



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 05:47 AM UTC

PDB ID : 5DL8 / pdb_00005dl8
Title : Crystal structure of Acinetobacter baumannii OccAB4
Authors : Zahn, M.; Basle, A.; van den Berg, B.
Deposited on : 2015-09-04
Resolution : 2.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

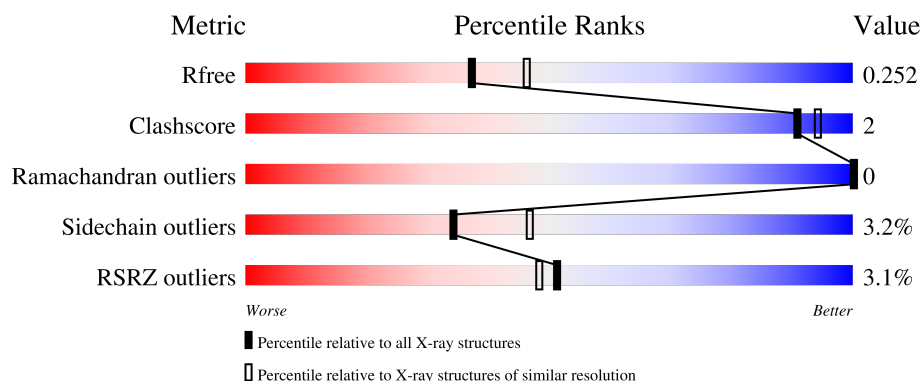
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	407	3% 74% 20% • •
1	B	407	3% 77% 17% • •

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6838 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 Benzoate transport porin BenP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	391	Total	C	N	O	S	0	4	0
			3217	2075	519	619	4			
1	A	391	Total	C	N	O	S	0	1	0
			3191	2056	515	617	3			

There are 30 discrepancies between the modelled and reference sequences:

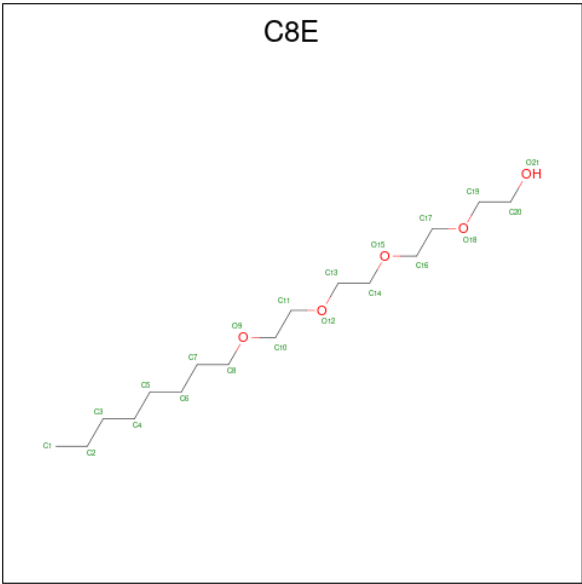
Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	ALA	-	expression tag	UNP A0A0D5YI36
B	-13	ASN	-	expression tag	UNP A0A0D5YI36
B	-12	VAL	-	expression tag	UNP A0A0D5YI36
B	-11	ARG	-	expression tag	UNP A0A0D5YI36
B	-10	LEU	-	expression tag	UNP A0A0D5YI36
B	-9	GLN	-	expression tag	UNP A0A0D5YI36
B	-8	HIS	-	expression tag	UNP A0A0D5YI36
B	-7	HIS	-	expression tag	UNP A0A0D5YI36
B	-6	HIS	-	expression tag	UNP A0A0D5YI36
B	-5	HIS	-	expression tag	UNP A0A0D5YI36
B	-4	HIS	-	expression tag	UNP A0A0D5YI36
B	-3	HIS	-	expression tag	UNP A0A0D5YI36
B	-2	HIS	-	expression tag	UNP A0A0D5YI36
B	-1	LEU	-	expression tag	UNP A0A0D5YI36
B	0	GLU	-	expression tag	UNP A0A0D5YI36
A	-14	ALA	-	expression tag	UNP A0A0D5YI36
A	-13	ASN	-	expression tag	UNP A0A0D5YI36
A	-12	VAL	-	expression tag	UNP A0A0D5YI36
A	-11	ARG	-	expression tag	UNP A0A0D5YI36
A	-10	LEU	-	expression tag	UNP A0A0D5YI36
A	-9	GLN	-	expression tag	UNP A0A0D5YI36
A	-8	HIS	-	expression tag	UNP A0A0D5YI36
A	-7	HIS	-	expression tag	UNP A0A0D5YI36
A	-6	HIS	-	expression tag	UNP A0A0D5YI36
A	-5	HIS	-	expression tag	UNP A0A0D5YI36

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	HIS	-	expression tag	UNP A0A0D5YI36
A	-3	HIS	-	expression tag	UNP A0A0D5YI36
A	-2	HIS	-	expression tag	UNP A0A0D5YI36
A	-1	LEU	-	expression tag	UNP A0A0D5YI36
A	0	GLU	-	expression tag	UNP A0A0D5YI36

- Molecule 2 is (HYDROXYETHYLOXY)TRI(ETHYLOXY)OCTANE (CCD ID: C8E) (formula: C₁₆H₃₄O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			10	6	4		
2	B	1	Total	C	O	0	0
			7	4	3		
2	B	1	Total	C	O	0	0
			14	9	5		
2	B	1	Total	C	O	0	0
			21	16	5		
2	A	1	Total	C	O	0	0
			17	12	5		
2	A	1	Total	C	O	0	0
			10	9	1		
2	A	1	Total	C	O	0	0
			21	16	5		
2	A	1	Total	C		0	0
			8	8			

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total 2	Ca 2	0	0
3	A	2	Total 2	Ca 2	0	0

