



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 8, 2024 – 11:57 AM EDT

PDB ID : 3RBH
Title : Structure of alginate export protein AlgE from *Pseudomonas aeruginosa*
Authors : Whitney, J.C.; Hay, I.D.; Li, C.; Eckford, P.D.; Robinson, H.; Amaya, M.F.;
Wood, L.F.; Ohman, D.E.; Bear, C.E.; Rehm, B.H.; Howell, P.L.
Deposited on : 2011-03-29
Resolution : 2.30 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 : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.20.1
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.003 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

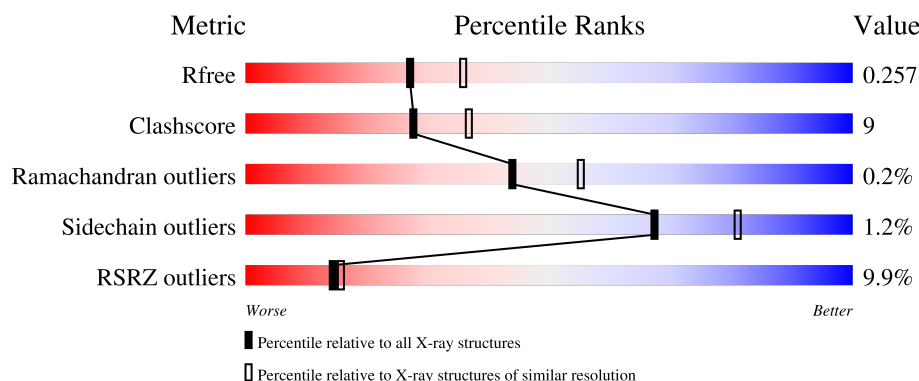
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	164625	5963 (2.30-2.30)
Clashscore	180529	6698 (2.30-2.30)
Ramachandran outliers	177936	6640 (2.30-2.30)
Sidechain outliers	177891	6640 (2.30-2.30)
RSRZ outliers	164620	5963 (2.30-2.30)

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	479	<div> <div>10%</div> <div> <div></div> <div>75%</div> <div>14%</div> <div>11%</div> </div> </div>
1	B	479	<div> <div>6%</div> <div> <div></div> <div>72%</div> <div>17%</div> <div>10%</div> </div> </div>
1	C	479	<div> <div>10%</div> <div> <div></div> <div>70%</div> <div>15%</div> <div>15%</div> </div> </div>
1	D	479	<div> <div>9%</div> <div> <div></div> <div>72%</div> <div>13%</div> <div>14%</div> </div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14038 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 Alginate production protein AlgE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	428	Total	C	N	O	Se	0	2	0
			3305	2073	585	643	4			
1	B	429	Total	C	N	O	Se	0	5	0
			3328	2084	588	652	4			
1	C	409	Total	C	N	O	Se	0	1	0
			3165	1987	564	610	4			
1	D	410	Total	C	N	O	Se	0	1	0
			3165	1992	560	609	4			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	12	MSE	-	expression tag	UNP P18895
A	13	GLY	-	expression tag	UNP P18895
A	14	SER	-	expression tag	UNP P18895
A	15	SER	-	expression tag	UNP P18895
A	16	HIS	-	expression tag	UNP P18895
A	17	HIS	-	expression tag	UNP P18895
A	18	HIS	-	expression tag	UNP P18895
A	19	HIS	-	expression tag	UNP P18895
A	20	HIS	-	expression tag	UNP P18895
A	21	HIS	-	expression tag	UNP P18895
A	22	SER	-	expression tag	UNP P18895
A	23	SER	-	expression tag	UNP P18895
A	24	GLY	-	expression tag	UNP P18895
A	25	LEU	-	expression tag	UNP P18895
A	26	VAL	-	expression tag	UNP P18895
A	27	PRO	-	expression tag	UNP P18895
A	28	ARG	-	expression tag	UNP P18895
A	29	GLY	-	expression tag	UNP P18895
A	30	SER	-	expression tag	UNP P18895
A	31	HIS	-	expression tag	UNP P18895
A	32	MSE	-	expression tag	UNP P18895

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Chain	Residue	Modelled	Actual	Comment	Reference
B	12	MSE	-	expression tag	UNP P18895
B	13	GLY	-	expression tag	UNP P18895
B	14	SER	-	expression tag	UNP P18895
B	15	SER	-	expression tag	UNP P18895
B	16	HIS	-	expression tag	UNP P18895
B	17	HIS	-	expression tag	UNP P18895
B	18	HIS	-	expression tag	UNP P18895
B	19	HIS	-	expression tag	UNP P18895
B	20	HIS	-	expression tag	UNP P18895
B	21	HIS	-	expression tag	UNP P18895
B	22	SER	-	expression tag	UNP P18895
B	23	SER	-	expression tag	UNP P18895
B	24	GLY	-	expression tag	UNP P18895
B	25	LEU	-	expression tag	UNP P18895
B	26	VAL	-	expression tag	UNP P18895
B	27	PRO	-	expression tag	UNP P18895
B	28	ARG	-	expression tag	UNP P18895
B	29	GLY	-	expression tag	UNP P18895
B	30	SER	-	expression tag	UNP P18895
B	31	HIS	-	expression tag	UNP P18895
B	32	MSE	-	expression tag	UNP P18895
C	12	MSE	-	expression tag	UNP P18895
C	13	GLY	-	expression tag	UNP P18895
C	14	SER	-	expression tag	UNP P18895
C	15	SER	-	expression tag	UNP P18895
C	16	HIS	-	expression tag	UNP P18895
C	17	HIS	-	expression tag	UNP P18895
C	18	HIS	-	expression tag	UNP P18895
C	19	HIS	-	expression tag	UNP P18895
C	20	HIS	-	expression tag	UNP P18895
C	21	HIS	-	expression tag	UNP P18895
C	22	SER	-	expression tag	UNP P18895
C	23	SER	-	expression tag	UNP P18895
C	24	GLY	-	expression tag	UNP P18895
C	25	LEU	-	expression tag	UNP P18895
C	26	VAL	-	expression tag	UNP P18895
C	27	PRO	-	expression tag	UNP P18895
C	28	ARG	-	expression tag	UNP P18895
C	29	GLY	-	expression tag	UNP P18895
C	30	SER	-	expression tag	UNP P18895
C	31	HIS	-	expression tag	UNP P18895
C	32	MSE	-	expression tag	UNP P18895

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Chain	Residue	Modelled	Actual	Comment	Reference
D	12	MSE	-	expression tag	UNP P18895
D	13	GLY	-	expression tag	UNP P18895
D	14	SER	-	expression tag	UNP P18895
D	15	SER	-	expression tag	UNP P18895
D	16	HIS	-	expression tag	UNP P18895
D	17	HIS	-	expression tag	UNP P18895
D	18	HIS	-	expression tag	UNP P18895
D	19	HIS	-	expression tag	UNP P18895
D	20	HIS	-	expression tag	UNP P18895
D	21	HIS	-	expression tag	UNP P18895
D	22	SER	-	expression tag	UNP P18895
D	23	SER	-	expression tag	UNP P18895
D	24	GLY	-	expression tag	UNP P18895
D	25	LEU	-	expression tag	UNP P18895
D	26	VAL	-	expression tag	UNP P18895
D	27	PRO	-	expression tag	UNP P18895
D	28	ARG	-	expression tag	UNP P18895
D	29	GLY	-	expression tag	UNP P18895
D	30	SER	-	expression tag	UNP P18895
D	31	HIS	-	expression tag	UNP P18895
D	32	MSE	-	expression tag	UNP P18895

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



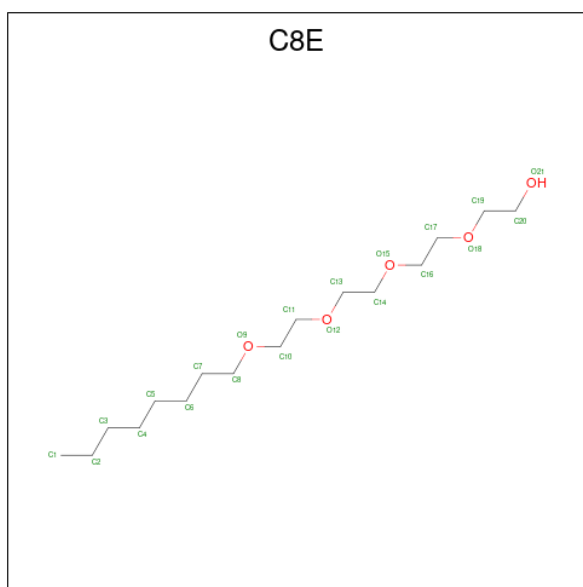
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total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

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

- Molecule 4 is (HYDROXYETHYLOXY)TRI(ETHYLOXY)OCTANE (three-letter code: C8E) (formula: $C_{16}H_{34}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	11	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			11	10	1		
4	A	1	Total	C	O	0	0
			10	9	1		
4	A	1	Total	C	O	0	0
			10	9	1		
4	B	1	Total	C	O	0	0
			9	8	1		
4	B	1	Total	C	O	0	0
			12	10	2		
4	B	1	Total	C	O	0	0
			21	16	5		
4	B	1	Total	C	O	0	0
			9	8	1		
4	B	1	Total	C	O	0	0
			9	8	1		
4	B	1	Total	C	O	0	0
			13	11	2		
4	B	1	Total	C	O	0	0
			10	9	1		
4	B	1	Total	C	O	0	0
			8	6	2		
4	C	1	Total	C	O	0	0
			21	16	5		
4	C	1	Total	C	O	0	0
			12	10	2		
4	C	1	Total	C	O	0	0
			12	10	2		
4	C	1	Total	C	O	0	0
			10	8	2		
4	C	1	Total	C	O	0	0
			9	8	1		
4	C	1	Total	C	O	0	0
			18	14	4		
4	D	1	Total	C	O	0	0
			11	10	1		
4	D	1	Total	C	O	0	0
			21	16	5		
4	D	1	Total	C	O	0	0
			19	15	4		
4	D	1	Total	C	O	0	0
			16	13	3		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	D	1	Total C O 9 8 1	0	0
4	D	1	Total C 8 8	0	0
4	D	1	Total C O 12 10 2	0	0
4	D	1	Total C O 13 11 2	0	0
4	D	1	Total C O 15 12 3	0	0
4	D	1	Total C O 13 11 2	0	0
4	D	1	Total C O 9 8 1	0	0

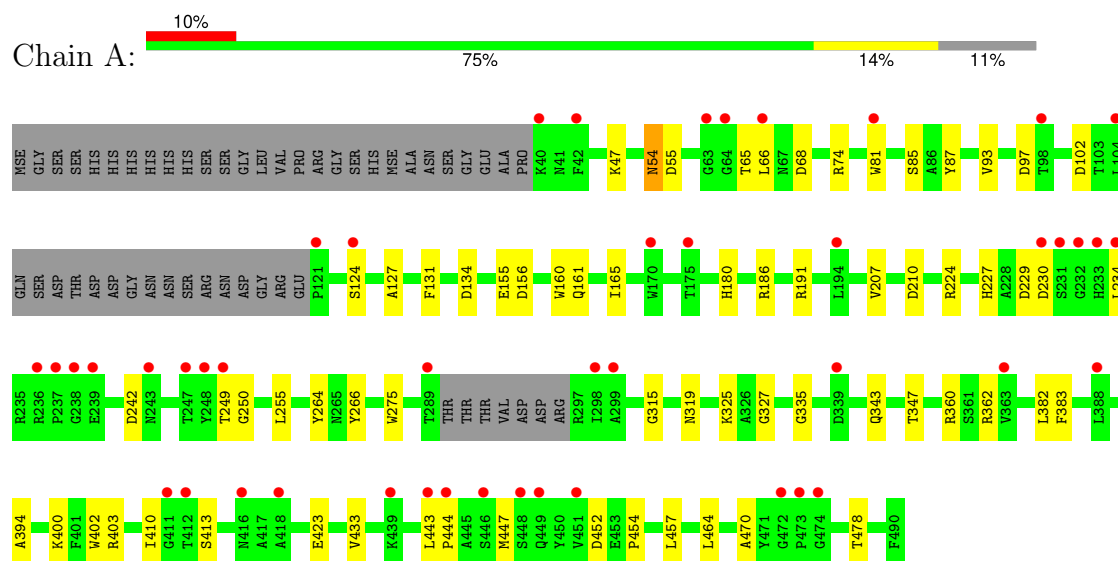
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	166	Total O 166 166	0	0
5	B	155	Total O 155 155	0	0
5	C	142	Total O 142 142	0	0
5	D	149	Total O 149 149	0	0

