



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:59 PM UTC

PDB ID : 4C94 / pdb_00004c94
Title : Crystal Structure of the Strawberry Pathogenesis-Related 10 (PR-10) Fra a 3 protein in complex with Catechin
Authors : Casanal, A.; Zander, U.; Valpuesta, V.; Marquez, J.A.
Deposited on : 2013-10-02
Resolution : 3.00 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

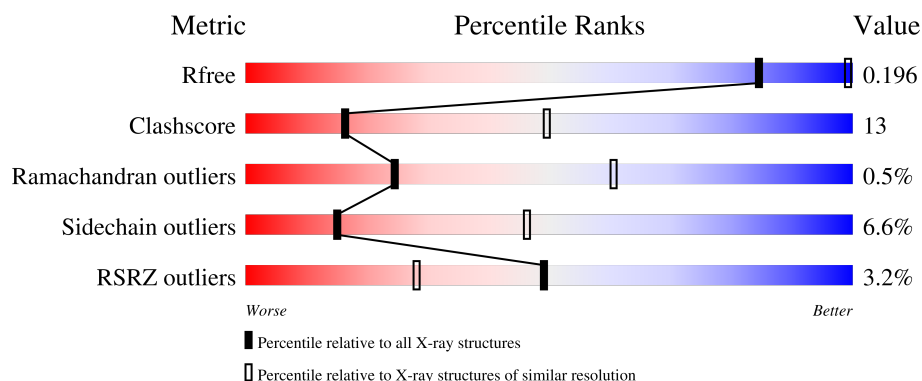
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	161	0% 61% 30% 7% .
1	B	161	3% 70% 24% 6%
1	C	161	5% 66% 29% .
1	D	161	2% 68% 23% 6% . .
1	E	161	5% 57% 32% 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
2	KXN	E	161	-	X	-	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6318 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.

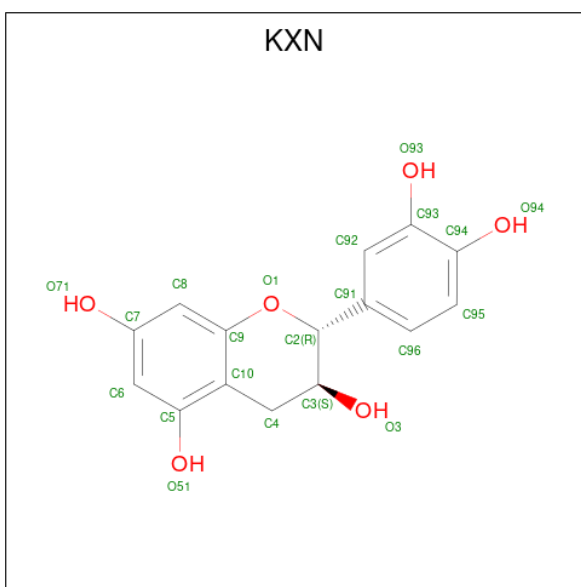
- Molecule 1 is a protein called FRA A 3 ALLERGEN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	161	Total	C	N	O	S	0	0	0
			1244	800	201	242	1			
1	B	161	Total	C	N	O	S	0	0	0
			1244	800	201	242	1			
1	C	161	Total	C	N	O	S	0	0	0
			1244	800	201	242	1			
1	D	156	Total	C	N	O	S	0	0	0
			1204	776	196	231	1			
1	E	161	Total	C	N	O	S	0	0	0
			1244	800	201	242	1			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	ALA	-	expression tag	UNP D0E0C7
A	0	MET	-	expression tag	UNP D0E0C7
A	1	ALA	-	expression tag	UNP D0E0C7
B	-1	ALA	-	expression tag	UNP D0E0C7
B	0	MET	-	expression tag	UNP D0E0C7
B	1	ALA	-	expression tag	UNP D0E0C7
C	-1	ALA	-	expression tag	UNP D0E0C7
C	0	MET	-	expression tag	UNP D0E0C7
C	1	ALA	-	expression tag	UNP D0E0C7
D	-1	ALA	-	expression tag	UNP D0E0C7
D	0	MET	-	expression tag	UNP D0E0C7
D	1	ALA	-	expression tag	UNP D0E0C7
E	-1	ALA	-	expression tag	UNP D0E0C7
E	0	MET	-	expression tag	UNP D0E0C7
E	1	ALA	-	expression tag	UNP D0E0C7

- Molecule 2 is (2R,3S)-2-(3,4-dihydroxyphenyl)-3,4-dihydro-2H-chromene-3,5,7-triol (CCD ID: KXN) (formula: C₁₅H₁₄O₆).



