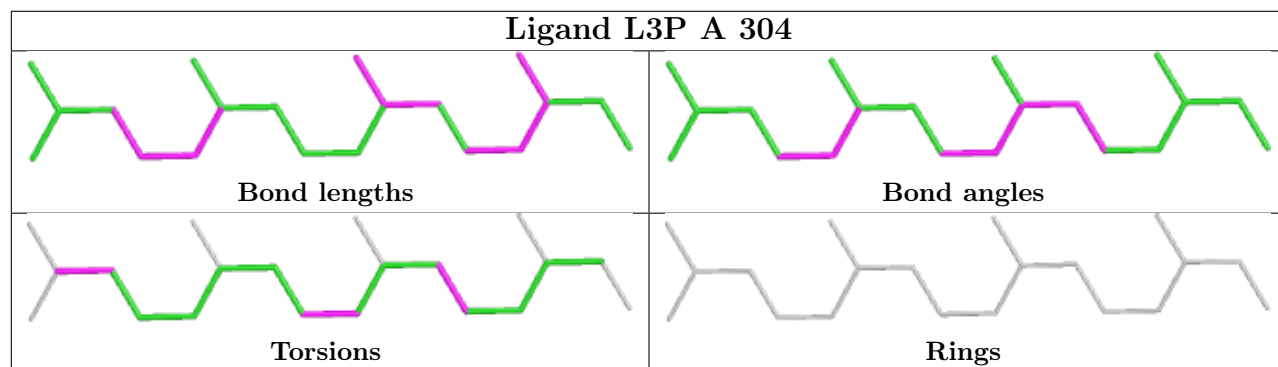
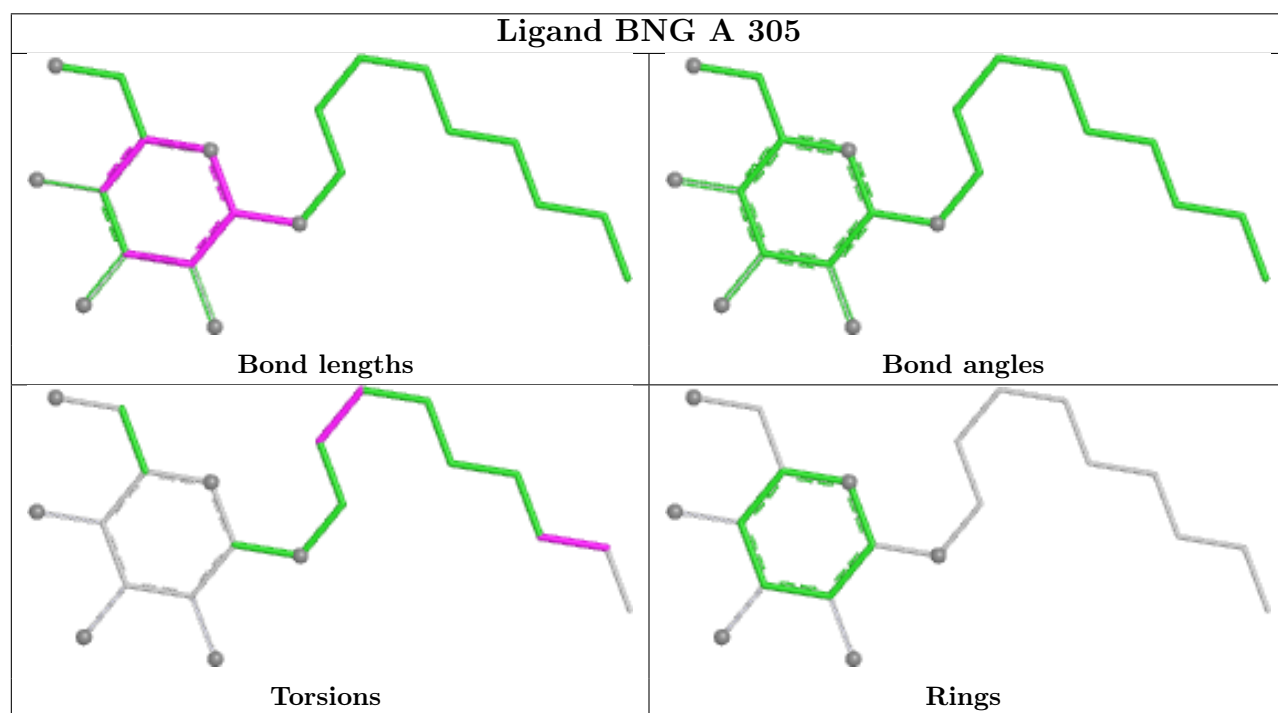