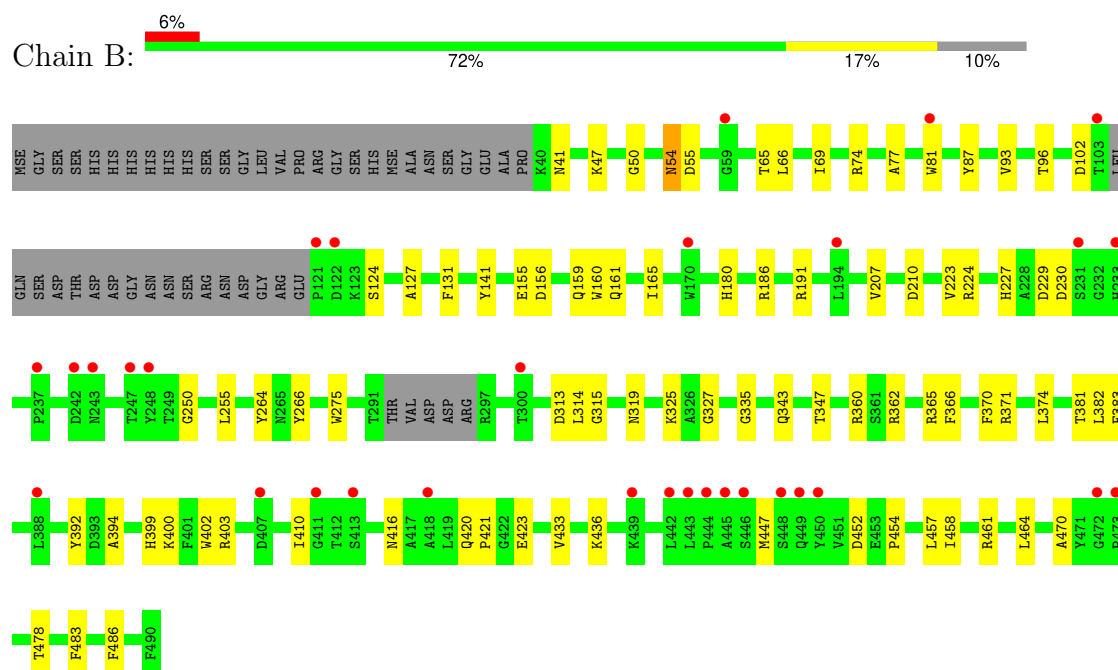
3 Residue-property plots [i](#)

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.

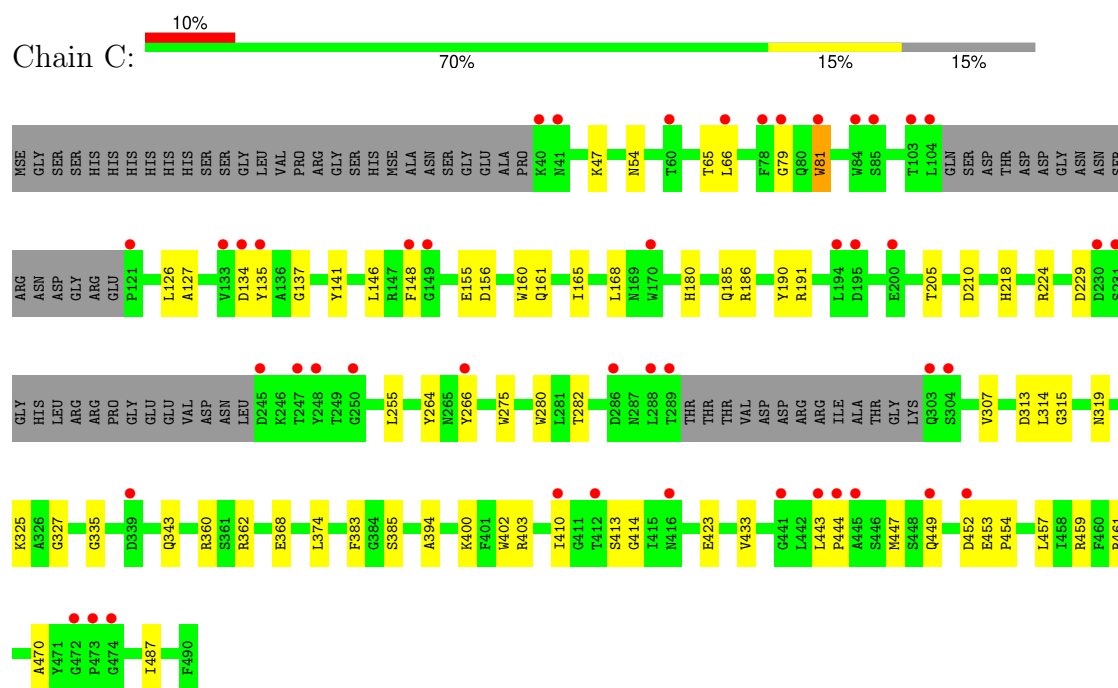
• Molecule 1: Alginate production protein AlgE



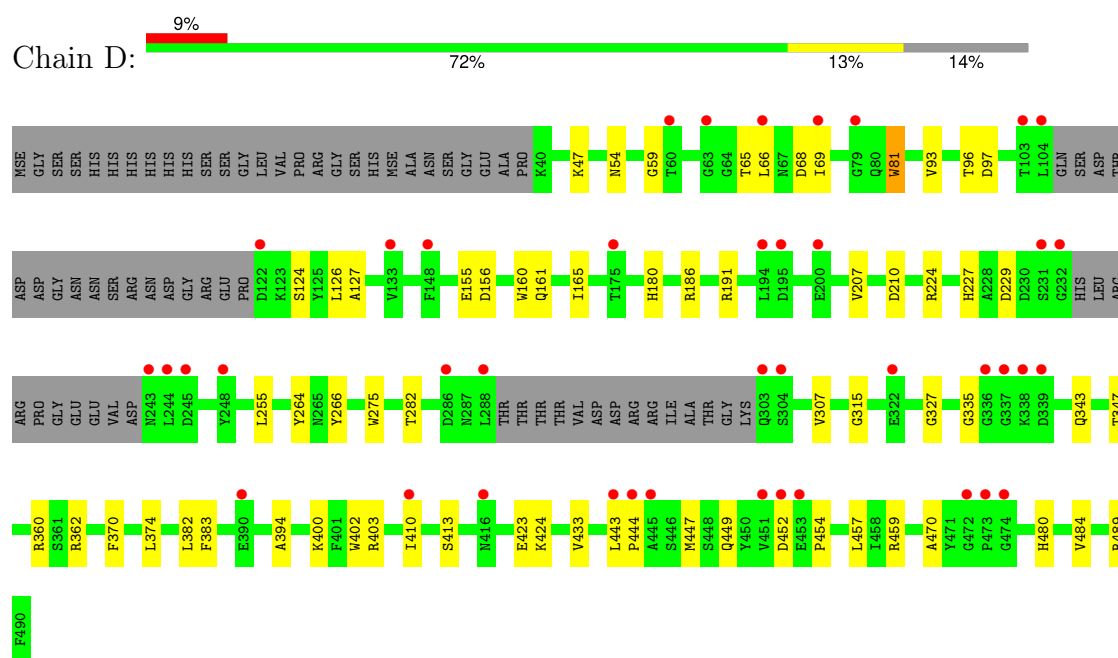
• Molecule 1: Alginate production protein AlgE



• Molecule 1: Alginate production protein AlgE



• Molecule 1: Alginate production protein AlgE



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	162.02Å 90.70Å 160.28Å 90.00° 107.65° 90.00°	Depositor
Resolution (Å)	44.76 – 2.30 44.76 – 2.30	Depositor EDS
% Data completeness (in resolution range)	94.0 (44.76-2.30) 99.6 (44.76-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.49 (at 2.29Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, R_{free}	0.221 , 0.259 0.220 , 0.257	Depositor DCC
R_{free} test set	4891 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	34.7	Xtriage
Anisotropy	0.481	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 67.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for $1/2^*h-3/2^*k,-1/2^*h-1/2^*k,-1/2^*h+1/2^*k-l$ 0.000 for $1/2^*h+3/2^*k,1/2^*h-1/2^*k,-1/2^*h-1/2^*k-l$	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14038	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 25.60 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.0790e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: C8E, CA, EDO

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.41	0/3387	0.55	0/4598
1	B	0.42	0/3410	0.55	0/4633
1	C	0.42	0/3244	0.55	0/4401
1	D	0.42	0/3244	0.56	0/4403
All	All	0.42	0/13285	0.56	0/18035

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3305	0	2965	48	0
1	B	3328	0	2978	69	0
1	C	3165	0	2842	61	0
1	D	3165	0	2842	49	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	24	0	36	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	32	0	48	4	0
3	C	28	0	42	2	0
3	D	12	0	18	2	0
4	A	44	0	74	3	0
4	B	91	0	142	14	0
4	C	82	0	129	7	0
4	D	146	0	244	8	0
5	A	166	0	0	1	0
5	B	155	0	0	11	0
5	C	142	0	0	10	0
5	D	149	0	0	6	0
All	All	14038	0	12360	229	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 9.

The worst 5 of 229 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:370:PHE:HB3	5:B:603:HOH:O	1.53	1.09
1:B:366:PHE:O	5:B:603:HOH:O	1.84	0.95
1:B:381[B]:THR:HG22	1:B:399:HIS:ND1	1.86	0.90
1:D:443:LEU:HD12	1:D:444:PRO:HD2	1.60	0.83
1:D:480:HIS:ND1	4:D:498:C8E:H102	1.97	0.79

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	424/479 (88%)	404 (95%)	19 (4%)	1 (0%)	44 55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	428/479 (89%)	411 (96%)	16 (4%)	1 (0%)	44	55
1	C	402/479 (84%)	387 (96%)	14 (4%)	1 (0%)	44	55
1	D	403/479 (84%)	386 (96%)	16 (4%)	1 (0%)	44	55
All	All	1657/1916 (86%)	1588 (96%)	65 (4%)	4 (0%)	44	55

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	54	ASN
1	B	54	ASN
1	C	54	ASN
1	D	54	ASN

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	316/382 (83%)	311 (98%)	5 (2%)	58	74
1	B	320/382 (84%)	317 (99%)	3 (1%)	75	87
1	C	302/382 (79%)	299 (99%)	3 (1%)	73	85
1	D	301/382 (79%)	297 (99%)	4 (1%)	65	79
All	All	1239/1528 (81%)	1224 (99%)	15 (1%)	67	81

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	382	LEU
1	D	229	ASP
1	C	47	LYS
1	D	382	LEU
1	D	47	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such

sidechains are listed below:

Mol	Chain	Res	Type
1	B	41	ASN
1	B	161	GLN

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 57 ligands modelled in this entry, 4 are monoatomic - leaving 53 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	EDO	B	491	-	3,3,3	0.43	0	2,2,2	0.46	0
3	EDO	C	491	-	3,3,3	0.43	0	2,2,2	0.34	0
4	C8E	B	501	-	9,9,20	0.26	0	8,8,19	0.60	0
4	C8E	C	497	-	8,8,20	0.27	0	7,7,19	0.50	0
4	C8E	B	498	-	8,8,20	0.25	0	7,7,19	0.60	0
4	C8E	B	8	-	20,20,20	0.42	0	19,19,19	0.34	0
3	EDO	A	492	-	3,3,3	0.46	0	2,2,2	0.45	0
4	C8E	C	498	-	17,17,20	0.42	0	16,16,19	0.34	0
4	C8E	D	495	-	8,8,20	0.25	0	7,7,19	0.52	0
3	EDO	C	493	-	3,3,3	0.50	0	2,2,2	0.22	0
4	C8E	A	10	-	10,10,20	0.37	0	9,9,19	0.44	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	C8E	C	7	-	11,11,20	0.30	0	10,10,19	0.65	0
3	EDO	D	7	-	3,3,3	0.53	0	2,2,2	0.62	0
4	C8E	D	493	-	10,10,20	0.38	0	9,9,19	0.43	0
3	EDO	A	493	-	3,3,3	0.45	0	2,2,2	0.38	0
4	C8E	D	501	-	8,8,20	0.23	0	7,7,19	0.64	0
4	C8E	A	11	-	9,9,20	0.31	0	8,8,19	0.44	0
3	EDO	C	11	-	3,3,3	0.48	0	2,2,2	0.43	0
3	EDO	B	6	-	3,3,3	0.53	0	2,2,2	0.27	0
3	EDO	B	4	-	3,3,3	0.43	0	2,2,2	0.53	0
4	C8E	B	497	-	11,11,20	0.37	0	10,10,19	0.39	0
3	EDO	A	8	-	3,3,3	0.46	0	2,2,2	0.42	0
3	EDO	B	493	-	3,3,3	0.50	0	2,2,2	0.36	0
4	C8E	B	500	-	12,12,20	0.35	0	11,11,19	0.37	0
3	EDO	C	1	-	3,3,3	0.50	0	2,2,2	0.44	0
3	EDO	D	491	-	3,3,3	0.46	0	2,2,2	0.44	0
4	C8E	C	494	-	20,20,20	0.47	0	19,19,19	0.38	0
4	C8E	B	502	-	7,7,20	0.46	0	6,6,19	0.40	0
4	C8E	D	9	-	18,18,20	0.43	0	17,17,19	0.38	0
4	C8E	A	494	-	12,12,20	0.34	0	11,11,19	0.41	0
3	EDO	D	492	-	3,3,3	0.51	0	2,2,2	0.26	0
3	EDO	C	492	-	3,3,3	0.43	0	2,2,2	0.46	0
4	C8E	B	496	-	8,8,20	0.41	0	7,7,19	0.36	0
4	C8E	D	499	-	14,14,20	0.39	0	13,13,19	0.42	0
4	C8E	D	498	-	12,12,20	0.36	0	11,11,19	0.34	0
3	EDO	B	495	-	3,3,3	0.41	0	2,2,2	0.44	0
4	C8E	C	496	-	9,9,20	0.38	0	8,8,19	0.33	0
3	EDO	A	3	-	3,3,3	0.56	0	2,2,2	0.26	0
3	EDO	A	491	-	3,3,3	0.43	0	2,2,2	0.44	0
3	EDO	C	10	-	3,3,3	0.46	0	2,2,2	0.36	0
4	C8E	D	5	-	20,20,20	0.44	0	19,19,19	0.36	0
4	C8E	D	496	-	7,7,20	0.30	0	6,6,19	0.43	0
3	EDO	A	2	-	3,3,3	0.39	0	2,2,2	0.40	0
3	EDO	B	492	-	3,3,3	0.48	0	2,2,2	0.27	0
3	EDO	B	9	-	3,3,3	0.47	0	2,2,2	0.38	0
4	C8E	B	499	-	8,8,20	0.23	0	7,7,19	0.68	0
4	C8E	D	500	-	12,12,20	0.33	0	11,11,19	0.40	0
3	EDO	B	494	-	3,3,3	0.59	0	2,2,2	0.04	0
4	C8E	D	494	-	15,15,20	0.41	0	14,14,19	0.42	0
3	EDO	C	5	-	3,3,3	0.50	0	2,2,2	0.10	0
4	C8E	C	495	-	11,11,20	0.38	0	10,10,19	0.30	0
4	C8E	A	495	-	9,9,20	0.29	0	8,8,19	0.55	0
4	C8E	D	497	-	11,11,20	0.37	0	10,10,19	0.35	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	B	491	-	-	0/1/1/1	-
3	EDO	C	491	-	-	0/1/1/1	-
4	C8E	B	501	-	-	7/7/7/18	-
4	C8E	C	497	-	-	4/6/6/18	-
4	C8E	B	498	-	-	2/6/6/18	-
4	C8E	B	8	-	-	12/18/18/18	-
3	EDO	A	492	-	-	0/1/1/1	-
4	C8E	C	498	-	-	9/15/15/18	-
4	C8E	D	495	-	-	4/6/6/18	-
3	EDO	C	493	-	-	1/1/1/1	-
4	C8E	A	10	-	-	5/8/8/18	-
4	C8E	C	7	-	-	4/9/9/18	-
3	EDO	D	7	-	-	0/1/1/1	-
4	C8E	D	493	-	-	5/8/8/18	-
3	EDO	A	493	-	-	0/1/1/1	-
4	C8E	D	501	-	-	2/6/6/18	-
4	C8E	A	11	-	-	4/7/7/18	-
3	EDO	C	11	-	-	0/1/1/1	-
3	EDO	B	6	-	-	0/1/1/1	-
3	EDO	B	4	-	-	1/1/1/1	-
4	C8E	B	497	-	-	6/9/9/18	-
3	EDO	A	8	-	-	1/1/1/1	-
3	EDO	B	493	-	-	0/1/1/1	-
4	C8E	B	500	-	-	7/10/10/18	-
3	EDO	C	1	-	-	0/1/1/1	-
3	EDO	D	491	-	-	1/1/1/1	-
4	C8E	C	494	-	-	12/18/18/18	-
4	C8E	B	502	-	-	2/5/5/18	-
4	C8E	D	9	-	-	9/16/16/18	-
4	C8E	A	494	-	-	7/10/10/18	-
3	EDO	D	492	-	-	0/1/1/1	-
3	EDO	C	492	-	-	0/1/1/1	-
4	C8E	B	496	-	-	2/6/6/18	-
4	C8E	D	499	-	-	7/12/12/18	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	C8E	D	498	-	-	7/10/10/18	-
3	EDO	B	495	-	-	1/1/1/1	-
4	C8E	C	496	-	-	4/7/7/18	-
3	EDO	A	3	-	-	0/1/1/1	-
3	EDO	A	491	-	-	0/1/1/1	-
3	EDO	C	10	-	-	0/1/1/1	-
4	C8E	D	5	-	-	6/18/18/18	-
4	C8E	D	496	-	-	2/5/5/18	-
3	EDO	A	2	-	-	0/1/1/1	-
3	EDO	B	492	-	-	0/1/1/1	-
3	EDO	B	9	-	-	0/1/1/1	-
4	C8E	B	499	-	-	2/6/6/18	-
4	C8E	D	500	-	-	6/10/10/18	-
3	EDO	B	494	-	-	0/1/1/1	-
4	C8E	D	494	-	-	10/13/13/18	-
3	EDO	C	5	-	-	0/1/1/1	-
4	C8E	C	495	-	-	5/9/9/18	-
4	C8E	A	495	-	-	5/7/7/18	-
4	C8E	D	497	-	-	2/9/9/18	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 164 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	7	C8E	C7-C8-O9-C10
4	B	8	C8E	O12-C13-C14-O15
4	C	494	C8E	O9-C10-C11-O12
4	B	8	C8E	C17-C16-O15-C14
4	C	494	C8E	O12-C13-C14-O15

There are no ring outliers.

23 monomers are involved in 40 short contacts:

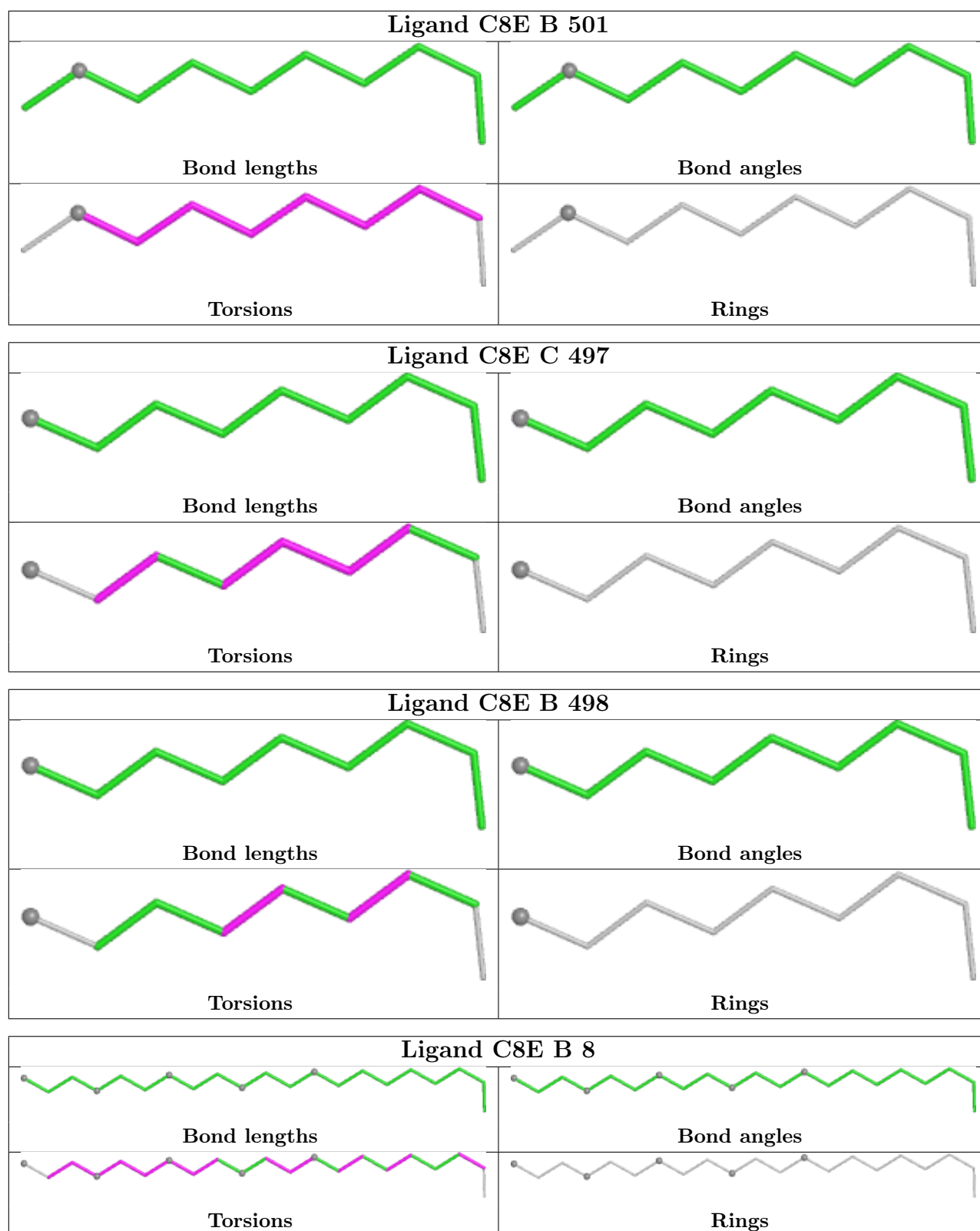
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	501	C8E	1	0
4	C	497	C8E	1	0