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

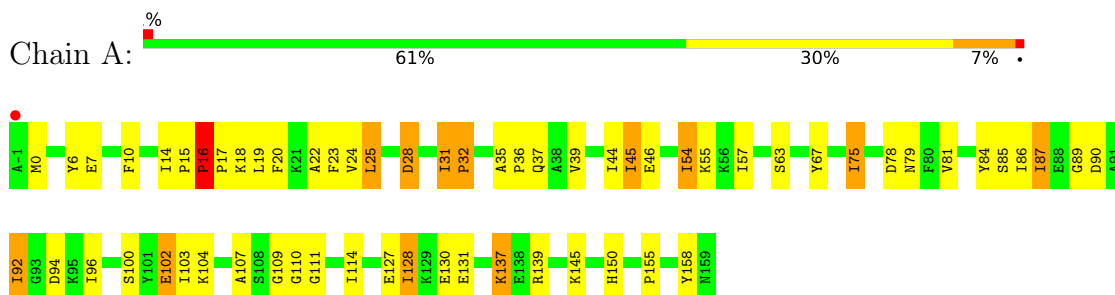
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	5	Total	O	0	0
			5	5		
3	B	1	Total	O	0	0
			1	1		
3	C	2	Total	O	0	0
			2	2		
3	D	2	Total	O	0	0
			2	2		
3	E	2	Total	O	0	0
			2	2		

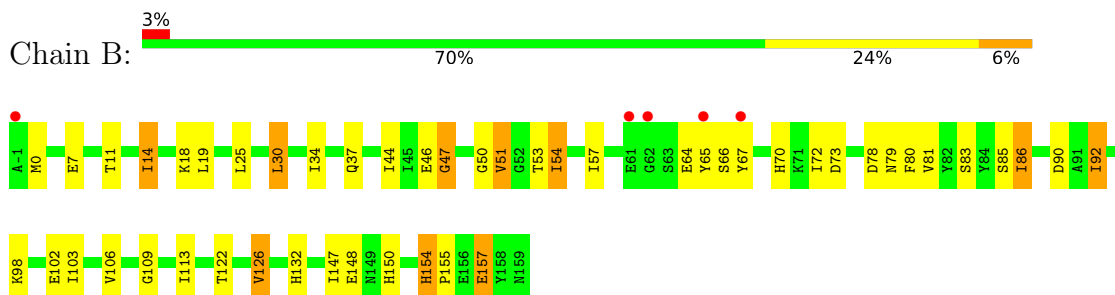
3 Residue-property plots [i](#)

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.