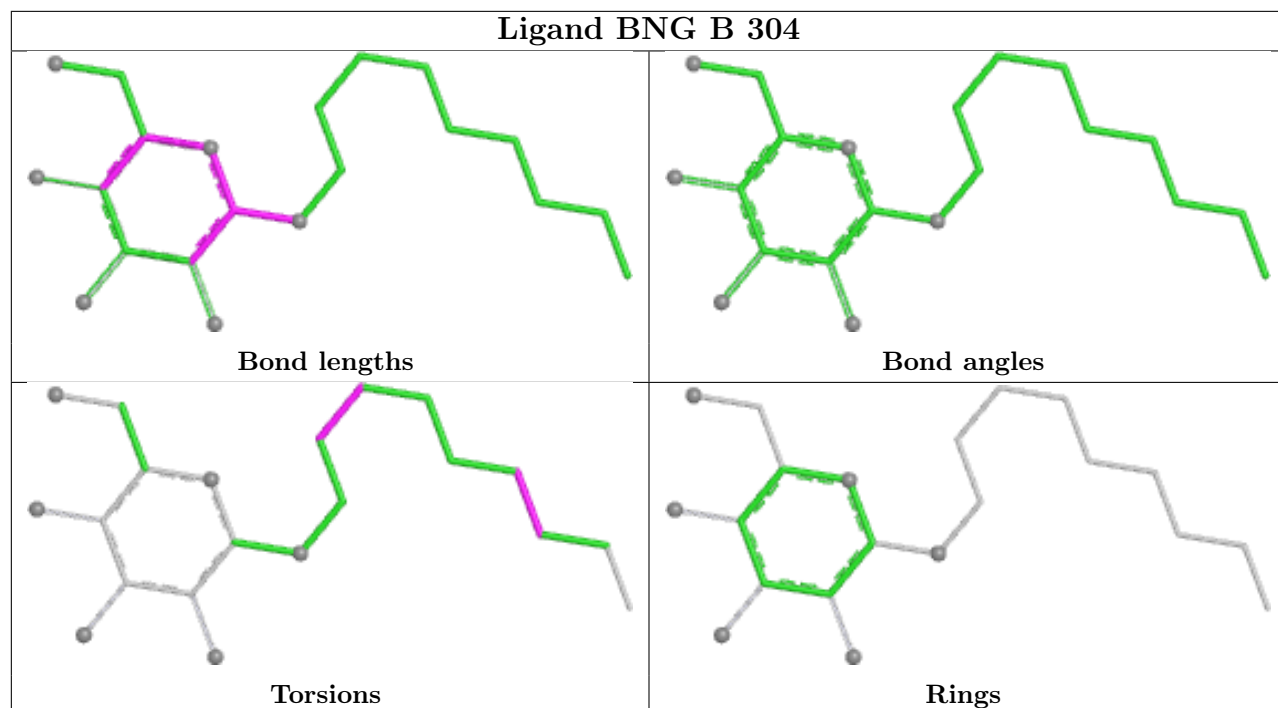
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