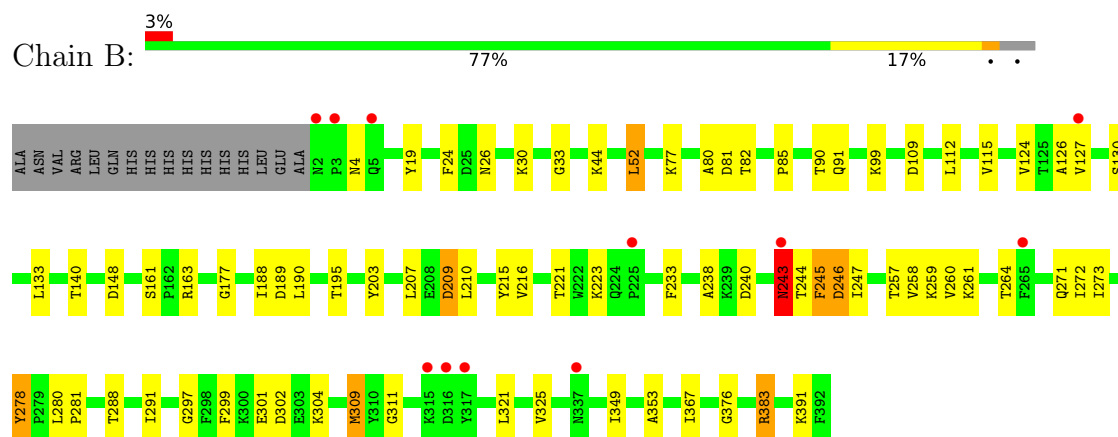
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	157	Total 157	O 157	0	0
4	A	161	Total 161	O 161	0	0

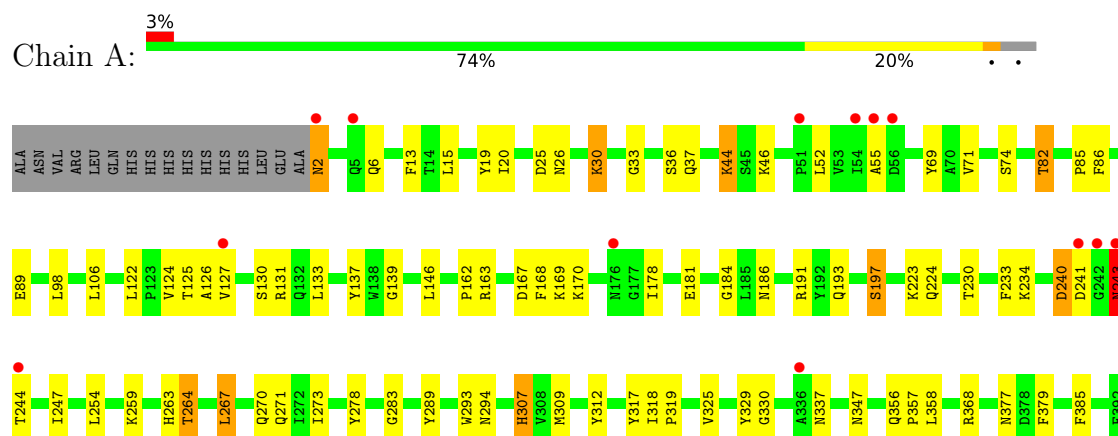
3 Residue-property plots [i](#)

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: Benzoate transport porin BenP



• Molecule 1: Benzoate transport porin BenP



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	170.30Å 90.56Å 101.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.01 – 2.20 50.01 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.7 (50.01-2.20) 99.7 (50.01-2.20)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.48 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0131	Depositor
R, R_{free}	0.207 , 0.248 0.212 , 0.252	Depositor DCC
R_{free} test set	2055 reflections (2.55%)	wwPDB-VP
Wilson B-factor (Å ²)	30.0	Xtriage
Anisotropy	0.635	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 32.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6838	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.09% 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: C8E, CA