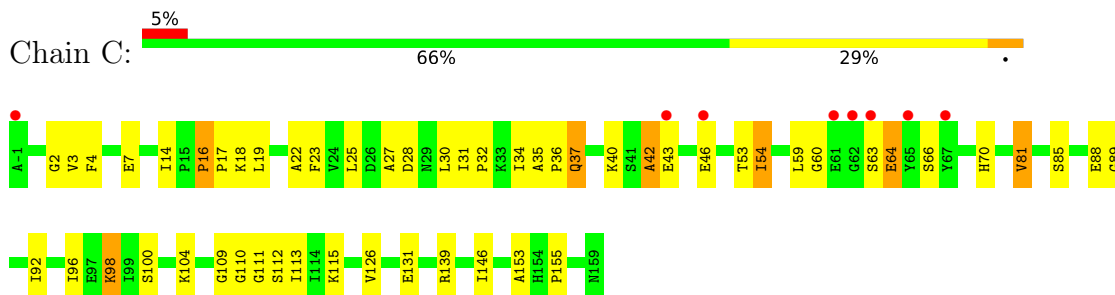
• Molecule 1: FRA A 3 ALLERGEN



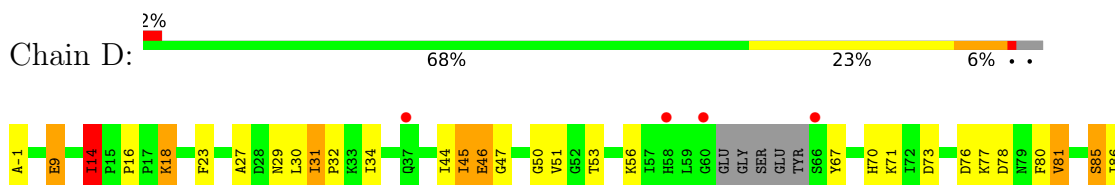
• Molecule 1: FRA A 3 ALLERGEN



• Molecule 1: FRA A 3 ALLERGEN

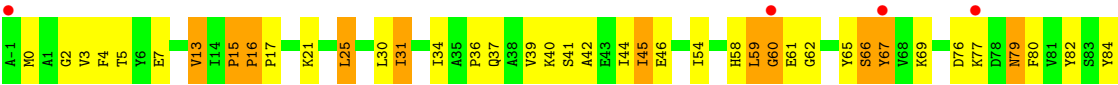


• Molecule 1: FRA A 3 ALLERGEN





● Molecule 1: FRA A 3 ALLERGEN



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	137.90Å 206.59Å 174.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.67 – 3.00 29.67 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.4 (29.67-3.00) 99.4 (29.67-3.00)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.80 (at 3.00Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.178 , 0.199 0.176 , 0.196	Depositor DCC
R_{free} test set	2536 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	73.1	Xtriage
Anisotropy	0.051	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 42.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6318	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.06% 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: KXN

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	1.72	13/1270 (1.0%)	1.68	18/1709 (1.1%)
1	B	1.76	16/1270 (1.3%)	1.54	18/1709 (1.1%)
1	C	1.39	4/1270 (0.3%)	1.54	12/1709 (0.7%)
1	D	1.47	6/1228 (0.5%)	1.55	16/1651 (1.0%)
1	E	1.54	15/1270 (1.2%)	1.68	31/1709 (1.8%)
All	All	1.58	54/6308 (0.9%)	1.60	95/8487 (1.1%)