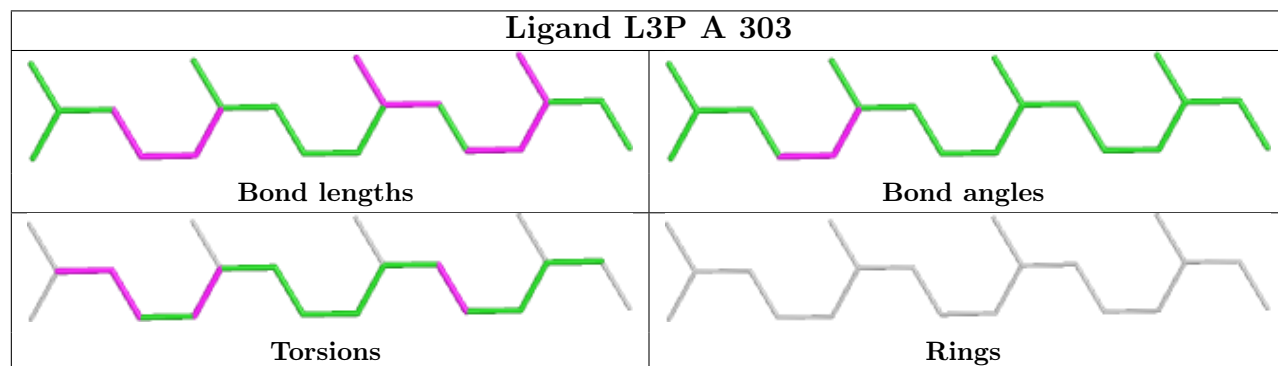
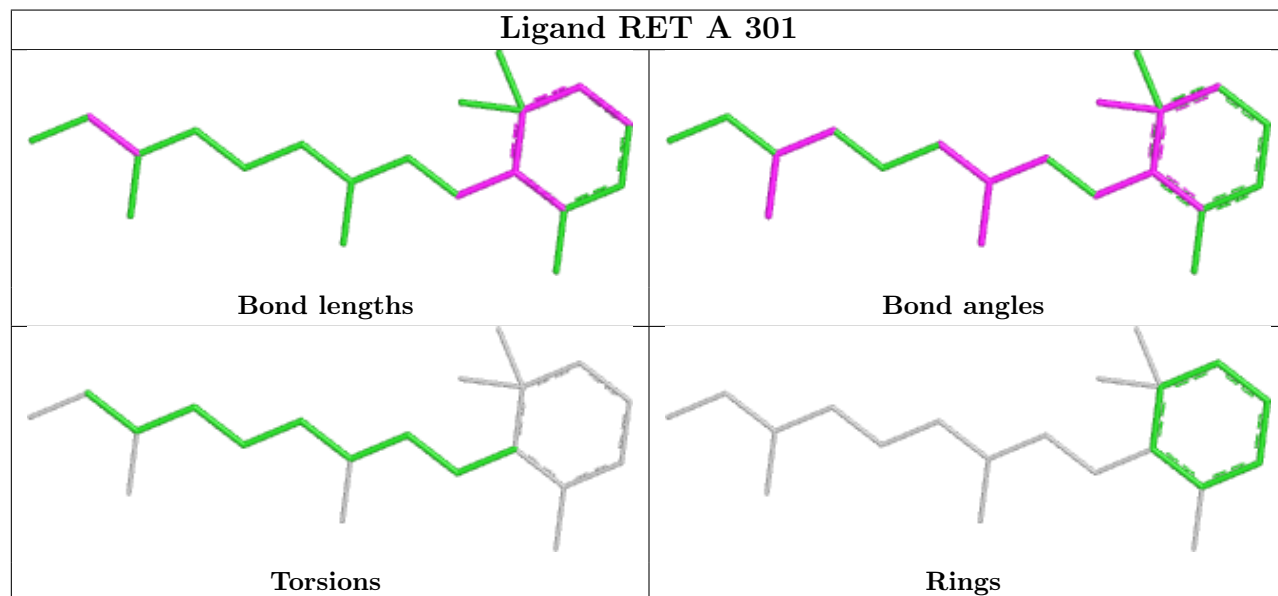
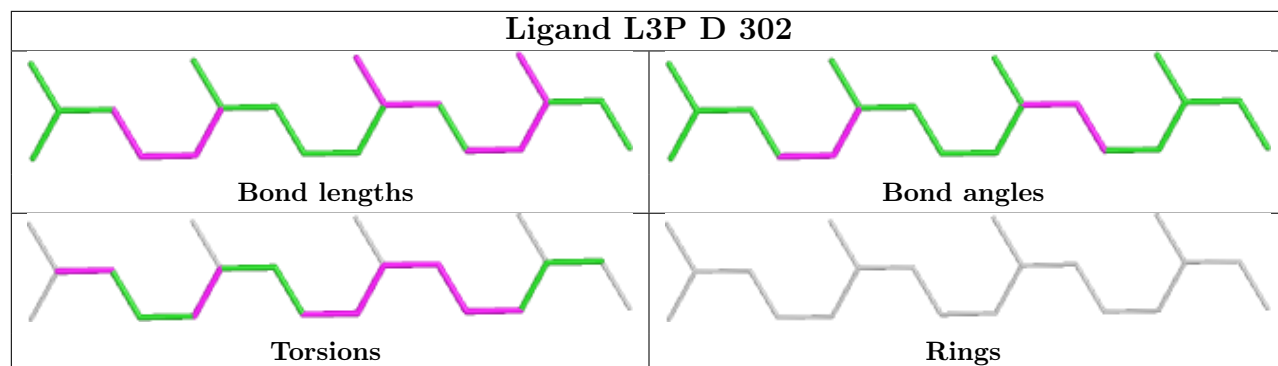
average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