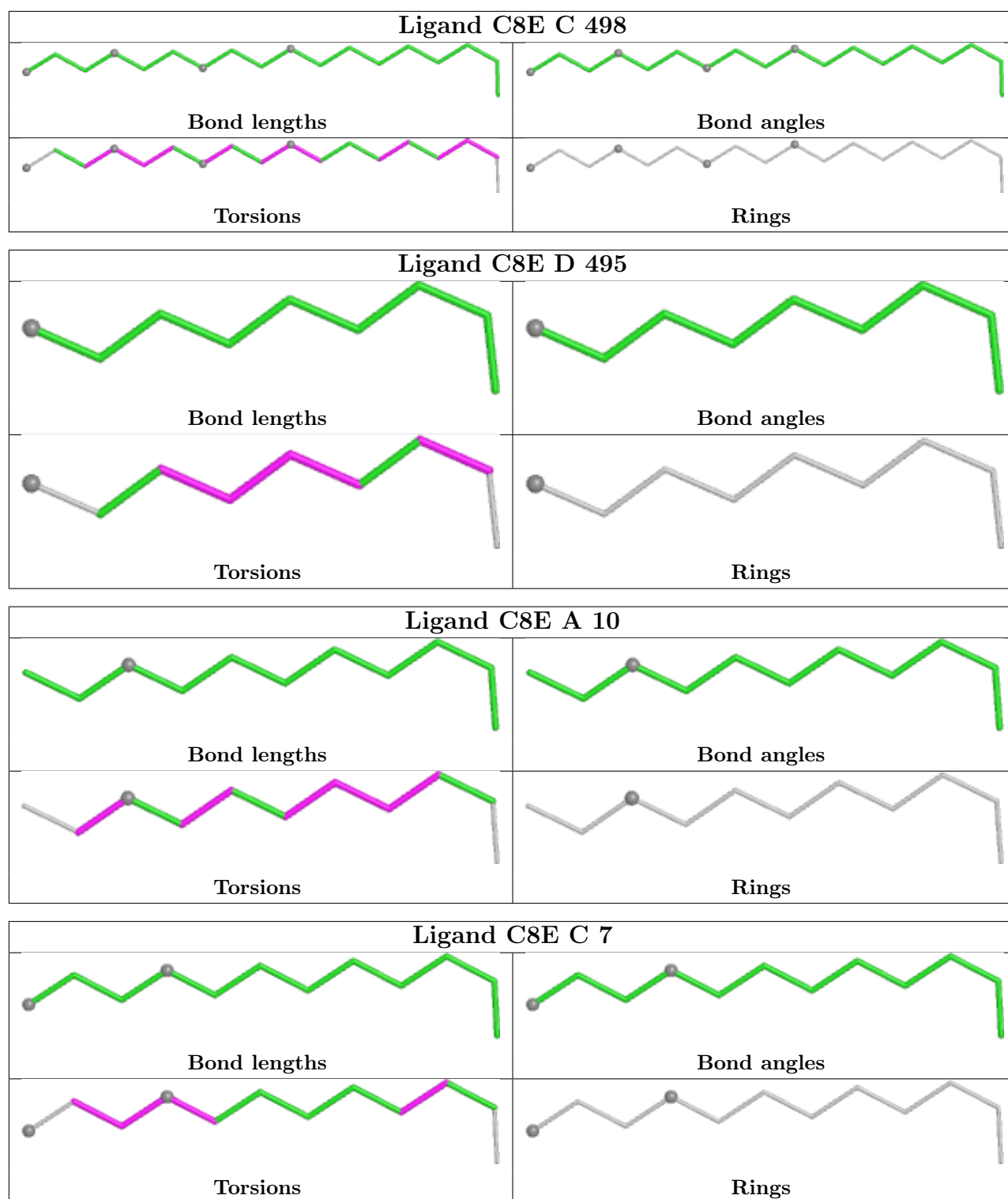
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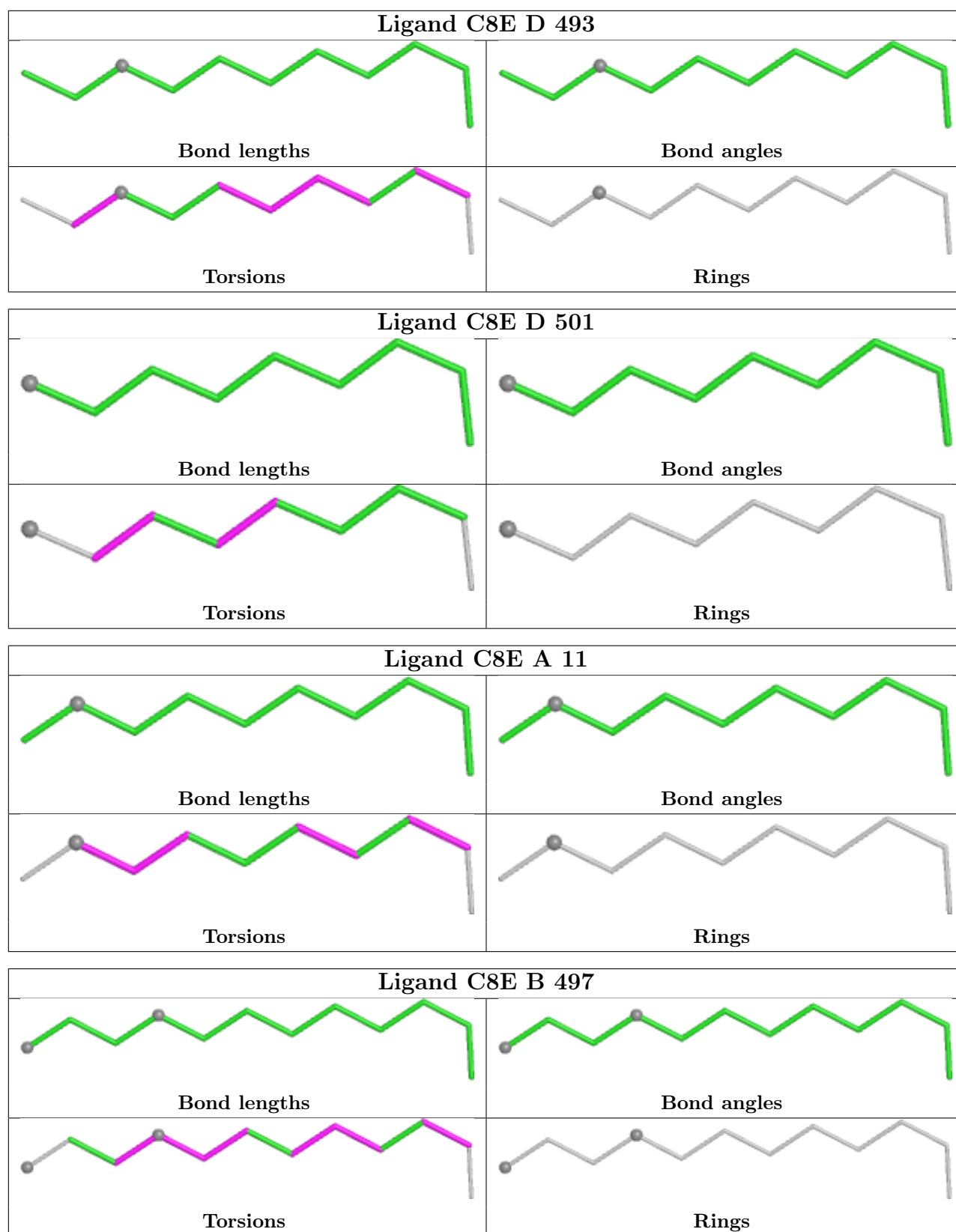
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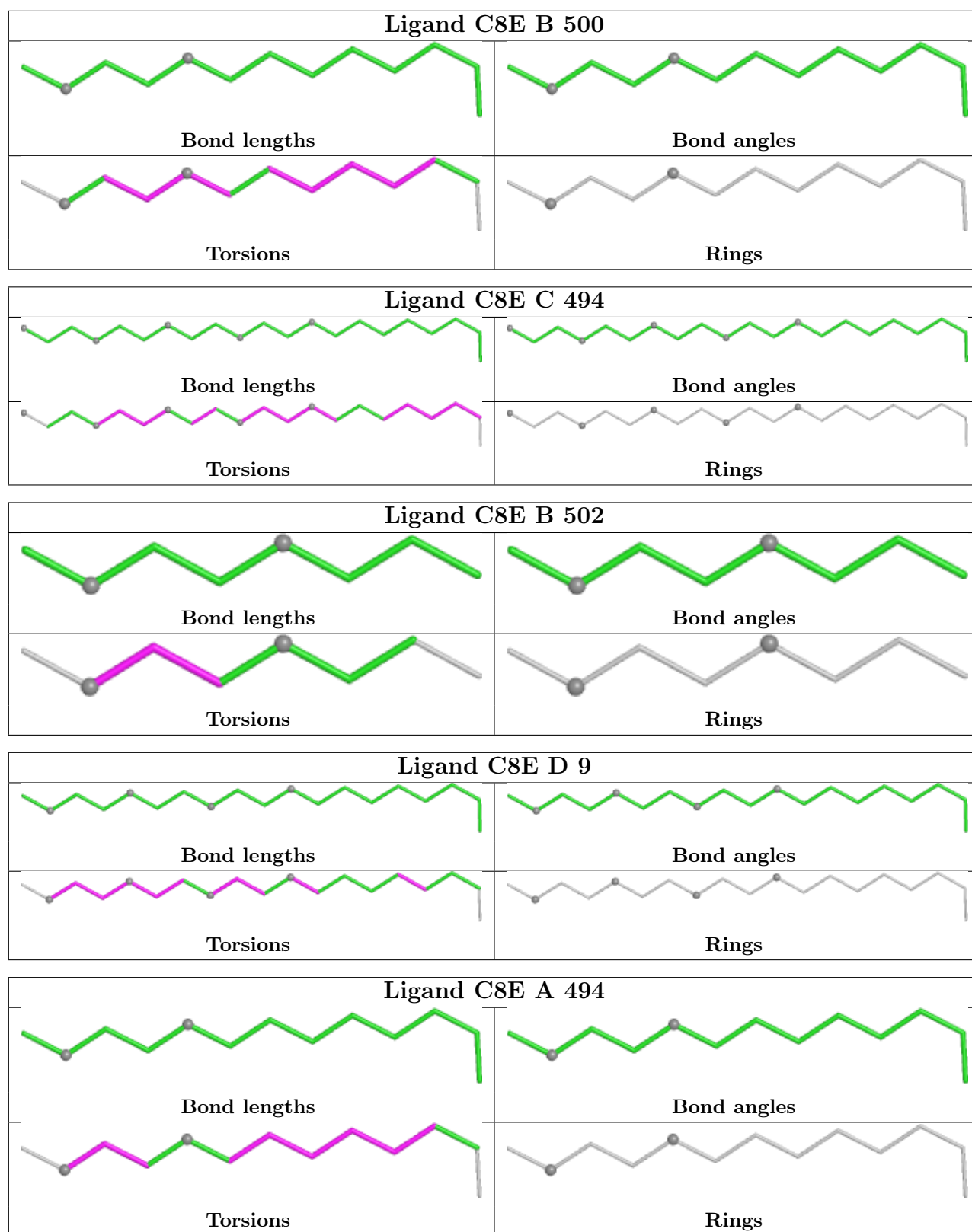
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	8	C8E	8	0
4	C	498	C8E	3	0
4	D	495	C8E	1	0
3	C	493	EDO	1	0
4	C	7	C8E	2	0
3	D	7	EDO	1	0
3	C	11	EDO	1	0
3	B	6	EDO	1	0
3	B	4	EDO	1	0
4	B	497	C8E	2	0
4	B	500	C8E	3	0
4	D	9	C8E	2	0
4	A	494	C8E	2	0
3	D	492	EDO	1	0
4	D	498	C8E	1	0
3	B	495	EDO	2	0
4	C	496	C8E	1	0
3	A	3	EDO	1	0
4	D	5	C8E	3	0
4	D	494	C8E	1	0
4	A	495	C8E	1	0