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
1	C	0	3
All	All	0	4

All (54) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	-1	ALA	N-CA	8.62	1.62	1.46
1	E	66	SER	N-CA	8.26	1.56	1.46
1	A	24	VAL	C-O	-8.22	1.14	1.24
1	B	14	ILE	CA-C	-8.04	1.46	1.53
1	B	113	ILE	C-O	-7.38	1.14	1.24
1	B	81	VAL	C-O	-7.37	1.16	1.24
1	B	37	GLN	C-O	-7.17	1.15	1.24
1	A	22	ALA	C-O	-7.13	1.15	1.24
1	A	44	ILE	C-O	-7.07	1.17	1.23
1	E	44	ILE	C-O	-6.97	1.17	1.24
1	E	91	ALA	CA-C	6.94	1.62	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	81	VAL	C-O	-6.92	1.17	1.24
1	B	11	THR	C-O	-6.85	1.15	1.23
1	E	92	ILE	CA-CB	6.83	1.60	1.53
1	A	78	ASP	CA-C	-6.74	1.45	1.52
1	E	67	TYR	N-CA	6.72	1.54	1.45
1	B	51	VAL	C-O	-6.60	1.17	1.24
1	A	32	PRO	N-CA	-6.57	1.38	1.47
1	D	9	GLU	C-O	-6.49	1.15	1.23
1	C	155	PRO	C-O	-6.29	1.15	1.24
1	B	25	LEU	C-O	-6.23	1.16	1.24
1	D	67	TYR	CA-C	6.22	1.60	1.52
1	D	16	PRO	C-O	-6.01	1.17	1.24
1	B	148	GLU	C-O	-5.94	1.17	1.24
1	A	28	ASP	C-O	-5.90	1.17	1.24
1	A	96	ILE	C-O	-5.85	1.17	1.24
1	E	37	GLN	C-O	-5.82	1.16	1.24
1	B	66	SER	C-O	5.81	1.32	1.23
1	B	103	ILE	C-O	-5.80	1.18	1.24
1	E	84	TYR	CA-C	-5.73	1.45	1.52
1	C	18	LYS	N-CA	5.73	1.53	1.46
1	A	25	LEU	C-O	-5.72	1.17	1.24
1	E	102	GLU	CA-C	-5.67	1.45	1.52
1	A	150	HIS	C-O	-5.64	1.17	1.24
1	A	107	ALA	C-O	-5.64	1.17	1.23
1	E	100	SER	CA-C	-5.50	1.45	1.52
1	A	92	ILE	N-CA	-5.45	1.39	1.47
1	D	81	VAL	CA-C	-5.43	1.46	1.52
1	A	75	ILE	C-O	-5.37	1.18	1.24
1	B	78	ASP	CA-C	-5.36	1.45	1.52
1	B	30	LEU	C-O	-5.33	1.17	1.24
1	C	22	ALA	C-O	-5.30	1.18	1.23
1	E	82	TYR	CA-C	-5.29	1.46	1.52
1	C	42	ALA	CA-C	-5.27	1.46	1.52
1	E	58	HIS	CA-C	-5.22	1.46	1.52
1	B	157	GLU	C-O	-5.19	1.17	1.23
1	E	42	ALA	CA-C	-5.15	1.46	1.52
1	E	150	HIS	CA-C	-5.09	1.45	1.52
1	B	147	ILE	C-O	-5.08	1.18	1.24
1	B	72	ILE	C-O	-5.07	1.18	1.24
1	E	39	VAL	N-CA	-5.06	1.40	1.46
1	A	16	PRO	CA-C	-5.04	1.47	1.52
1	B	106	VAL	C-O	-5.01	1.18	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	90	ASP	N-CA	-5.01	1.39	1.46