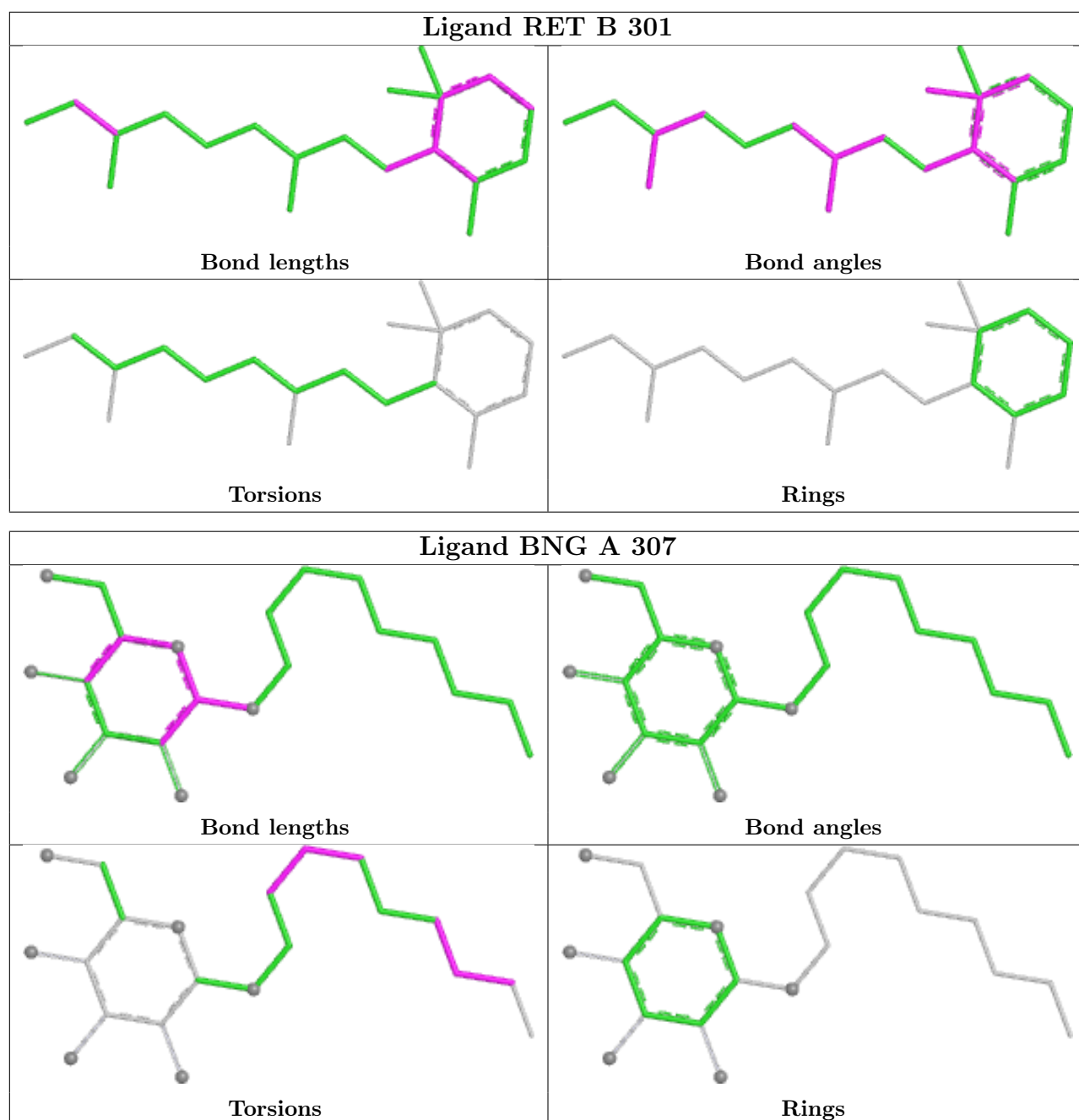












5.7 Other polymers [i](#)

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	261/291 (89%)	0.14	18 (6%) 23 21	15, 16, 34, 50	0
1	B	260/291 (89%)	0.52	24 (9%) 14 12	15, 23, 37, 56	0
1	D	260/291 (89%)	0.30	17 (6%) 25 23	15, 20, 38, 54	0
All	All	781/873 (89%)	0.32	59 (7%) 20 18	15, 20, 37, 56	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	277	SER	7.5
1	B	110	GLY	7.4
1	D	276	GLY	7.3
1	A	107	VAL	7.0
1	B	109	LEU	6.7
1	A	110	GLY	6.5
1	A	111	GLY	5.9
1	D	277	SER	5.7
1	D	30	ASN	5.5
1	A	160	CYS	5.4
1	B	276	GLY	5.0
1	B	107	VAL	4.8
1	B	29	LEU	4.4
1	B	268	THR	4.4
1	D	111	GLY	4.3
1	A	278	ILE	4.0
1	B	236	VAL	3.9
1	A	277	SER	3.7
1	A	112	GLU	3.6
1	D	258	ILE	3.6
1	B	258	ILE	3.5
1	B	108	MET	3.5
1	A	104	GLY	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	30	ASN	3.3
1	B	104	GLY	3.1
1	B	112	GLU	3.1
1	D	238	VAL	3.1
1	D	268	THR	3.1
1	D	275	SER	3.1
1	D	57	ARG	3.0
1	B	243	TYR	3.0
1	A	108	MET	3.0
1	D	243	TYR	2.9
1	A	29	LEU	2.9
1	B	19	VAL	2.8
1	A	109	LEU	2.7
1	B	105	SER	2.7
1	D	106	SER	2.6
1	D	113	GLU	2.6
1	A	106	SER	2.5
1	A	113	GLU	2.5
1	A	276	GLY	2.5
1	B	238	VAL	2.5
1	D	29	LEU	2.4
1	B	18	GLU	2.4
1	B	103	GLU	2.4
1	A	126	THR	2.3
1	D	59	LEU	2.3
1	D	109	LEU	2.3
1	B	101	PHE	2.2
1	B	125	LEU	2.2
1	B	200	GLN	2.2
1	B	106	SER	2.2
1	D	32	PRO	2.1
1	A	22	ARG	2.1
1	B	30	ASN	2.1
1	A	103	GLU	2.0
1	B	244	THR	2.0
1	D	244	THR	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 ⓘ