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	1.92	76/3280 (2.3%)	1.40	21/4444 (0.5%)
1	B	1.74	53/3304 (1.6%)	1.35	16/4476 (0.4%)
All	All	1.83	129/6584 (2.0%)	1.37	37/8920 (0.4%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (129) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	243	ASN	CA-C	11.44	1.65	1.53
1	A	55	ALA	C-O	9.72	1.36	1.24
1	A	244	THR	CA-C	9.01	1.64	1.52
1	A	131	ARG	N-CA	8.76	1.51	1.46
1	B	80	ALA	C-O	-8.35	1.14	1.23
1	A	130	SER	CA-C	8.09	1.64	1.52
1	A	193	GLN	C-O	-8.06	1.14	1.23
1	A	163	ARG	C-O	-7.95	1.14	1.24
1	A	358	LEU	C-O	-7.93	1.14	1.24
1	A	319	PRO	C-O	7.90	1.32	1.23
1	B	246	ASP	CA-C	7.85	1.63	1.53
1	A	126	ALA	CA-C	7.83	1.63	1.52
1	B	210	LEU	CA-C	7.49	1.58	1.52
1	A	44	LYS	CA-C	-7.45	1.43	1.52
1	B	130	SER	C-O	7.44	1.33	1.24
1	A	243	ASN	N-CA	7.20	1.56	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	130	SER	C-O	7.10	1.33	1.24
1	A	278	TYR	CA-C	7.09	1.60	1.52
1	B	221	THR	CA-C	6.94	1.60	1.52
1	A	347	ASN	C-O	6.94	1.32	1.23
1	A	273	ILE	N-CA	6.91	1.54	1.46
1	A	124	VAL	CA-C	6.88	1.61	1.52
1	B	190	LEU	C-O	6.88	1.31	1.24
1	A	36	SER	N-CA	6.83	1.54	1.45
1	A	234	LYS	C-O	-6.81	1.16	1.24
1	A	162	PRO	CA-C	6.81	1.60	1.52
1	A	19	TYR	CA-C	6.79	1.61	1.52
1	A	264	THR	C-O	6.78	1.32	1.23
1	A	86	PHE	C-O	-6.77	1.16	1.24
1	B	353	ALA	CA-C	6.74	1.61	1.52
1	A	85	PRO	C-O	6.67	1.31	1.23
1	A	240	ASP	N-CA	6.60	1.54	1.46
1	B	291	ILE	N-CA	6.54	1.54	1.46
1	A	20	ILE	CA-C	-6.49	1.44	1.52
1	A	89	GLU	C-O	-6.46	1.16	1.24
1	A	254	LEU	CB-CG	6.45	1.66	1.53
1	A	325	VAL	CA-C	6.42	1.60	1.52
1	A	146	LEU	C-O	-6.39	1.15	1.24
1	B	130	SER	CA-C	6.38	1.61	1.52
1	B	281	PRO	N-CA	-6.32	1.39	1.47
1	A	125	THR	C-O	6.19	1.32	1.23
1	B	272	ILE	C-O	6.19	1.31	1.24
1	B	195	THR	C-O	6.07	1.30	1.24
1	B	148	ASP	C-O	-6.04	1.17	1.24
1	A	98	LEU	C-O	6.04	1.31	1.24
1	A	270	GLN	C-O	-6.04	1.16	1.23
1	A	69	TYR	N-CA	6.00	1.53	1.46
1	A	307	HIS	C-O	5.96	1.31	1.24
1	B	189	ASP	C-O	-5.95	1.17	1.24
1	A	368	ARG	C-O	5.95	1.31	1.24
1	B	209	ASP	CG-OD2	5.93	1.36	1.25
1	A	193	GLN	CA-CB	5.92	1.60	1.53
1	B	207	LEU	C-O	-5.89	1.15	1.23
1	A	26	ASN	CA-C	5.86	1.60	1.52
1	B	163	ARG	CA-C	5.85	1.60	1.52
1	B	233	PHE	CA-C	-5.82	1.45	1.52
1	A	169	LYS	CA-C	5.82	1.60	1.52
1	A	224	GLN	CA-C	5.80	1.58	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	178	ILE	N-CA	5.78	1.53	1.46
1	B	367	ILE	C-O	5.78	1.30	1.24
1	B	240	ASP	CB-CG	-5.75	1.37	1.52
1	A	170	LYS	C-O	5.74	1.30	1.23
1	A	37	GLN	CA-C	-5.73	1.45	1.52
1	A	312	TYR	C-O	5.73	1.30	1.23
1	A	191	ARG	C-O	-5.68	1.17	1.24
1	B	85	PRO	C-O	5.67	1.30	1.23
1	A	139	GLY	N-CA	5.65	1.51	1.45
1	B	221	THR	C-O	5.62	1.30	1.24
1	B	243	ASN	C-O	5.61	1.31	1.24
1	B	325	VAL	CA-C	5.61	1.59	1.52
1	A	368	ARG	CA-C	5.60	1.59	1.52
1	A	25	ASP	N-CA	5.60	1.53	1.46
1	A	233	PHE	CA-CB	-5.60	1.45	1.53
1	A	137	TYR	CA-C	5.59	1.59	1.52
1	B	124	VAL	CA-C	5.58	1.59	1.52
1	B	261	LYS	N-CA	5.58	1.53	1.46
1	B	163	ARG	CZ-NH1	5.57	1.40	1.32
1	A	127	VAL	CA-C	5.55	1.59	1.52
1	A	337	ASN	N-CA	5.53	1.53	1.46
1	A	271	GLN	CA-C	-5.53	1.45	1.52
1	A	197	SER	CA-C	5.51	1.60	1.52
1	A	82	THR	CA-CB	5.50	1.62	1.53
1	A	122	LEU	C-O	5.50	1.28	1.24
1	B	240	ASP	N-CA	5.49	1.52	1.45
1	A	133	LEU	CA-C	5.48	1.60	1.53
1	B	112	LEU	N-CA	-5.48	1.39	1.46
1	B	278	TYR	C-O	-5.48	1.17	1.24
1	A	294	ASN	CA-C	5.47	1.60	1.52
1	A	30	LYS	C-O	-5.44	1.17	1.24
1	B	349	ILE	C-O	5.44	1.30	1.24
1	A	247	ILE	C-O	-5.42	1.18	1.24
1	B	243	ASN	CA-C	5.41	1.60	1.52
1	B	99	LYS	N-CA	5.40	1.52	1.45
1	A	289	TYR	N-CA	5.39	1.53	1.46
1	A	230	THR	C-O	-5.38	1.17	1.24
1	B	311	GLY	CA-C	5.38	1.56	1.51
1	A	181	GLU	CD-OE1	-5.36	1.15	1.25
1	B	177	GLY	N-CA	5.36	1.53	1.45
1	B	273	ILE	N-CA	5.35	1.52	1.46
1	A	330	GLY	CA-C	5.34	1.56	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	209	ASP	N-CA	5.33	1.53	1.46
1	B	44	LYS	CA-C	-5.32	1.46	1.52
1	B	24	PHE	C-O	-5.28	1.17	1.23
1	B	376	GLY	C-O	5.28	1.30	1.23
1	A	124	VAL	CA-CB	5.27	1.61	1.54
1	B	133	LEU	N-CA	5.27	1.52	1.45
1	B	238	ALA	CA-C	5.26	1.58	1.52
1	B	288	THR	CB-CG2	5.25	1.69	1.52
1	A	385	PHE	N-CA	-5.23	1.39	1.46
1	B	82	THR	CA-CB	5.22	1.61	1.53
1	A	74	SER	CA-C	5.22	1.60	1.53
1	A	241	ASP	CB-CG	5.22	1.65	1.52
1	A	186	ASN	C-O	-5.21	1.17	1.24
1	B	109	ASP	CA-C	5.20	1.59	1.52
1	B	195	THR	C-N	5.20	1.40	1.33
1	B	52	LEU	N-CA	5.19	1.52	1.46
1	B	321	LEU	CA-C	5.19	1.59	1.52
1	B	216	VAL	C-O	5.19	1.29	1.24
1	A	15	LEU	CA-C	-5.17	1.46	1.52
1	B	81	ASP	CA-CB	5.15	1.61	1.54
1	A	6	GLN	CA-C	5.12	1.59	1.52
1	A	293	TRP	CA-C	5.12	1.59	1.52
1	A	318	ILE	N-CA	-5.12	1.40	1.46
1	A	317	TYR	N-CA	5.10	1.52	1.46
1	B	383	ARG	CZ-NH1	5.08	1.39	1.32
1	B	26	ASN	C-O	5.07	1.29	1.24
1	A	13	PHE	CA-C	-5.07	1.46	1.52
1	B	161	SER	N-CA	5.06	1.52	1.46
1	A	263	HIS	C-O	5.03	1.30	1.23