All (95) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	16	PRO	CA-C-N	-10.75	107.79	119.19
1	C	16	PRO	C-N-CA	-10.75	107.79	119.19
1	D	46	GLU	CA-C-N	-10.72	114.78	122.18
1	D	46	GLU	C-N-CA	-10.72	114.78	122.18
1	A	45	ILE	CB-CA-C	-10.07	98.74	112.24
1	E	60	GLY	N-CA-C	-9.66	97.58	112.84
1	E	67	TYR	N-CA-C	8.25	122.54	109.50
1	C	14	ILE	N-CA-C	8.24	115.72	108.63
1	E	87	ILE	CB-CA-C	-8.06	101.09	112.22
1	B	0	MET	N-CA-C	7.59	120.75	109.59
1	B	109	GLY	CA-C-N	-7.45	111.61	123.31
1	B	109	GLY	C-N-CA	-7.45	111.61	123.31
1	B	7	GLU	N-CA-C	7.43	121.60	109.72
1	E	154	HIS	CA-C-N	-7.39	113.29	120.83
1	E	154	HIS	C-N-CA	-7.39	113.29	120.83
1	E	30	LEU	CA-C-N	-7.16	115.73	120.24
1	E	30	LEU	C-N-CA	-7.16	115.73	120.24
1	E	41	SER	N-CA-C	7.14	119.00	108.14
1	E	66	SER	N-CA-C	7.13	125.98	110.80
1	B	126	VAL	CB-CA-C	-7.11	101.36	111.31
1	B	14	ILE	CB-CA-C	-6.97	104.46	110.94
1	A	54	ILE	CB-CA-C	-6.89	100.33	110.81
1	D	157	GLU	N-CA-C	6.89	120.22	110.50
1	B	132	HIS	N-CA-C	-6.74	103.74	112.23
1	A	31	ILE	CA-C-N	6.71	127.25	119.47
1	A	31	ILE	C-N-CA	6.71	127.25	119.47
1	E	143	LEU	N-CA-C	-6.70	105.11	113.28
1	E	122	THR	N-CA-C	6.66	118.61	110.41
1	E	87	ILE	CB-CG1-CD1	-6.66	99.82	113.80
1	E	31	ILE	CA-C-N	-6.62	112.17	119.19
1	E	31	ILE	C-N-CA	-6.62	112.17	119.19
1	D	154	HIS	CA-C-N	-6.56	112.84	120.12
1	D	154	HIS	C-N-CA	-6.56	112.84	120.12
1	E	144	PHE	N-CA-C	-6.49	103.44	112.45
1	E	15	PRO	CA-C-N	6.42	126.99	120.38
1	E	15	PRO	C-N-CA	6.42	126.99	120.38
1	A	14	ILE	CB-CA-C	-6.40	104.99	110.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	18	LYS	N-CA-C	-6.35	103.49	111.11
1	C	14	ILE	CB-CA-C	-6.28	105.10	110.94
1	D	106	VAL	CB-CA-C	-6.28	101.34	110.63
1	B	72	ILE	CB-CA-C	-6.27	103.75	111.08
1	D	29	ASN	CB-CA-C	-6.23	101.06	110.90
1	C	18	LYS	N-CA-C	-6.21	104.43	111.07
1	E	106	VAL	CB-CA-C	-6.13	101.48	110.62
1	B	154	HIS	CA-C-N	-6.11	113.67	120.45
1	B	154	HIS	C-N-CA	-6.11	113.67	120.45
1	D	16	PRO	N-CA-C	6.06	118.10	110.70
1	E	153	ALA	CA-C-N	-6.04	116.21	122.85
1	E	153	ALA	C-N-CA	-6.04	116.21	122.85
1	B	37	GLN	CB-CG-CD	6.03	122.86	112.60
1	A	131	GLU	N-CA-C	6.03	117.93	111.36
1	E	148	GLU	N-CA-C	-5.96	103.75	111.02
1	E	59	LEU	N-CA-C	5.83	118.05	110.53
1	E	0	MET	N-CA-C	5.82	117.53	109.15
1	B	86	ILE	N-CA-C	-5.81	98.66	107.73
1	A	67	TYR	N-CA-C	5.81	118.19	110.53
1	C	37	GLN	N-CA-C	-5.80	104.32	111.33
1	D	-1	ALA	N-CA-C	5.75	127.09	111.00
1	C	25	LEU	N-CA-C	5.70	119.75	112.34
1	E	45	ILE	CB-CA-C	-5.66	103.67	111.65
1	E	79	ASN	N-CA-C	5.60	120.10	113.16
1	E	131	GLU	N-CA-C	5.54	117.40	111.36
1	C	96	ILE	N-CA-C	5.54	116.55	107.24
1	E	21	LYS	N-CA-C	-5.54	105.14	111.07
1	E	37	GLN	N-CA-C	-5.50	106.33	113.16
1	C	88	GLU	N-CA-C	5.50	117.43	109.07
1	C	70	HIS	N-CA-C	-5.45	100.14	109.24
1	D	94	ASP	CB-CA-C	-5.43	99.84	110.11
1	C	40	LYS	N-CA-C	-5.42	104.78	111.40
1	A	94	ASP	N-CA-C	-5.42	105.78	112.72
1	A	79	ASN	N-CA-C	5.39	119.84	113.16
1	B	37	GLN	O-C-N	-5.33	115.50	122.59
1	D	14	ILE	CA-C-N	-5.33	114.89	120.38
1	D	14	ILE	C-N-CA	-5.33	114.89	120.38
1	A	130	GLU	CA-C-N	5.32	127.85	120.29
1	A	130	GLU	C-N-CA	5.32	127.85	120.29
1	A	102	GLU	CA-CB-CG	5.30	124.70	114.10
1	B	92	ILE	N-CA-C	5.29	115.72	107.99
1	C	3	VAL	N-CA-C	5.28	115.87	108.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	90	ASP	N-CA-C	-5.26	105.44	111.07
1	B	102	GLU	CA-CB-CG	5.26	124.63	114.10
1	D	-1	ALA	CB-CA-C	-5.25	102.63	110.50
1	E	16	PRO	N-CA-C	5.22	117.06	110.70
1	B	106	VAL	CB-CA-C	-5.19	102.94	110.63
1	D	108	SER	N-CA-CB	5.12	119.21	110.71
1	A	57	ILE	CB-CG1-CD1	-5.11	103.07	113.80
1	E	7	GLU	N-CA-C	5.09	117.20	108.90
1	A	0	MET	N-CA-C	5.08	117.53	109.96
1	A	7	GLU	CA-CB-CG	-5.08	103.95	114.10
1	D	18	LYS	CG-CD-CE	5.04	122.89	111.30
1	B	66	SER	O-C-N	-5.03	116.75	122.68
1	E	156	GLU	N-CA-C	5.01	119.11	113.15
1	A	87	ILE	CB-CA-C	-5.00	104.59	110.84
1	A	84	TYR	CA-C-N	-5.00	115.44	122.94
1	A	84	TYR	C-N-CA	-5.00	115.44	122.94