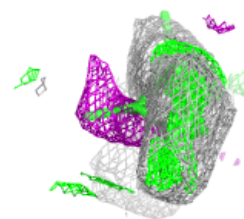
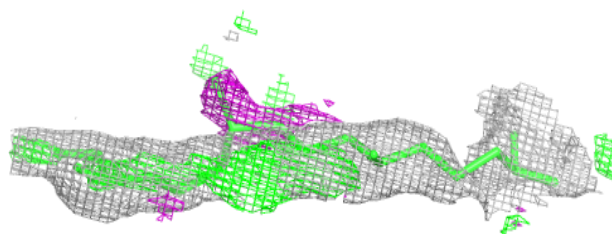
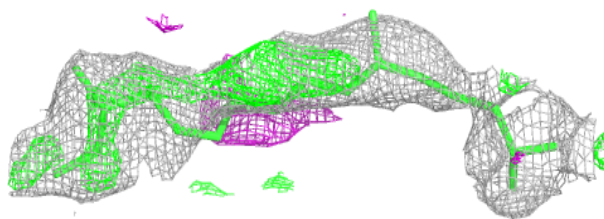
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	L3P	B	302	20/59	0.37	0.42	82,83,83,84	0
3	22B	A	302	37/54	0.42	0.30	24,52,64,65	0
5	BNG	A	306	21/21	0.51	0.44	85,86,87,87	0
4	L3P	A	303	20/59	0.58	0.42	90,91,94,94	0
4	L3P	D	303	20/59	0.62	0.42	92,92,95,95	0
4	L3P	B	303	20/59	0.62	0.45	87,89,89,89	0
4	L3P	D	302	20/59	0.63	0.40	77,79,81,81	0
4	L3P	A	304	20/59	0.67	0.43	78,80,82,82	0
5	BNG	D	304	21/21	0.68	0.37	74,77,78,79	0
5	BNG	A	307	21/21	0.69	0.32	78,79,85,86	0
5	BNG	A	305	21/21	0.73	0.42	81,82,87,88	0
5	BNG	B	305	21/21	0.75	0.35	79,81,81,81	0
5	BNG	B	304	21/21	0.90	0.13	26,30,58,61	0
2	RET	A	301	20/21	0.91	0.08	14,14,18,18	0
2	RET	D	301	20/21	0.92	0.08	14,15,19,19	0
2	RET	B	301	20/21	0.93	0.08	18,19,21,22	0

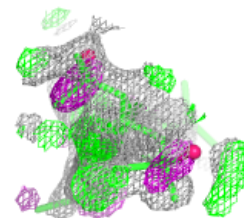
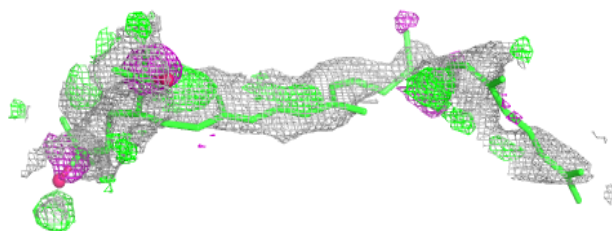
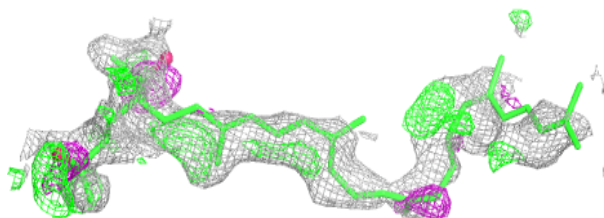
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around L3P B 302:

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

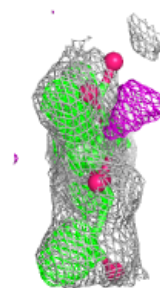
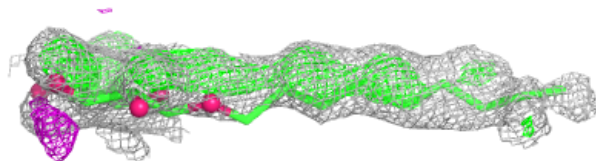
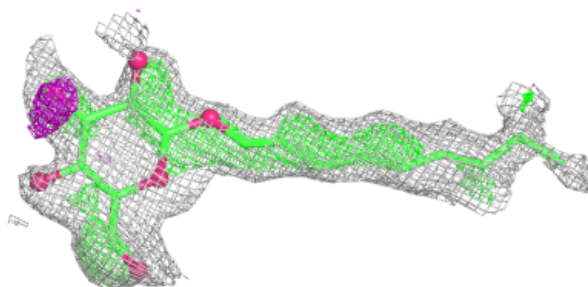
**Electron density around 22B A 302:**

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

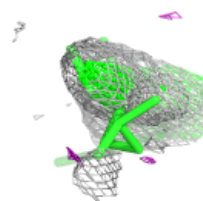
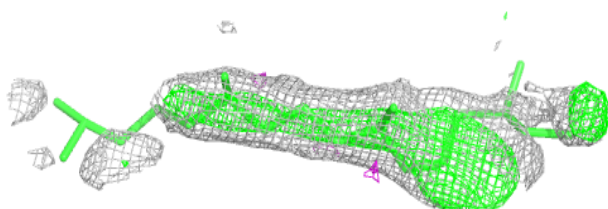
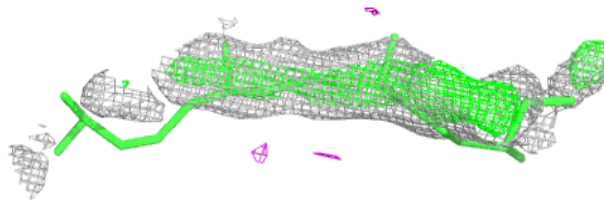