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	243	ASN	N-CA-C	9.99	123.81	107.32
1	B	245	PHE	CA-C-N	-7.93	111.02	122.68
1	B	245	PHE	C-N-CA	-7.93	111.02	122.68
1	A	168	PHE	N-CA-C	-7.13	97.61	109.24
1	A	127	VAL	N-CA-CB	6.93	118.72	110.95
1	A	329	TYR	CA-C-N	6.40	126.00	121.65
1	A	329	TYR	C-N-CA	6.40	126.00	121.65
1	A	2	ASN	CA-C-N	6.32	126.27	119.76
1	A	2	ASN	C-N-CA	6.32	126.27	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	240	ASP	O-C-N	6.16	130.39	122.81
1	B	127[A]	VAL	CA-C-O	5.85	128.09	120.78
1	B	127[B]	VAL	CA-C-O	5.85	128.09	120.78
1	A	184	GLY	N-CA-C	5.78	118.78	111.09
1	B	260	VAL	CB-CA-C	-5.67	102.73	110.77
1	B	245	PHE	N-CA-C	5.64	120.44	113.50
1	A	71	VAL	N-CA-C	-5.64	100.36	108.48
1	B	247	ILE	CB-CA-C	5.62	117.76	110.96
1	A	240	ASP	CA-C-N	5.59	131.57	123.13
1	A	240	ASP	C-N-CA	5.59	131.57	123.13
1	B	291	ILE	CB-CA-C	-5.57	103.53	112.16
1	B	44	LYS	CB-CA-C	-5.49	102.33	110.62
1	A	267	LEU	N-CA-CB	-5.45	101.66	110.81
1	A	377	ASN	N-CA-C	5.41	117.57	107.99
1	B	258	VAL	CB-CA-C	5.38	118.59	110.63
1	A	379	PHE	N-CA-C	5.33	116.91	108.96
1	A	283	GLY	CA-C-N	5.30	129.65	122.07
1	A	283	GLY	C-N-CA	5.30	129.65	122.07
1	B	30	LYS	N-CA-C	5.26	118.19	109.46
1	A	46	LYS	N-CA-C	-5.25	103.95	110.41
1	A	267	LEU	CB-CG-CD2	-5.23	95.01	110.70
1	B	127[A]	VAL	CA-C-N	-5.21	115.26	123.13
1	B	127[A]	VAL	C-N-CA	-5.21	115.26	123.13
1	B	127[B]	VAL	CA-C-N	-5.21	115.26	123.13
1	B	127[B]	VAL	C-N-CA	-5.21	115.26	123.13
1	A	33	GLY	N-CA-C	5.14	117.81	110.46
1	A	223	LYS	CD-CE-NZ	5.06	128.10	111.90
1	B	297	GLY	N-CA-C	5.01	119.65	113.79

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	243	ASN	Peptide

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	3191	0	3049	8	0
1	B	3217	0	3074	13	0
2	A	56	0	89	2	0
2	B	52	0	73	1	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	161	0	0	0	0
4	B	157	0	0	3	0
All	All	6838	0	6285	22	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (22) 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:A:240:ASP:CG	1:A:243:ASN:HD21	1.84	0.85
1:A:240:ASP:OD1	1:A:243:ASN:ND2	2.14	0.80
1:A:356:GLN:HE22	2:A:403:C8E:H72	1.71	0.55
1:A:356:GLN:HE22	2:A:403:C8E:C7	2.20	0.53
1:B:245:PHE:O	1:B:246:ASP:C	2.48	0.50
2:B:404:C8E:H202	4:B:649:HOH:O	2.11	0.50
1:A:240:ASP:CG	1:A:243:ASN:ND2	2.64	0.49
1:A:264:THR:HG22	1:A:309:MET:HE1	1.96	0.47
1:B:33:GLY:O	1:B:77:LYS:HE2	2.15	0.46
1:B:301:GLU:O	1:B:302:ASP:HB2	2.15	0.46
1:B:126[A]:ALA:HB2	4:B:507:HOH:O	2.14	0.46
1:B:90:THR:O	1:B:91:GLN:HB2	2.17	0.45
1:A:307:HIS:CD2	1:A:307:HIS:N	2.84	0.45
1:B:264:THR:CG2	1:B:309[B]:MET:HE1	2.48	0.44
1:A:264:THR:CG2	1:A:309:MET:HE1	2.48	0.44
1:B:115:VAL:HG22	1:B:140:THR:HG23	2.01	0.42
1:B:271:GLN:HG3	1:B:304:LYS:HG2	2.02	0.42
1:B:4:ASN:N	4:B:502:HOH:O	2.30	0.42
1:B:243:ASN:HB3	1:B:244:THR:H	1.77	0.41
1:B:203:TYR:HB3	1:B:215:TYR:HB3	2.03	0.41
1:B:19:TYR:O	1:B:383:ARG:HA	2.21	0.41
1:B:278:TYR:HB3	1:B:299:PHE:HB2	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	390/407 (96%)	374 (96%)	16 (4%)	0	100	100
1	B	393/407 (97%)	376 (96%)	17 (4%)	0	100	100
All	All	783/814 (96%)	750 (96%)	33 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	341/354 (96%)	328 (96%)	13 (4%)	29	40
1	B	343/354 (97%)	332 (97%)	11 (3%)	34	47
All	All	684/708 (97%)	660 (96%)	24 (4%)	34	43

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	52	LEU
1	B	188	ILE
1	B	209	ASP
1	B	223	LYS
1	B	243	ASN
1	B	257	THR
1	B	259	LYS
1	B	280	LEU

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Mol	Chain	Res	Type
1	B	309[A]	MET
1	B	309[B]	MET
1	B	391	LYS
1	A	2	ASN
1	A	30	LYS
1	A	44	LYS
1	A	52	LEU
1	A	82	THR
1	A	106	LEU
1	A	167[A]	ASP
1	A	167[B]	ASP
1	A	197	SER
1	A	243	ASN
1	A	259	LYS
1	A	267	LEU
1	A	357	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	78	HIS
1	B	145	GLN
1	B	224	GLN
1	B	237	ASN
1	B	292	ASN
1	B	342	HIS
1	B	365	GLN
1	A	21	ASN
1	A	243	ASN
1	A	270	GLN
1	A	292	ASN
1	A	322	ASN
1	A	331	HIS
1	A	351	ASN
1	A	365	GLN