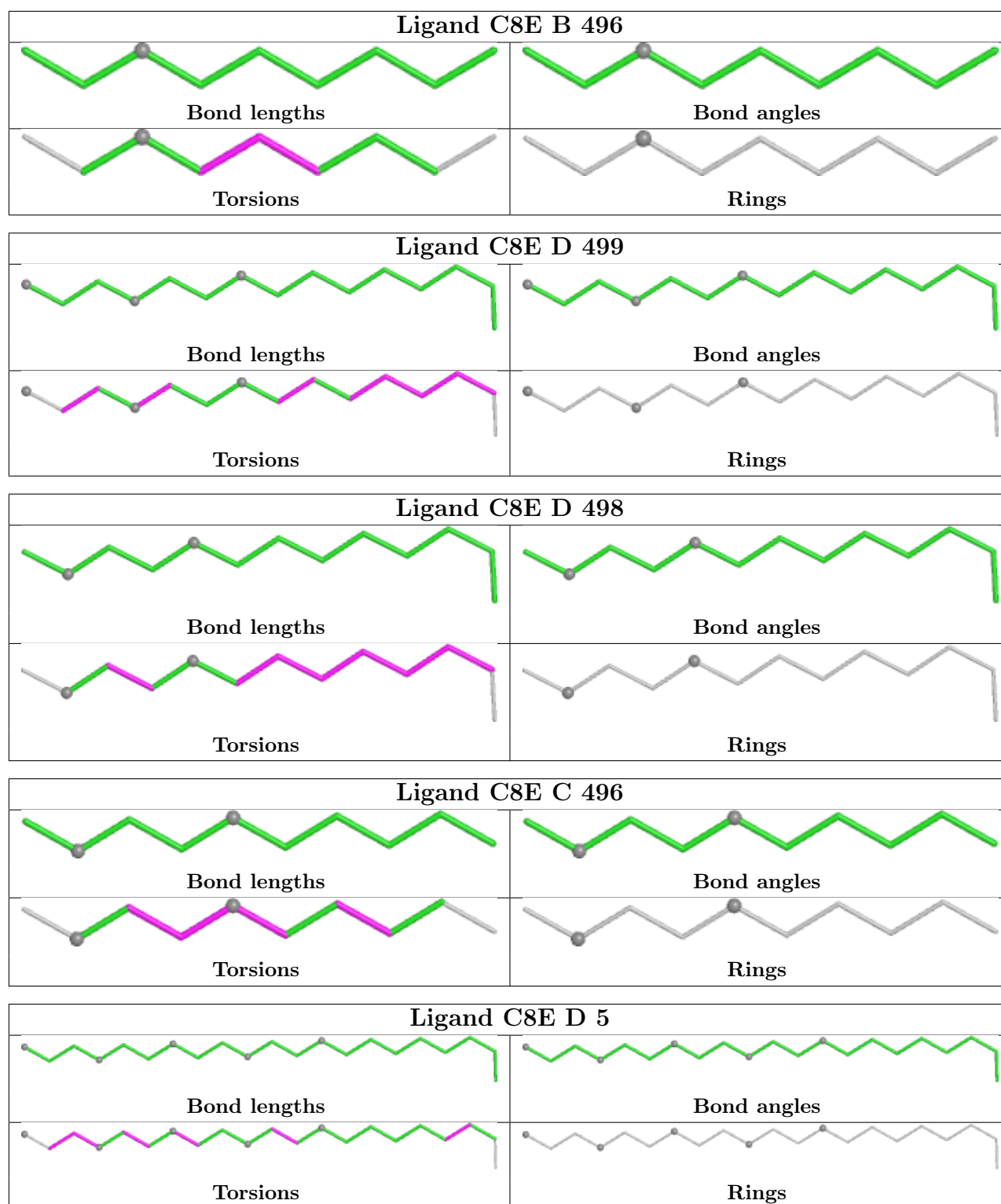
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

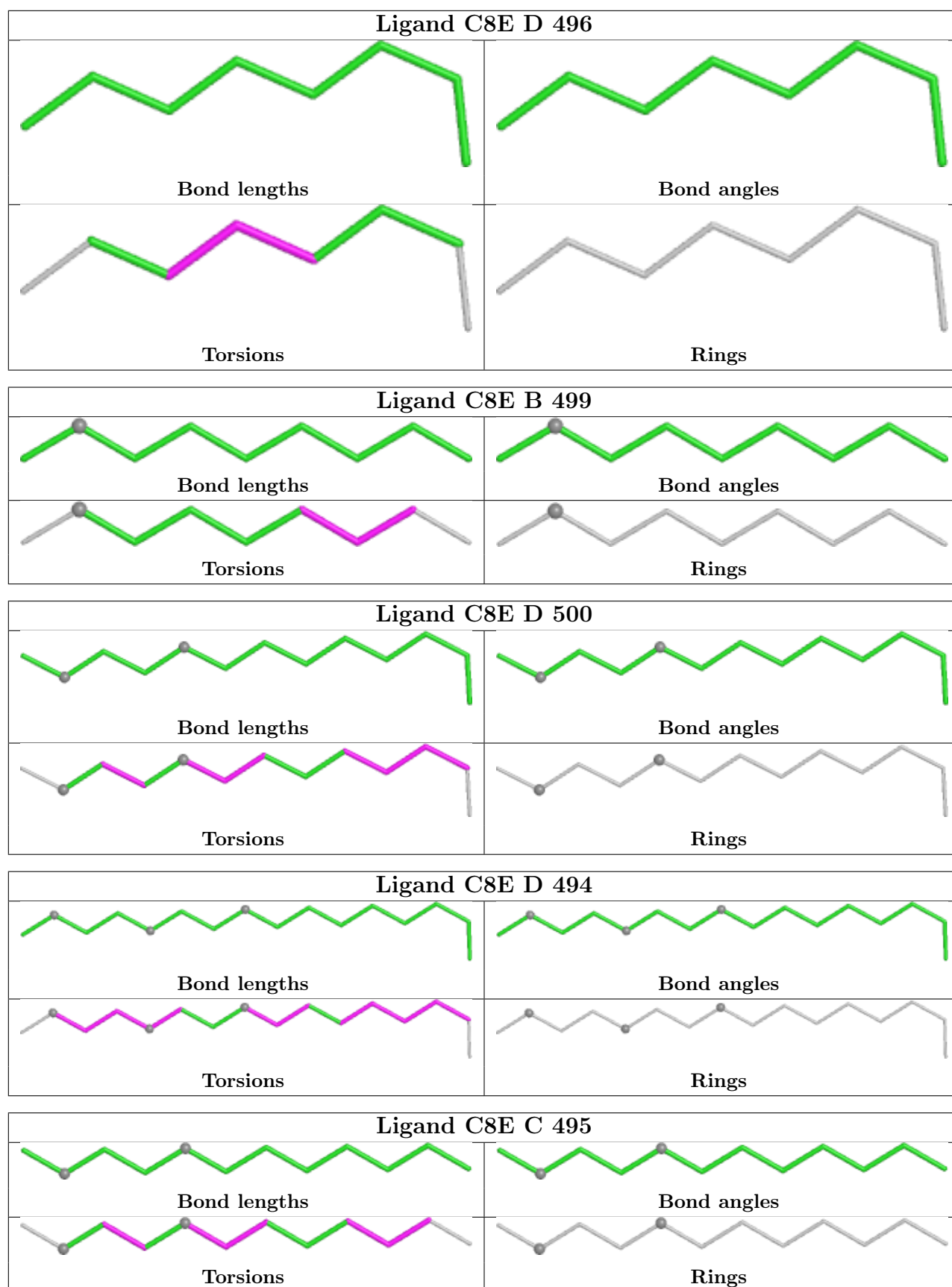


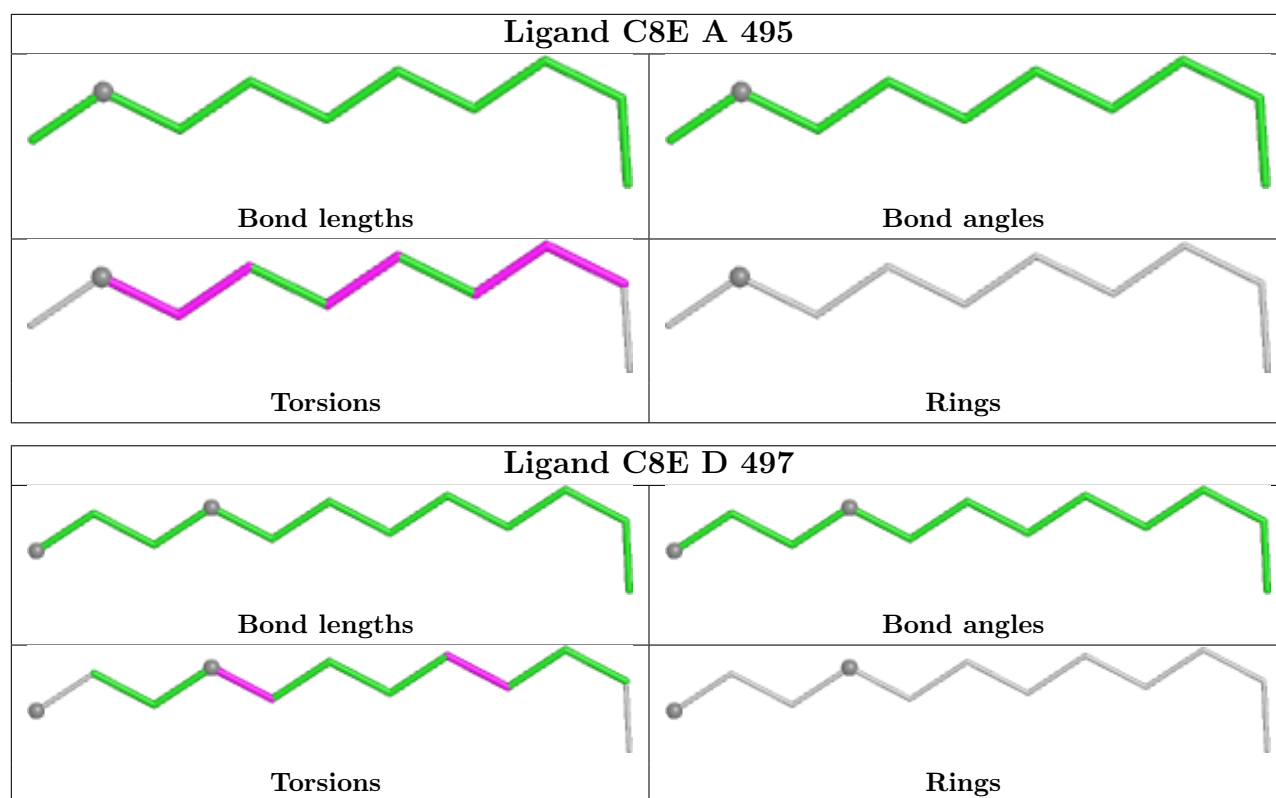












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	424/479 (88%)	0.62	46 (10%) 12 13	10, 36, 78, 105	2 (0%)
1	B	425/479 (88%)	0.55	31 (7%) 22 24	9, 36, 72, 102	5 (1%)
1	C	405/479 (84%)	0.65	46 (11%) 11 12	18, 38, 73, 102	1 (0%)
1	D	406/479 (84%)	0.59	41 (10%) 14 15	16, 36, 68, 100	1 (0%)
All	All	1660/1916 (86%)	0.61	164 (9%) 14 16	9, 36, 74, 105	9 (0%)

The worst 5 of 164 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	238	GLY	5.3
1	C	79	GLY	5.1
1	C	231	SER	4.9
1	C	245	ASP	4.9
1	D	288	LEU	4.6

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 monosaccharides 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(\AA^2)	Q<0.9
3	EDO	B	9	4/4	0.60	0.23	56,60,71,75	0
4	C8E	C	498	18/21	0.75	0.23	23,76,95,101	0
4	C8E	D	497	12/21	0.76	0.19	32,53,71,74	0
3	EDO	C	493	4/4	0.79	0.21	55,55,60,73	0
4	C8E	B	496	9/21	0.79	0.20	41,53,61,68	0
4	C8E	D	499	15/21	0.79	0.19	27,51,71,74	0
4	C8E	D	498	13/21	0.80	0.17	27,45,59,62	0
3	EDO	C	10	4/4	0.80	0.17	58,63,71,83	0
4	C8E	C	494	21/21	0.81	0.20	23,46,71,83	0
3	EDO	B	491	4/4	0.82	0.13	39,49,53,58	0
4	C8E	A	494	13/21	0.82	0.19	33,46,73,76	0
4	C8E	D	494	16/21	0.83	0.18	32,44,77,79	0
4	C8E	B	501	10/21	0.83	0.17	34,42,52,59	0
3	EDO	A	8	4/4	0.83	0.14	49,52,61,63	0
3	EDO	A	491	4/4	0.83	0.15	33,53,57,61	0
3	EDO	D	492	4/4	0.84	0.16	49,56,60,65	0
4	C8E	B	502	8/21	0.84	0.17	29,47,59,65	0
4	C8E	D	496	8/21	0.84	0.15	25,41,46,49	0
4	C8E	B	8	21/21	0.84	0.15	21,41,57,63	0
4	C8E	C	495	12/21	0.84	0.15	20,41,53,60	0
4	C8E	C	496	10/21	0.84	0.16	21,43,83,84	0
4	C8E	D	493	11/21	0.85	0.15	15,39,52,58	0
4	C8E	B	497	12/21	0.85	0.15	27,45,71,72	0
4	C8E	D	500	13/21	0.85	0.15	20,38,65,65	0
4	C8E	C	497	9/21	0.86	0.13	36,44,59,62	0
4	C8E	B	500	13/21	0.86	0.15	24,35,75,77	0
4	C8E	A	495	10/21	0.86	0.14	25,29,50,63	0
4	C8E	D	5	21/21	0.86	0.15	33,51,70,75	0
3	EDO	A	492	4/4	0.86	0.17	41,48,52,55	0
4	C8E	D	495	9/21	0.87	0.12	29,48,58,59	0
3	EDO	B	492	4/4	0.87	0.13	44,44,54,55	0
3	EDO	A	493	4/4	0.87	0.16	54,58,58,62	0
4	C8E	A	10	11/21	0.88	0.14	25,35,52,59	0
3	EDO	C	491	4/4	0.88	0.15	46,55,57,63	0
4	C8E	B	499	9/21	0.89	0.14	29,35,54,59	0
3	EDO	B	493	4/4	0.89	0.16	54,62,71,71	0
3	EDO	B	6	4/4	0.90	0.12	29,34,39,51	0
3	EDO	C	492	4/4	0.90	0.15	39,42,51,56	0
4	C8E	D	9	19/21	0.90	0.13	17,35,53,55	0
3	EDO	C	11	4/4	0.90	0.12	35,46,53,62	0
4	C8E	C	7	12/21	0.90	0.12	25,40,60,66	0
3	EDO	B	494	4/4	0.91	0.13	34,35,37,39	0
2	CA	C	3	1/1	0.92	0.12	71,71,71,71	0