Electron density around BNG A 306:

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

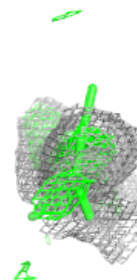
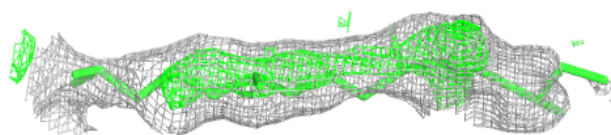
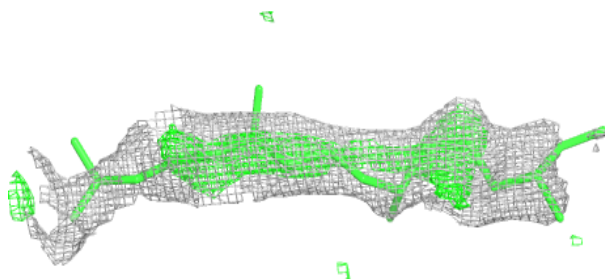
**Electron density around L3P A 303:**

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

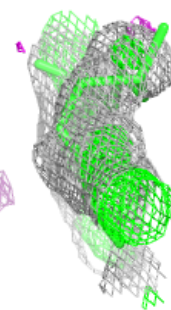
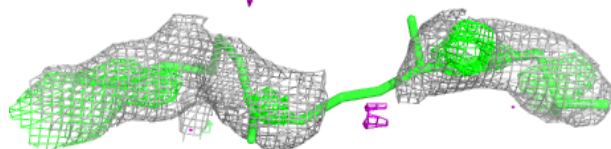
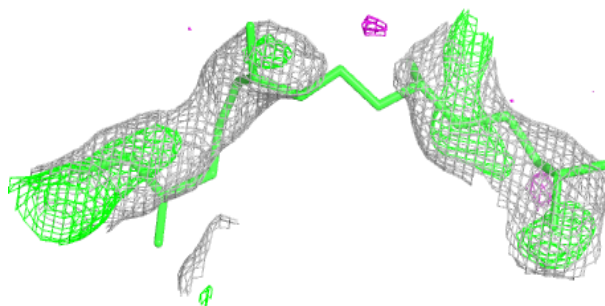


Electron density around L3P D 303:

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

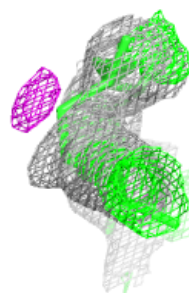
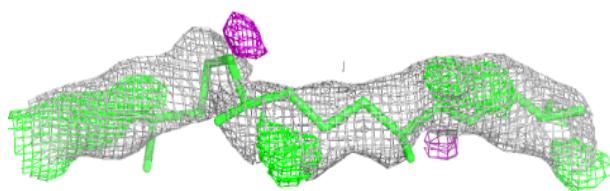
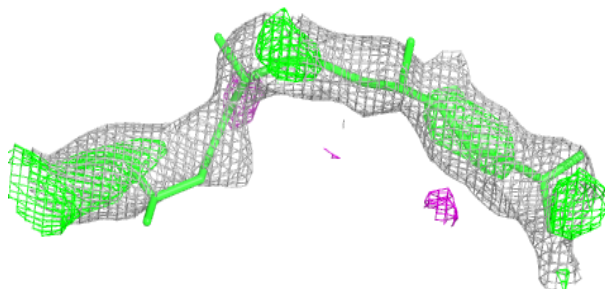
**Electron density around L3P B 303:**

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

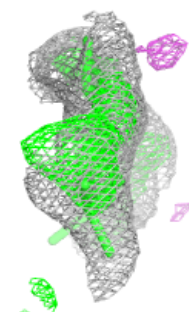
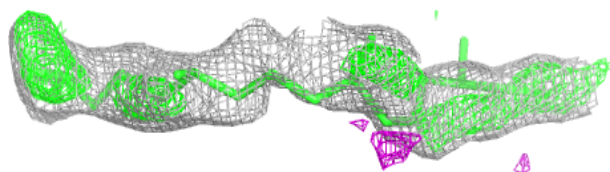
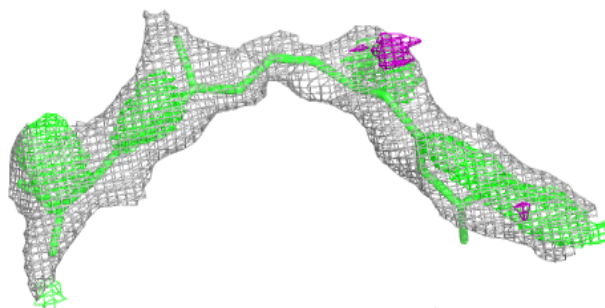