5.3.3 RNA ⓘ

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 12 ligands modelled in this entry, 4 are monoatomic - leaving 8 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	$\# Z > 2$
2	C8E	B	401	-	9,9,20	0.67	0	8,8,19	0.64	0
2	C8E	A	403	-	20,20,20	0.88	0	19,19,19	0.99	0
2	C8E	A	401	-	16,16,20	0.73	0	15,15,19	1.17	2 (13%)
2	C8E	A	402	-	9,9,20	0.65	0	8,8,19	0.84	0
2	C8E	B	404	-	20,20,20	0.90	0	19,19,19	0.82	1 (5%)
2	C8E	A	404	-	7,7,20	0.42	0	6,6,19	0.50	0
2	C8E	B	403	-	13,13,20	0.74	0	12,12,19	0.67	0
2	C8E	B	402	-	6,6,20	0.55	0	5,5,19	0.81	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
2	C8E	B	401	-	-	3/7/7/18	-
2	C8E	A	403	-	-	9/18/18/18	-
2	C8E	A	401	-	-	9/14/14/18	-
2	C8E	A	402	-	-	2/7/7/18	-
2	C8E	B	404	-	-	12/18/18/18	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	C8E	A	404	-	-	2/5/5/18	-
2	C8E	B	403	-	-	7/11/11/18	-
2	C8E	B	402	-	-	2/4/4/18	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	C8E	C10-O9-C8	2.66	124.88	113.26
2	B	404	C8E	C19-O18-C17	2.27	123.21	113.26
2	A	401	C8E	O12-C13-C14	2.15	120.17	110.35

There are no chirality outliers.

All (46) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	403	C8E	O12-C13-C14-O15
2	A	401	C8E	O12-C13-C14-O15
2	B	404	C8E	O9-C10-C11-O12
2	A	403	C8E	C5-C6-C7-C8
2	A	401	C8E	O15-C16-C17-O18
2	A	403	C8E	O9-C10-C11-O12
2	B	404	C8E	O18-C19-C20-O21
2	B	404	C8E	C16-C17-O18-C19
2	A	403	C8E	O18-C19-C20-O21
2	A	401	C8E	C6-C7-C8-O9
2	B	402	C8E	O15-C16-C17-O18
2	B	404	C8E	C3-C4-C5-C6
2	B	403	C8E	O15-C16-C17-O18
2	A	401	C8E	C5-C6-C7-C8
2	B	404	C8E	C4-C5-C6-C7
2	A	403	C8E	O15-C16-C17-O18
2	B	401	C8E	O12-C13-C14-O15
2	A	404	C8E	C2-C3-C4-C5
2	B	404	C8E	C5-C6-C7-C8
2	A	401	C8E	C20-C19-O18-C17
2	A	403	C8E	O12-C13-C14-O15
2	B	404	C8E	O15-C16-C17-O18
2	A	404	C8E	C3-C4-C5-C6
2	A	403	C8E	C16-C17-O18-C19

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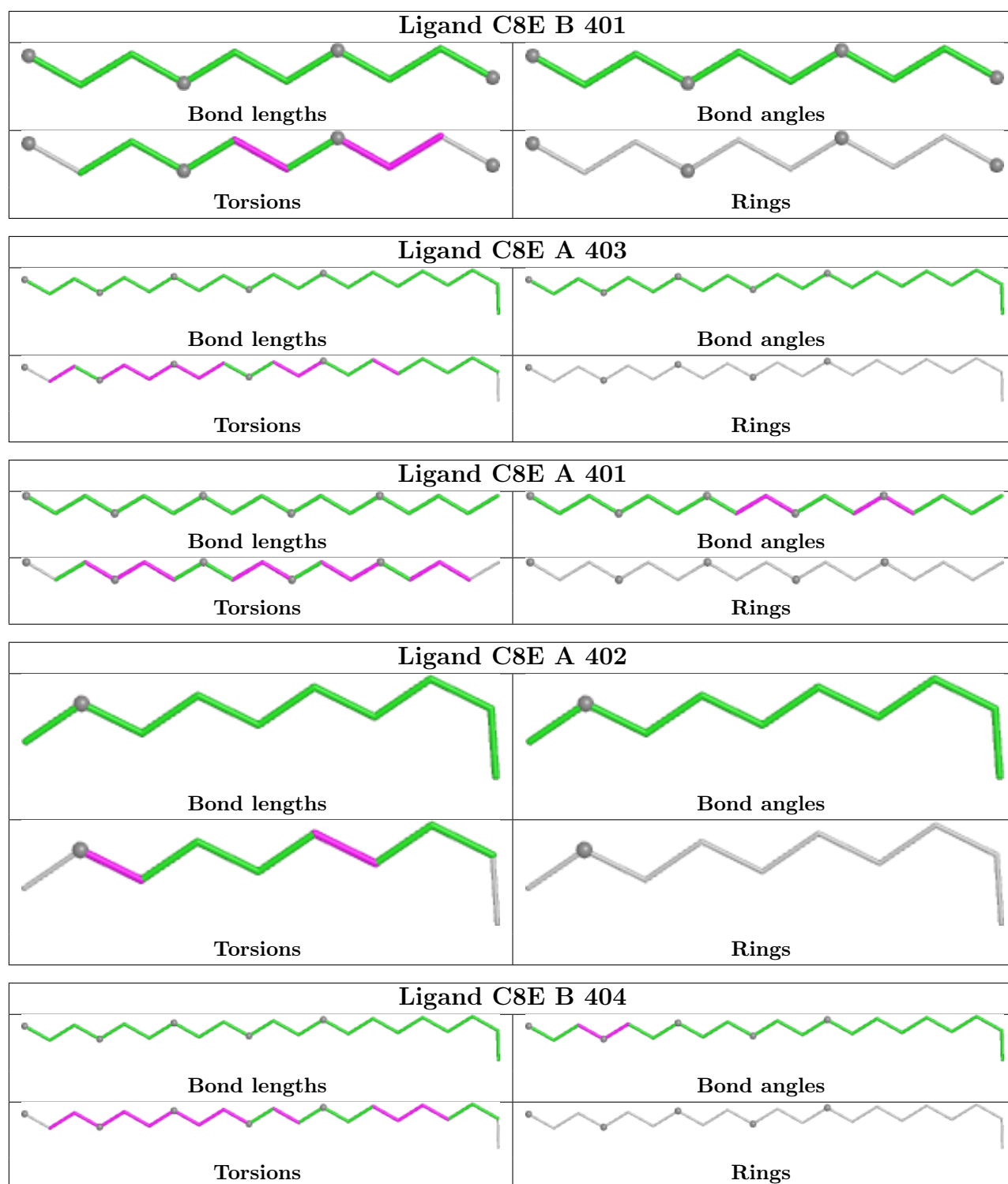
Mol	Chain	Res	Type	Atoms
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2	B	402	C8E	O18-C19-C20-O21
2	B	401	C8E	C13-C14-O15-C16
2	A	401	C8E	O9-C10-C11-O12
2	B	403	C8E	C13-C14-O15-C16
2	A	401	C8E	C11-C10-O9-C8
2	B	404	C8E	C14-C13-O12-C11
2	A	401	C8E	C16-C17-O18-C19
2	A	403	C8E	C17-C16-O15-C14
2	B	404	C8E	C13-C14-O15-C16
2	A	403	C8E	C11-C10-O9-C8
2	B	404	C8E	O12-C13-C14-O15
2	A	403	C8E	C13-C14-O15-C16
2	B	403	C8E	C20-C19-O18-C17
2	B	404	C8E	C17-C16-O15-C14
2	B	404	C8E	C20-C19-O18-C17
2	B	403	C8E	C16-C17-O18-C19
2	A	401	C8E	C14-C13-O12-C11
2	A	402	C8E	C7-C8-O9-C10
2	B	401	C8E	O15-C16-C17-O18
2	A	402	C8E	C3-C4-C5-C6
2	B	403	C8E	O9-C10-C11-O12