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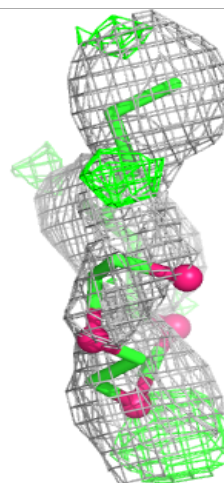
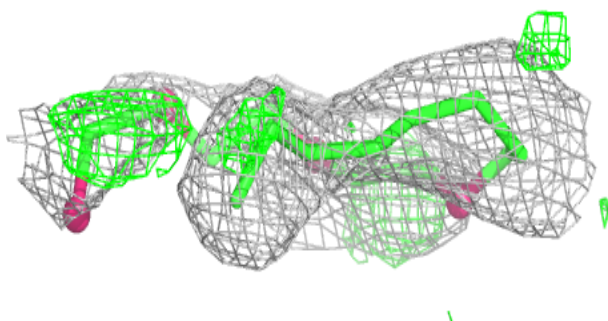
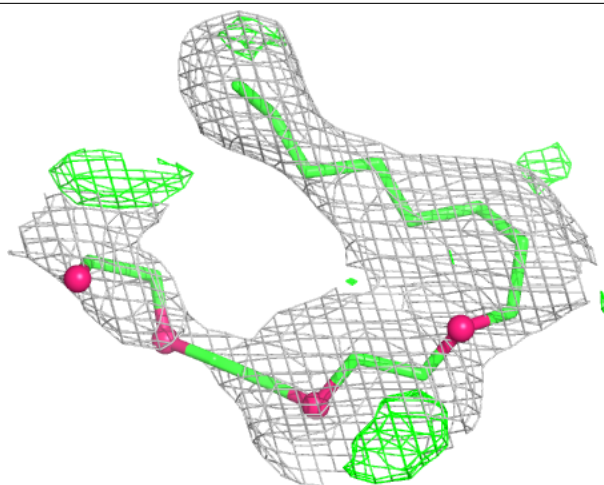
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	C8E	A	11	10/21	0.92	0.10	28,36,46,61	0
4	C8E	D	501	9/21	0.92	0.13	26,34,46,47	0
4	C8E	B	498	9/21	0.93	0.11	27,33,42,45	0
3	EDO	C	5	4/4	0.94	0.09	24,25,27,37	0
3	EDO	A	3	4/4	0.94	0.11	20,28,33,41	0
3	EDO	D	491	4/4	0.94	0.11	39,53,53,62	0
3	EDO	D	7	4/4	0.95	0.07	16,19,21,26	0
2	CA	A	4	1/1	0.95	0.14	65,65,65,65	0
3	EDO	B	495	4/4	0.95	0.12	39,48,52,55	0
3	EDO	C	1	4/4	0.95	0.08	14,18,25,36	0
3	EDO	A	2	4/4	0.96	0.10	17,30,34,40	0
2	CA	D	1	1/1	0.97	0.10	58,58,58,58	0
3	EDO	B	4	4/4	0.97	0.06	18,23,28,40	0
2	CA	B	2	1/1	0.97	0.11	61,61,61,61	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.

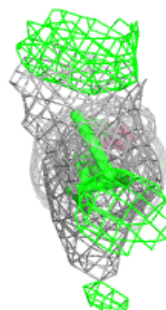
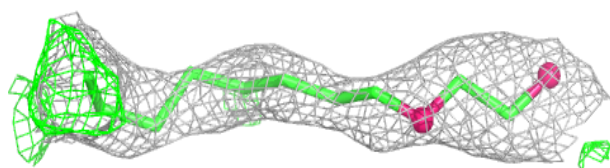
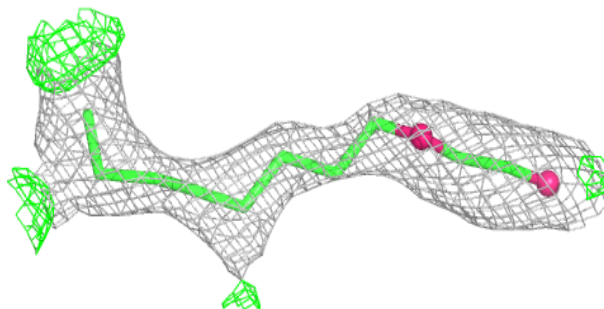
Electron density around C8E C 498:

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

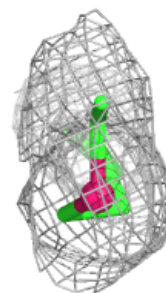
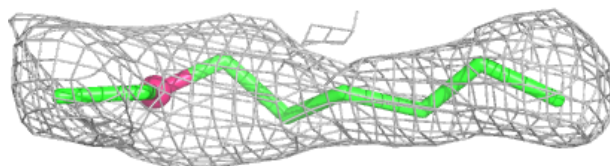
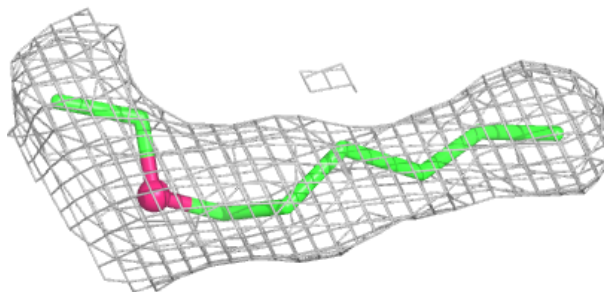


Electron density around C8E D 497:

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

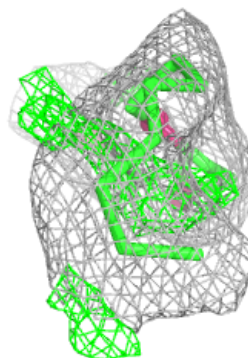
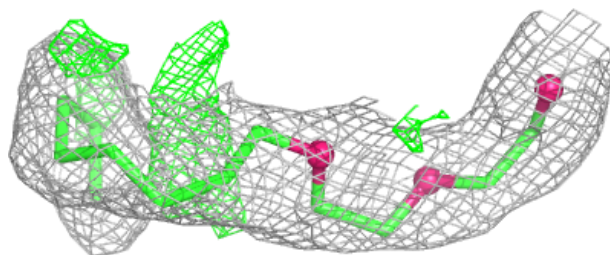
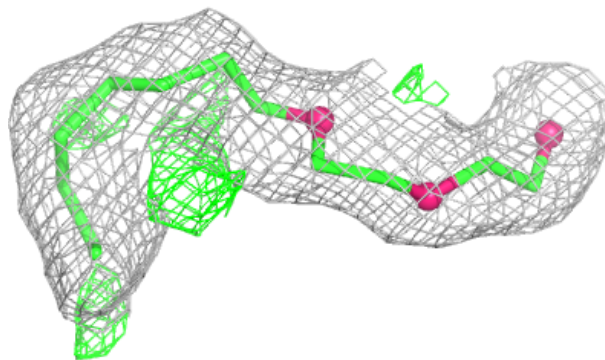
**Electron density around C8E B 496:**

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

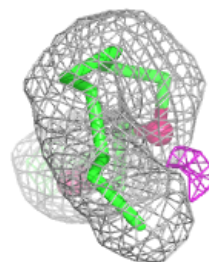
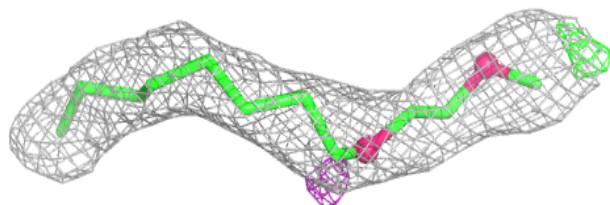
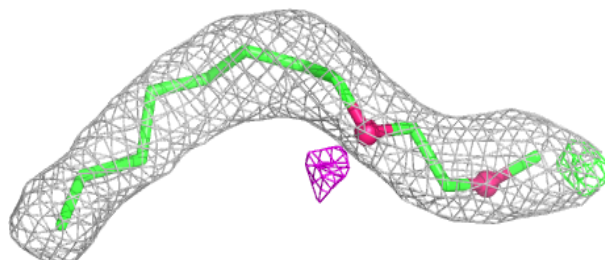


Electron density around C8E D 499:

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

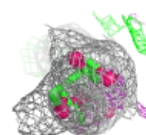
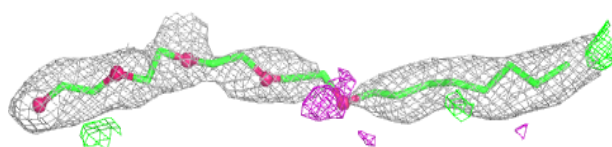
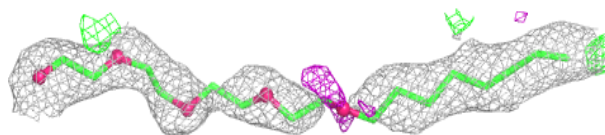
**Electron density around C8E D 498:**

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

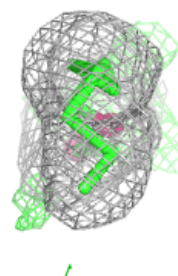
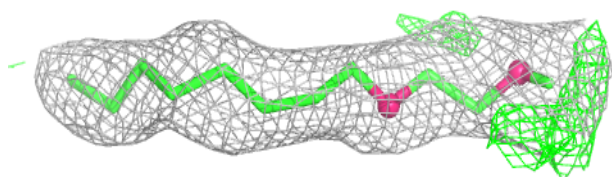
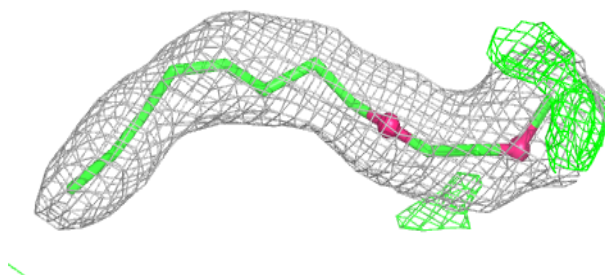


Electron density around C8E C 494:

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

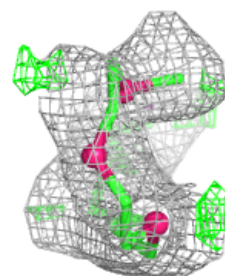
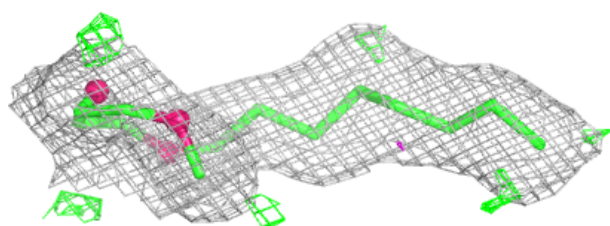
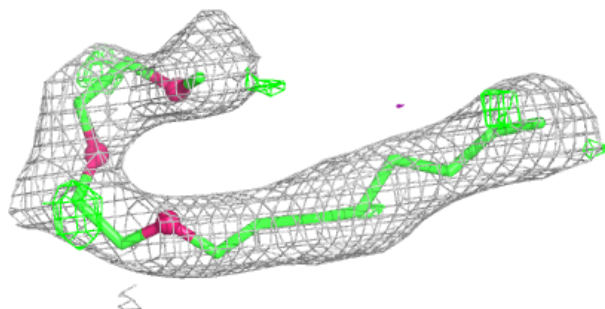
**Electron density around C8E A 494:**

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

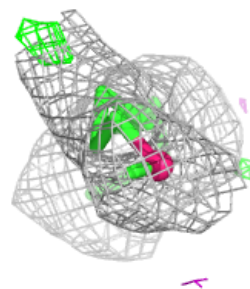
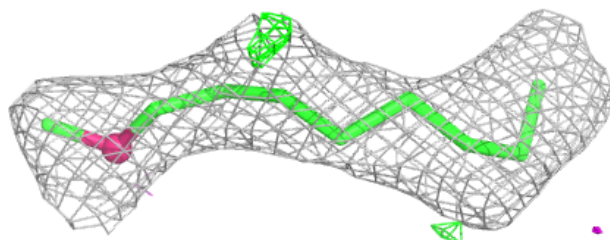
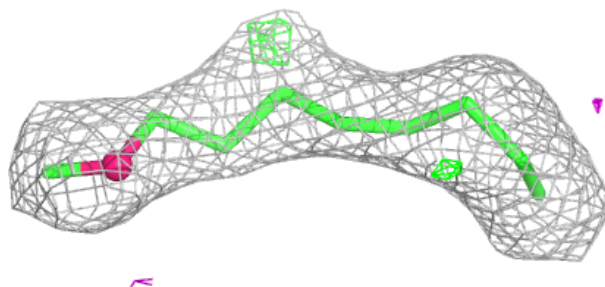


Electron density around C8E D 494:

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

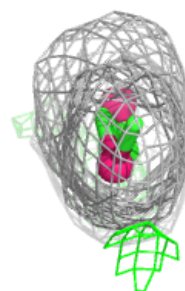
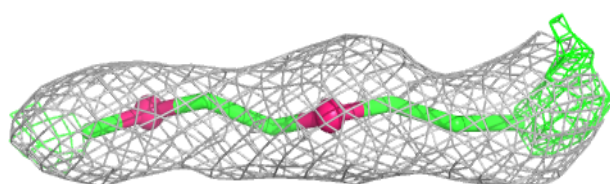
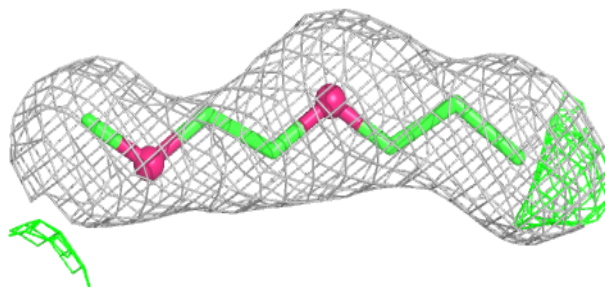
**Electron density around C8E B 501:**

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

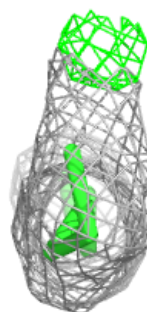
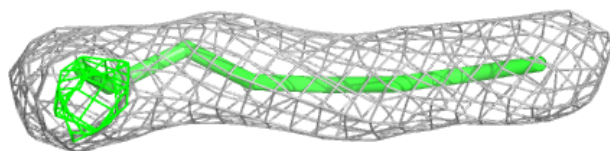
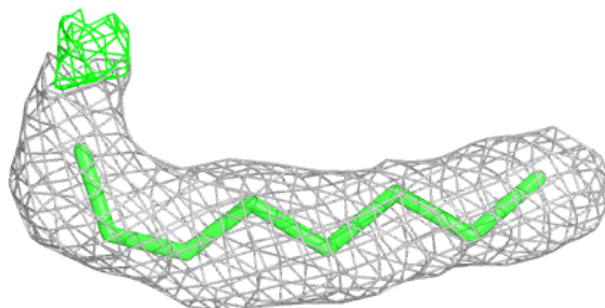


Electron density around C8E B 502:

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

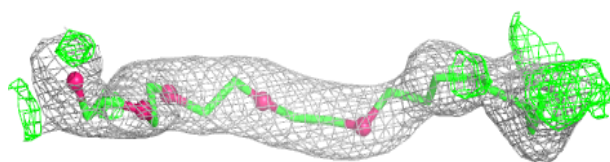
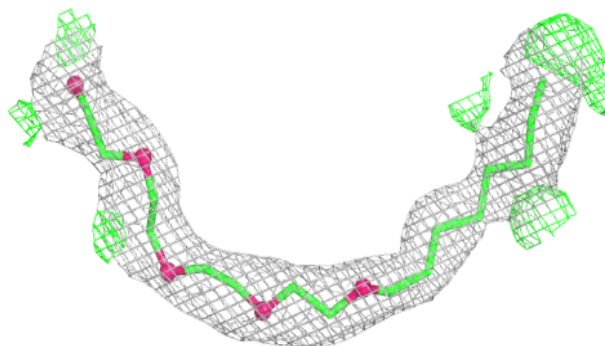
**Electron density around C8E D 496:**

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

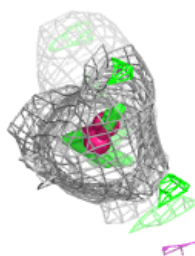
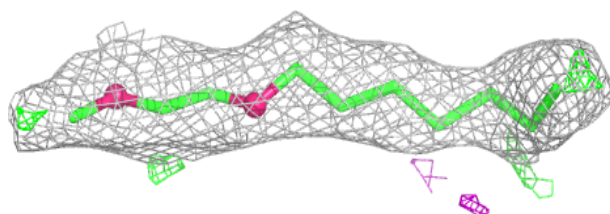
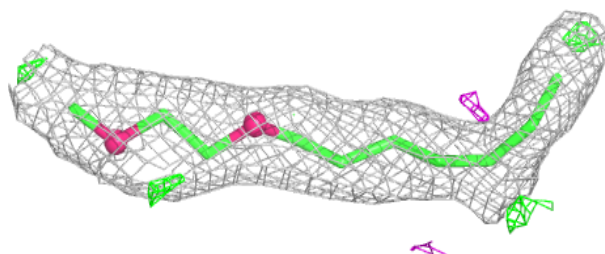


Electron density around C8E B 8:

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

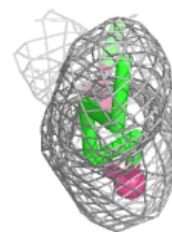
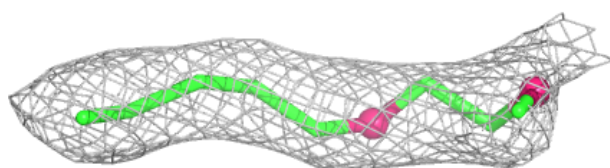
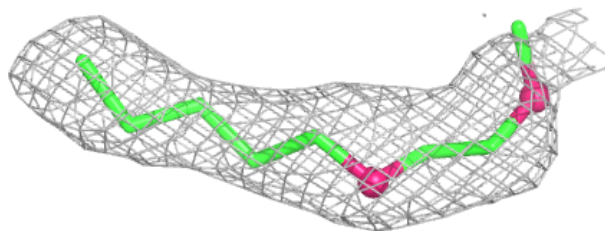
**Electron density around C8E C 495:**

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

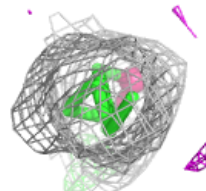
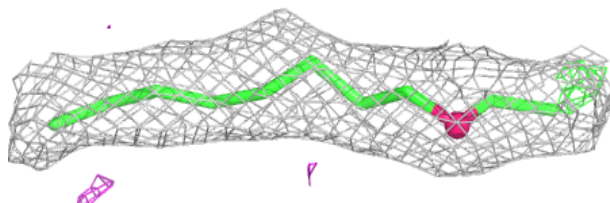
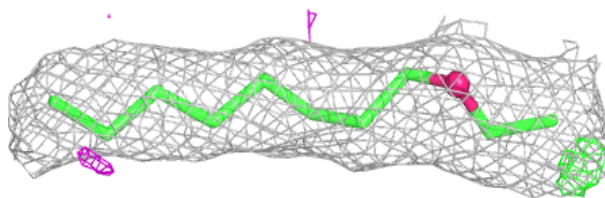


Electron density around C8E C 496:

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

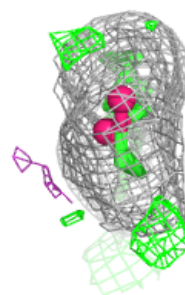
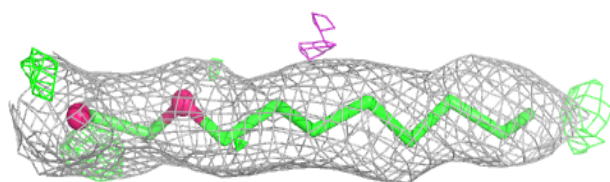
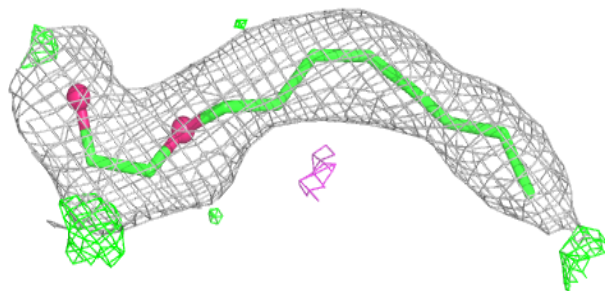
**Electron density around C8E D 493:**

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

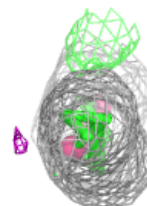
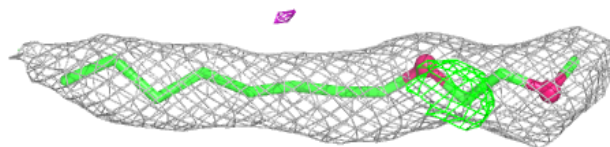
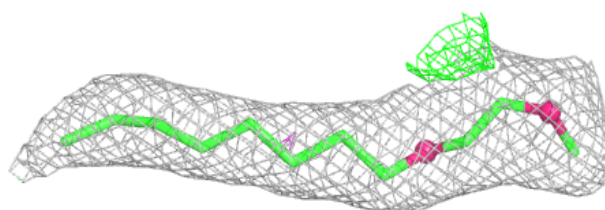


Electron density around C8E B 497:

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

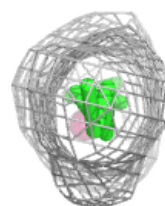
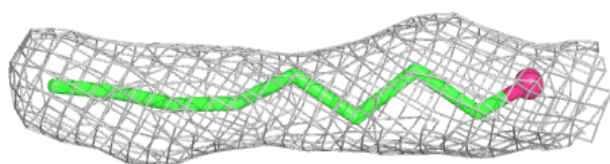
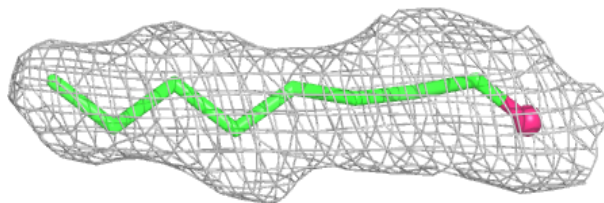
**Electron density around C8E D 500:**