Electron density around L3P D 302:

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

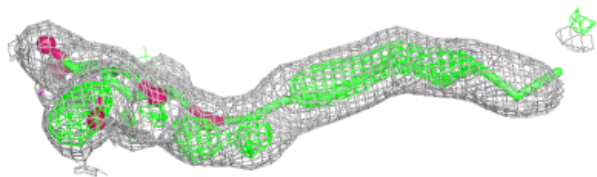
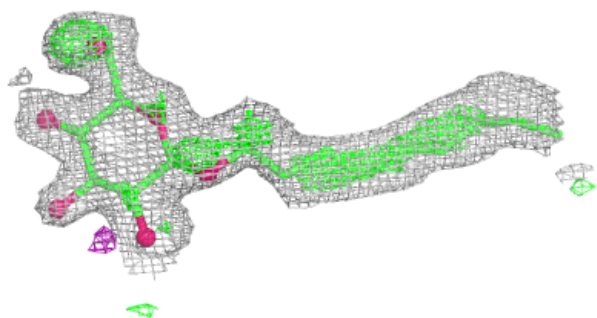
**Electron density around L3P A 304:**

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

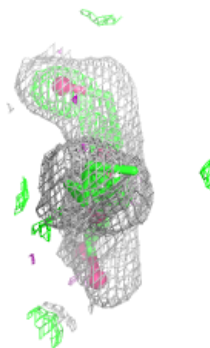
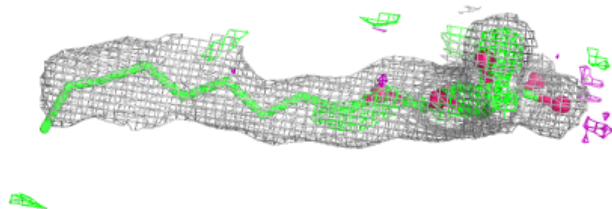
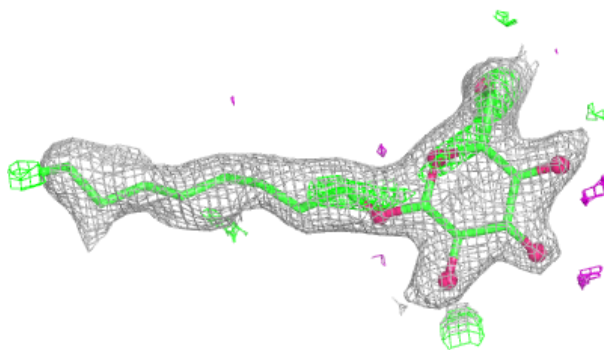


Electron density around BNG D 304:

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

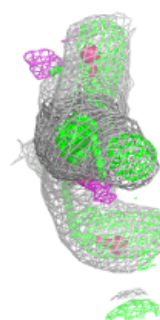
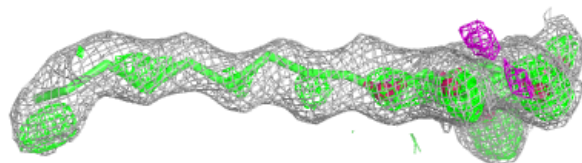
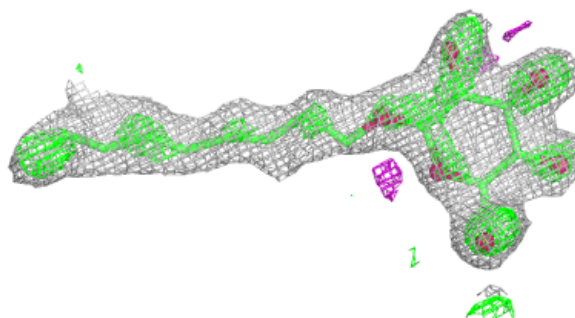
**Electron density around BNG A 307:**

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

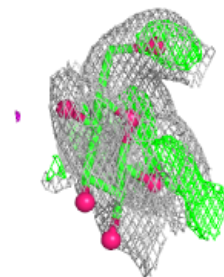
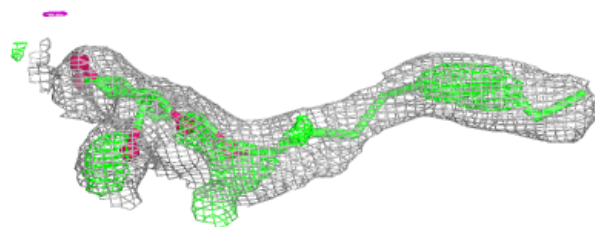
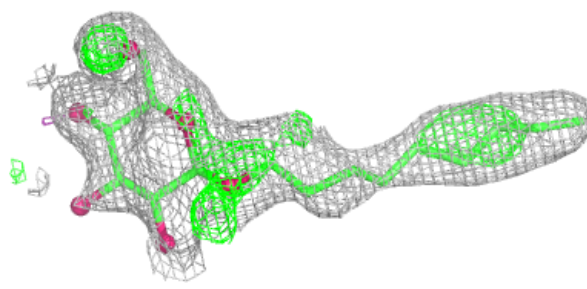