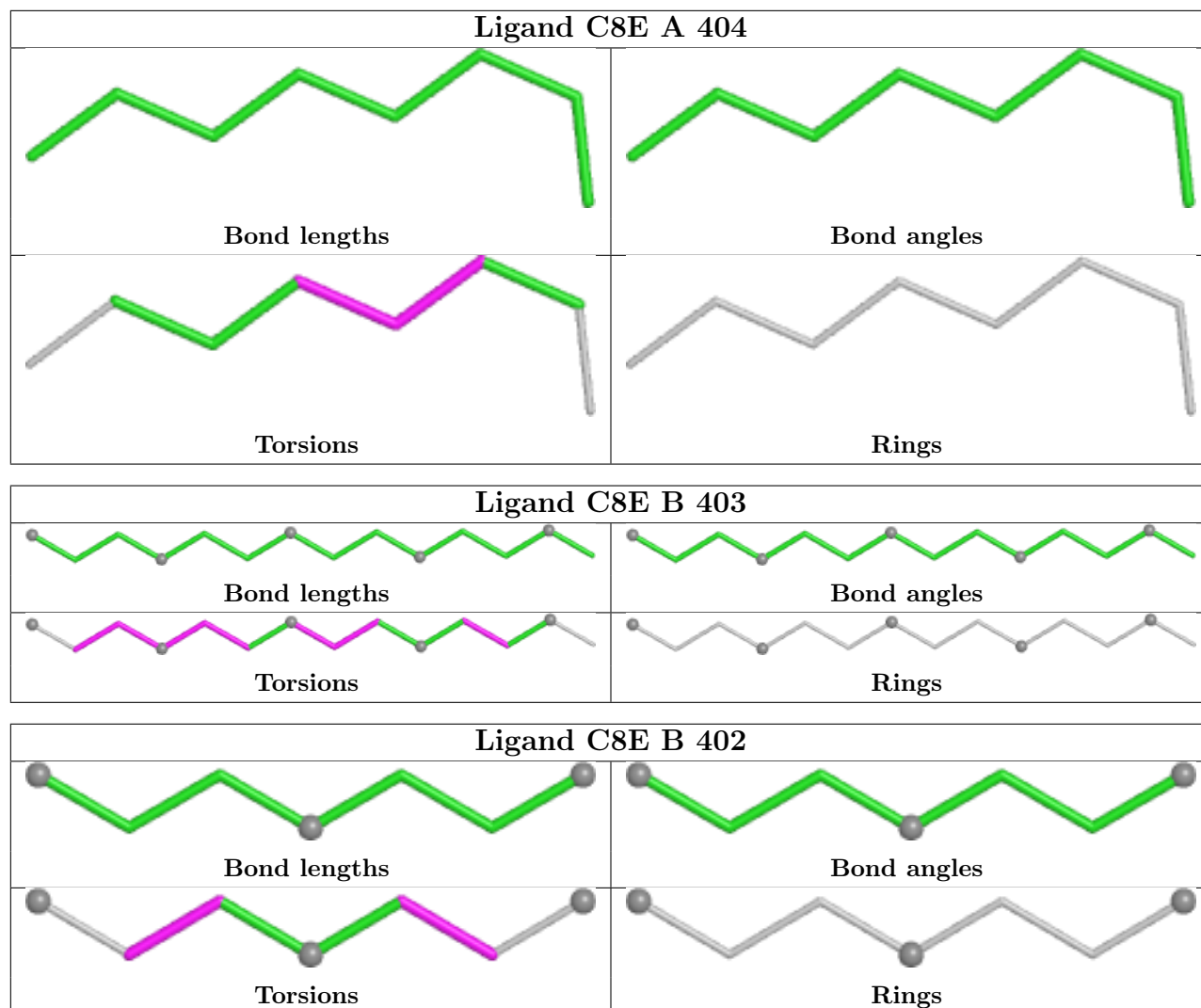
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	403	C8E	2	0
2	B	404	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

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	391/407 (96%)	-0.14	13 (3%)	49 46	20, 30, 60, 83	1 (0%)
1	B	391/407 (96%)	-0.05	11 (2%)	55 52	15, 33, 58, 84	4 (1%)
All	All	782/814 (96%)	-0.10	24 (3%)	51 48	15, 31, 59, 84	5 (0%)

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	127[A]	VAL	7.8
1	A	2	ASN	4.7
1	B	265[A]	PHE	3.6
1	A	55	ALA	3.3
1	B	317	TYR	3.1
1	B	2	ASN	2.9
1	A	243	ASN	2.7
1	A	5	GLN	2.6
1	A	242	GLY	2.6
1	B	5	GLN	2.6
1	B	316	ASP	2.6
1	B	225	PRO	2.6
1	A	54	ILE	2.6
1	A	176	ASN	2.4
1	B	3	PRO	2.3
1	A	51	PRO	2.3
1	B	243	ASN	2.2
1	B	315	LYS	2.2
1	A	56	ASP	2.2
1	A	127	VAL	2.1
1	A	336	ALA	2.1
1	A	241	ASP	2.1
1	B	337	ASN	2.0
1	A	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 ⓘ