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

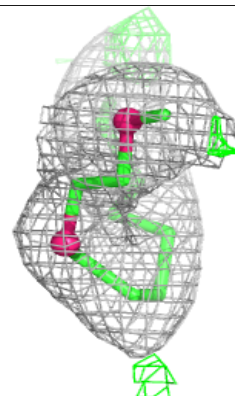
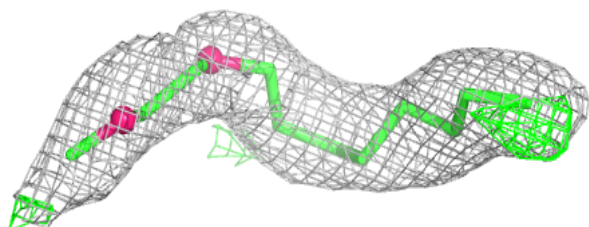
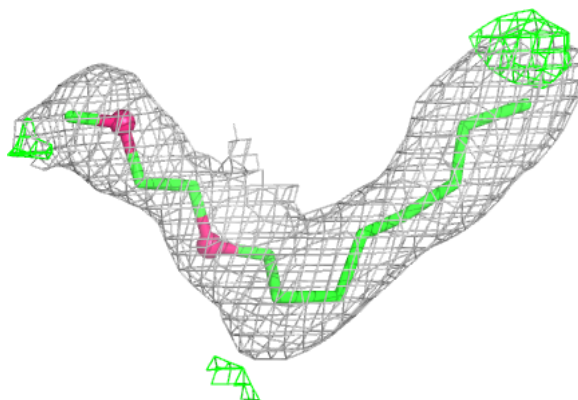


Electron density around C8E C 497:

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

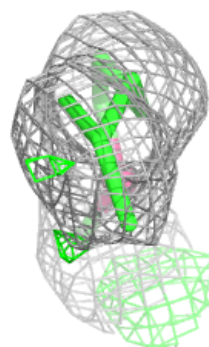
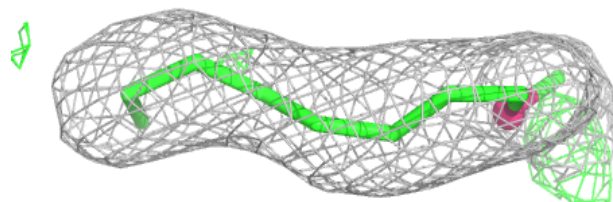
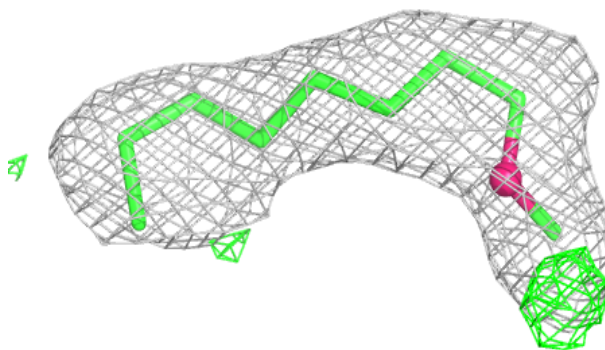
**Electron density around C8E B 500:**

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

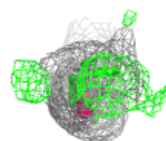
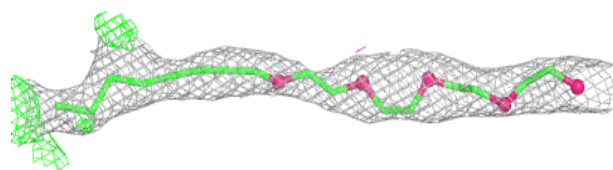
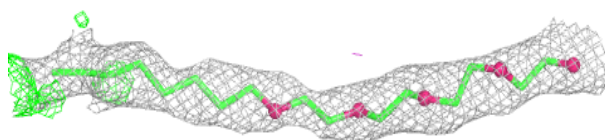


Electron density around C8E A 495:

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

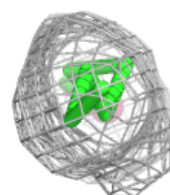
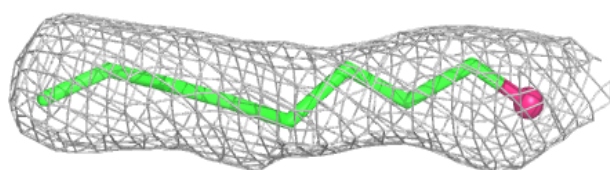
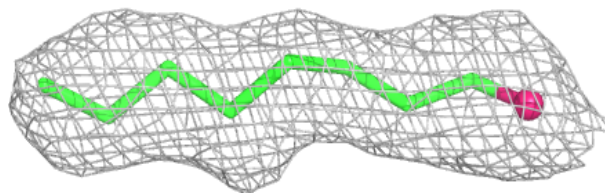
**Electron density around C8E D 5:**

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

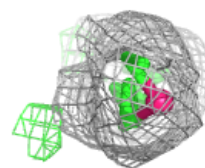
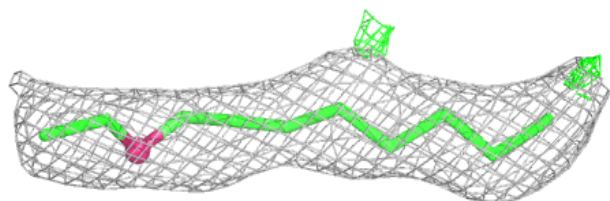
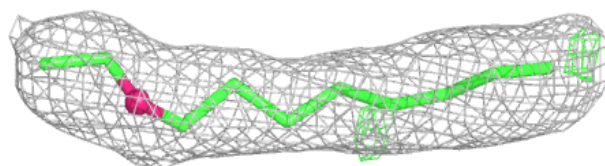


Electron density around C8E D 495:

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

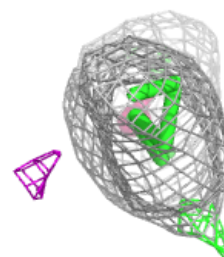
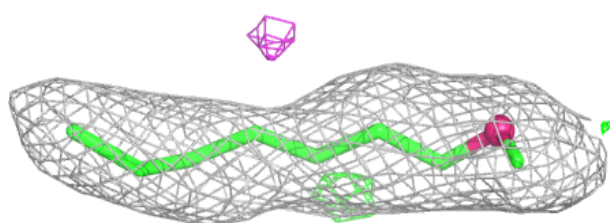
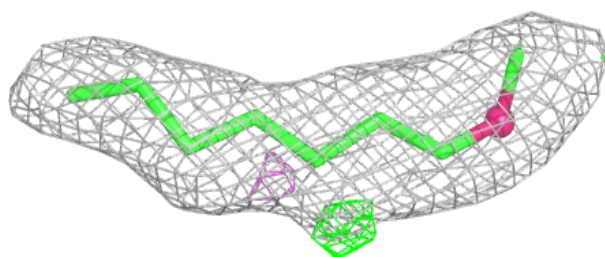
**Electron density around C8E A 10:**

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

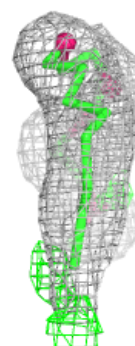
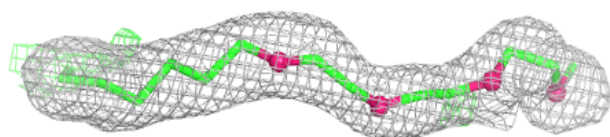
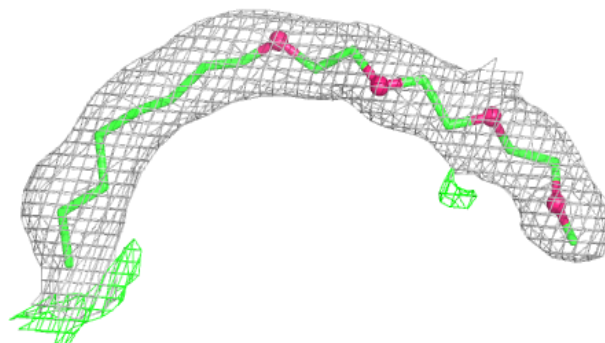


Electron density around C8E B 499:

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

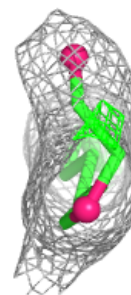
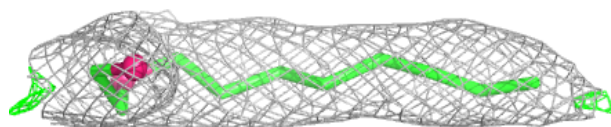
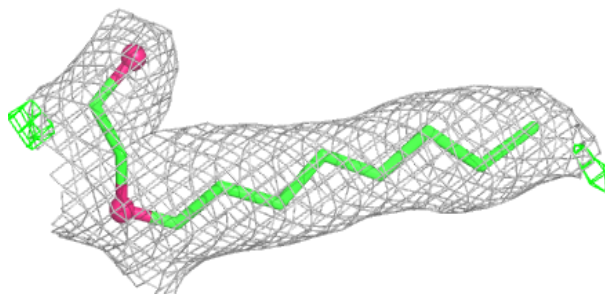
**Electron density around C8E D 9:**

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

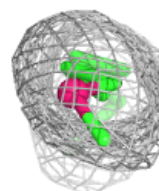
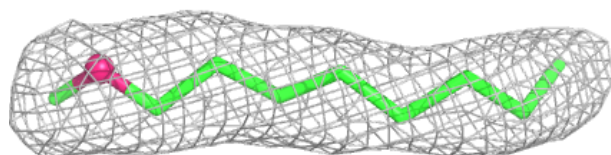
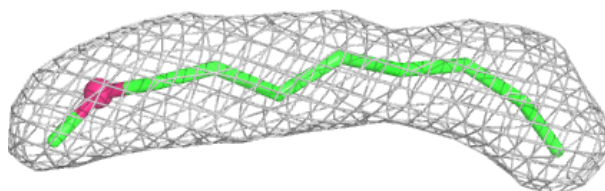


Electron density around C8E C 7:

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

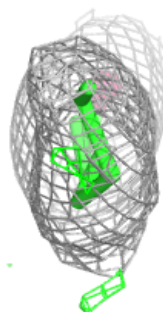
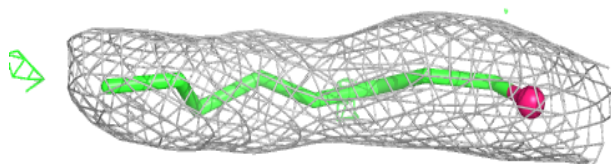
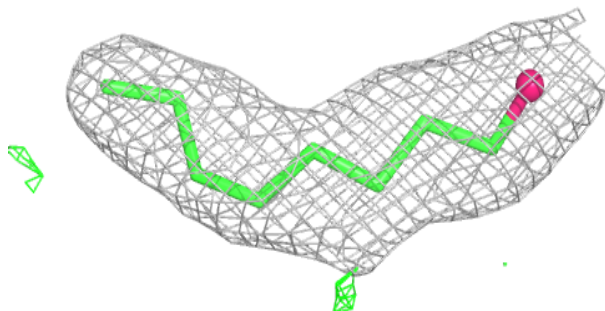
**Electron density around C8E A 11:**

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

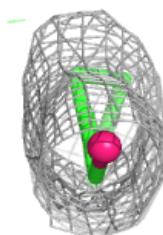
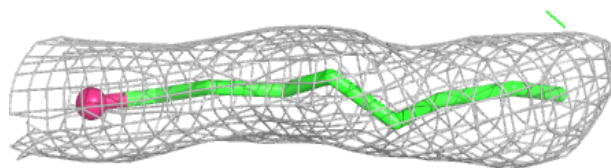
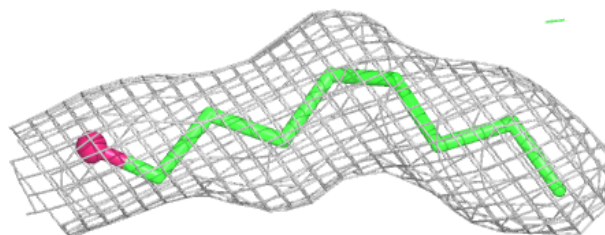


Electron density around C8E D 501:

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

**Electron density around C8E B 498:**

$2mF_o-DF_c$ (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.