Electron density around BNG A 305:

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

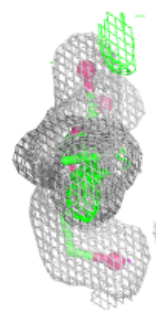
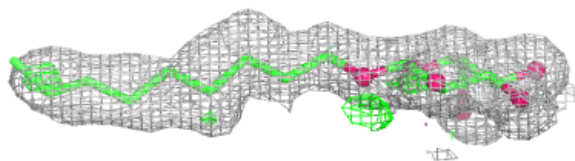
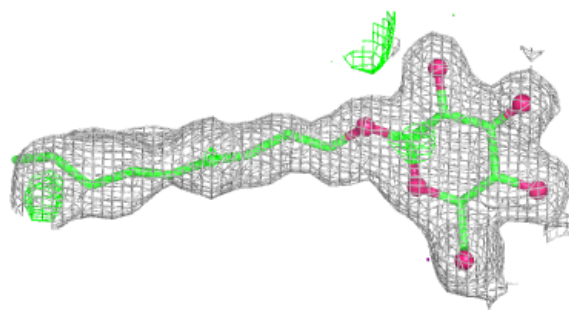
**Electron density around BNG B 305:**

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

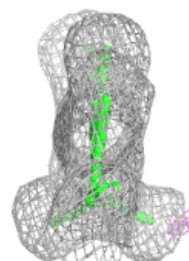
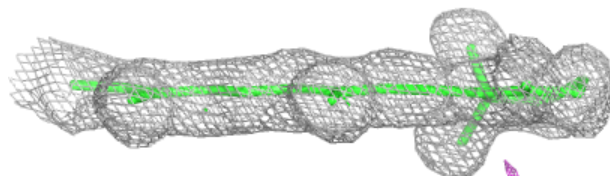
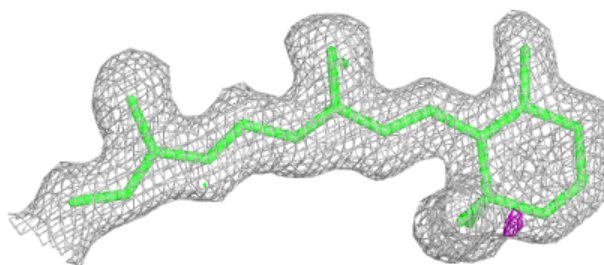


Electron density around BNG B 304:

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

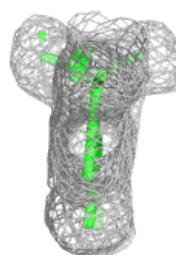
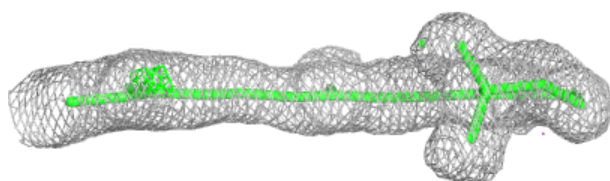
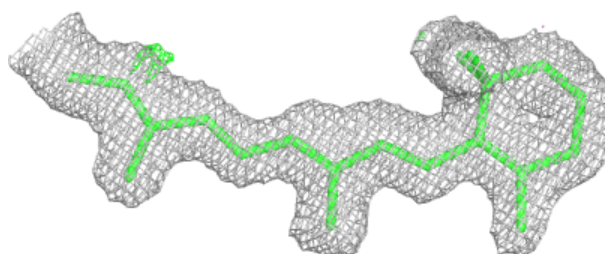
**Electron density around RET A 301:**

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

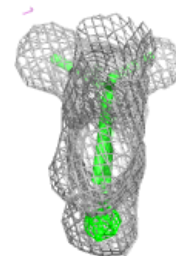
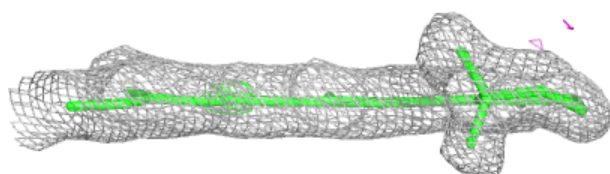
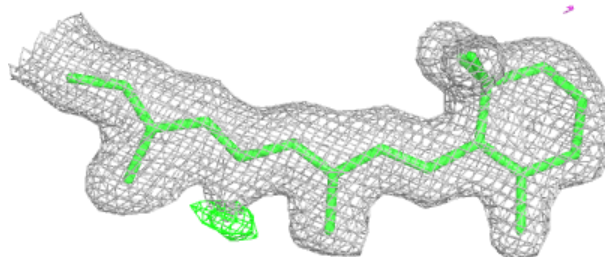


Electron density around RET D 301:

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

**Electron density around RET B 301:**

$2mF_o-DF_c$ (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.