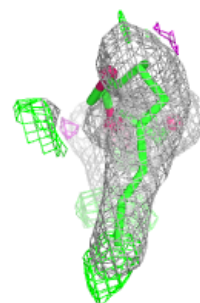
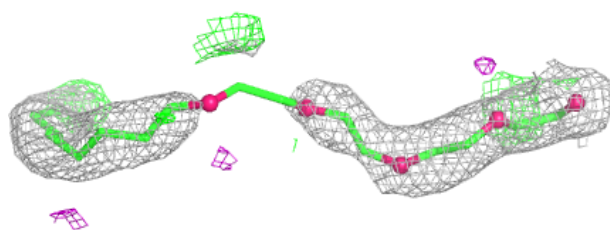
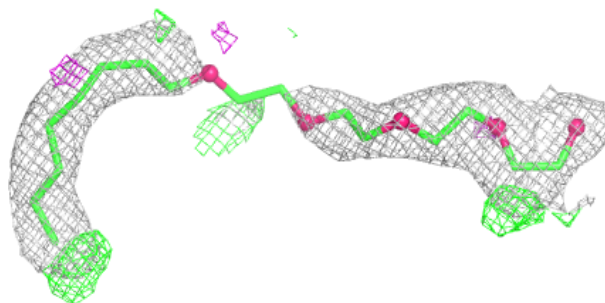
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	C8E	B	404	21/21	0.81	0.22	41,53,84,87	0
2	C8E	A	402	10/21	0.85	0.23	41,56,66,69	0
2	C8E	A	403	21/21	0.85	0.19	41,50,64,71	0
2	C8E	B	403	14/21	0.89	0.15	47,49,60,61	0
2	C8E	A	401	17/21	0.89	0.15	34,44,47,49	0
2	C8E	B	402	7/21	0.90	0.14	44,46,50,54	0
2	C8E	A	404	8/21	0.90	0.16	36,41,47,49	0
2	C8E	B	401	10/21	0.91	0.12	37,44,46,50	0
3	CA	B	406	1/1	0.97	0.05	43,43,43,43	0
3	CA	A	406	1/1	0.98	0.04	39,39,39,39	0
3	CA	B	405	1/1	0.99	0.06	43,43,43,43	0
3	CA	A	405	1/1	1.00	0.02	36,36,36,36	0

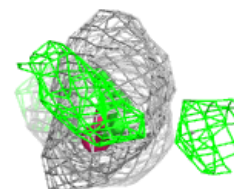
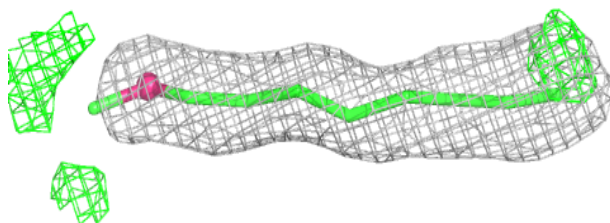
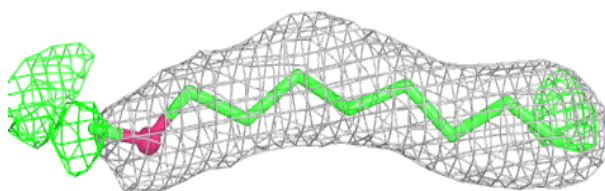
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around C8E B 404:

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

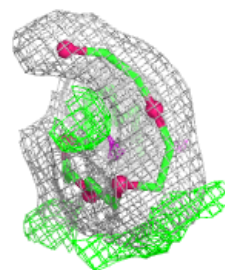
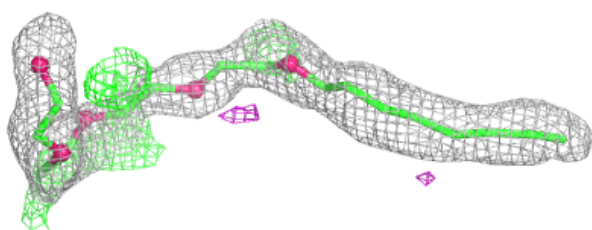
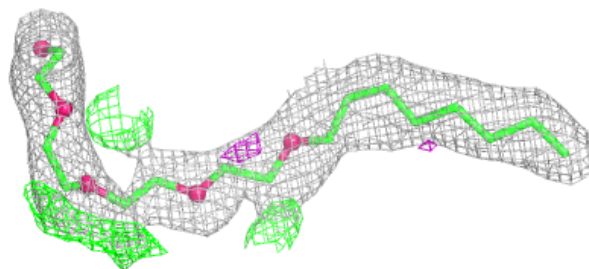
**Electron density around C8E A 402:**

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and green (positive)

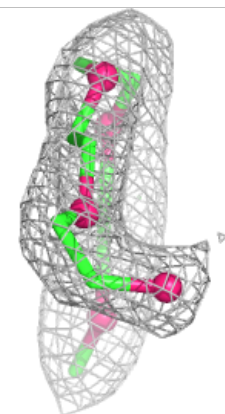
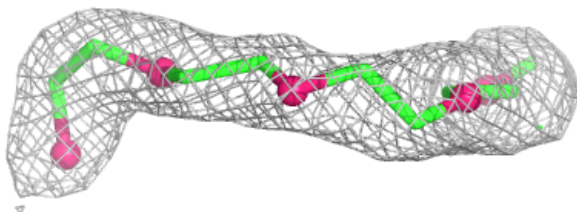
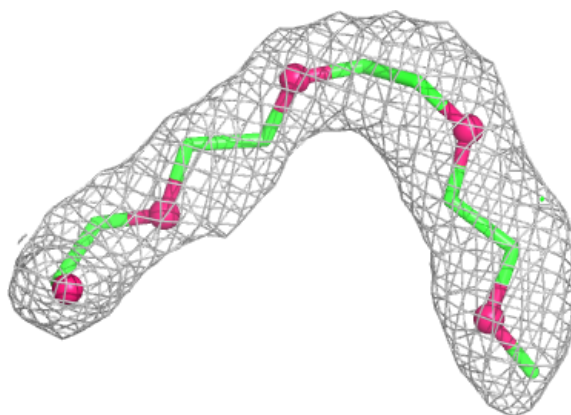


Electron density around C8E A 403:

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

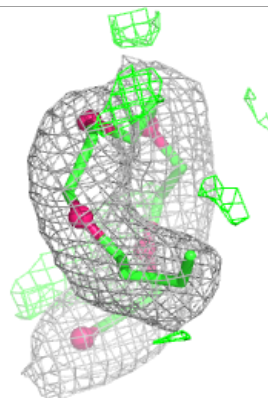
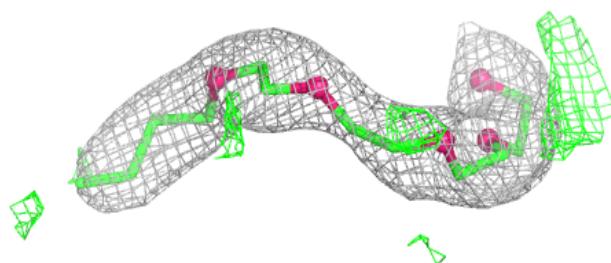
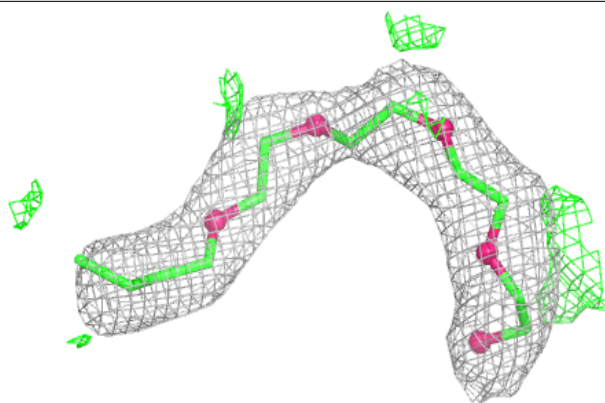
**Electron density around C8E B 403:**

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and green (positive)

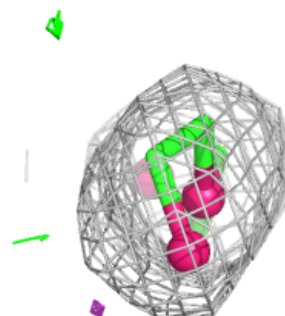
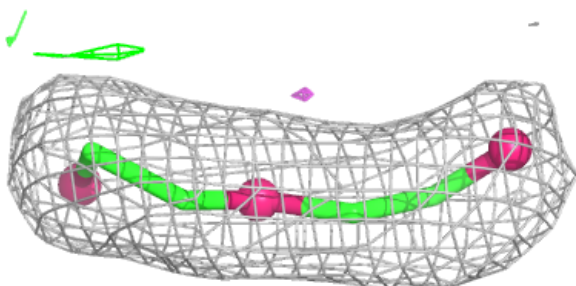
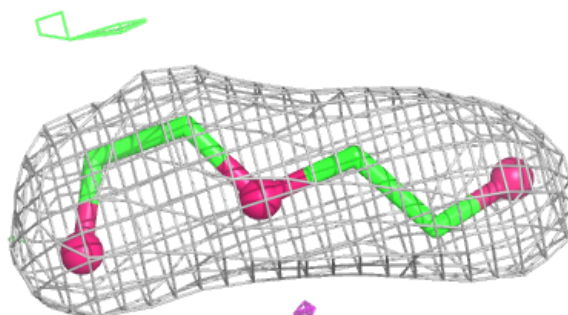


Electron density around C8E A 401:

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

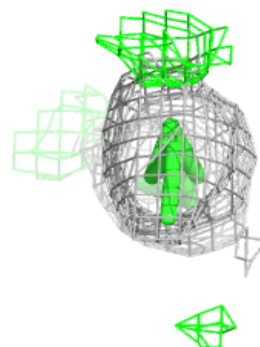
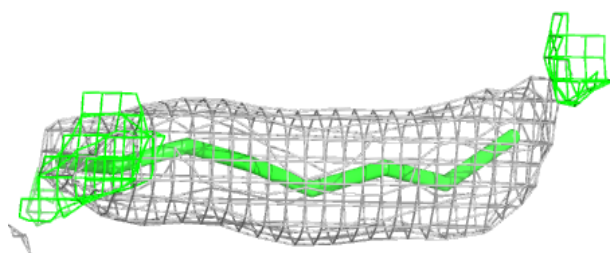
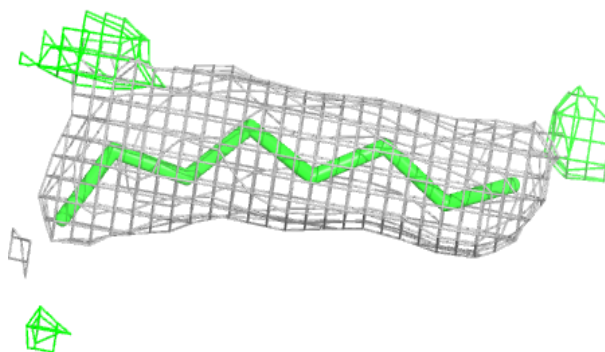
**Electron density around C8E B 402:**

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

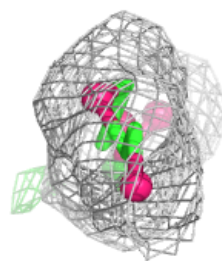
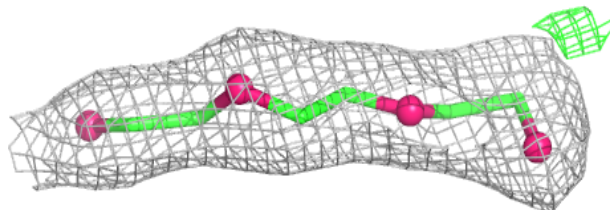
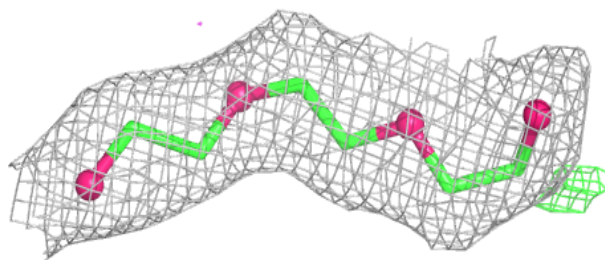


Electron density around C8E A 404:

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

**Electron density around C8E B 401:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.