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	110	GLY	Peptide
1	C	110	GLY	Peptide
1	C	64	GLU	Peptide
1	C	89	GLY	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	1244	0	1247	28	0
1	B	1244	0	1247	27	0
1	C	1244	0	1247	33	0
1	D	1204	0	1217	34	0
1	E	1244	0	1247	43	0
2	A	21	0	11	1	0
2	B	21	0	10	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	21	0	12	1	0
2	D	21	0	12	5	0
2	E	42	0	22	4	0
3	A	5	0	0	1	0
3	B	1	0	0	1	0
3	C	2	0	0	0	0
3	D	2	0	0	1	0
3	E	2	0	0	0	0
All	All	6318	0	6272	164	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 13.

All (164) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:161:KXN:H4A	2:E:161:KXN:H96	1.49	0.94
1:E:59:LEU:N	1:E:66:SER:O	2.10	0.83
1:D:86:ILE:O	1:D:92:ILE:HD11	1.84	0.78
1:D:31:ILE:HB	1:D:32:PRO:HD3	1.68	0.76
2:E:161:KXN:H96	2:E:161:KXN:C4	2.09	0.74
1:E:87:ILE:HG22	1:E:88:GLU:HB2	1.71	0.73
1:E:92:ILE:HD12	1:E:92:ILE:O	1.89	0.72
1:C:64:GLU:O	1:C:66:SER:N	2.24	0.70
1:A:31:ILE:N	1:A:32:PRO:CD	2.54	0.70
1:E:16:PRO:HD3	1:E:112:SER:OG	1.92	0.70
1:A:20:PHE:CE2	1:A:25:LEU:HD11	2.30	0.67
1:D:46:GLU:CG	1:D:46:GLU:O	2.42	0.67
1:C:42:ALA:O	1:C:43:GLU:HG3	1.97	0.65
1:C:23:PHE:O	1:C:27:ALA:HB2	1.97	0.65
1:E:15:PRO:C	1:E:17:PRO:HD2	2.22	0.64
1:E:31:ILE:HD13	1:E:143:LEU:CD1	2.28	0.64
1:D:30:LEU:C	1:D:30:LEU:HD13	2.22	0.64
2:D:160:KXN:O93	3:D:2001:HOH:O	2.15	0.64
2:B:160:KXN:O93	3:B:2001:HOH:O	2.15	0.63
1:C:2:GLY:HA3	1:E:4:PHE:CZ	2.34	0.63
1:C:28:ASP:O	1:C:32:PRO:HG2	1.98	0.62
1:A:10:PHE:HB2	1:A:114:ILE:HD12	1.81	0.62
1:E:31:ILE:HD13	1:E:143:LEU:HD11	1.80	0.61
1:D:14:ILE:HD13	1:D:14:ILE:N	2.15	0.61
1:A:63:SER:OG	2:A:160:KXN:H6	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:15:PRO:HB2	1:E:17:PRO:HD2	1.83	0.60
1:C:92:ILE:HG22	1:C:92:ILE:O	2.02	0.60
1:D:46:GLU:O	1:D:46:GLU:HG3	2.01	0.59
1:A:23:PHE:CD1	1:A:23:PHE:O	2.55	0.59
1:E:99:ILE:HD13	1:E:120:TYR:CE2	2.38	0.59
1:D:30:LEU:HD13	1:D:34:ILE:HG12	1.83	0.58
1:C:35:ALA:HB2	1:C:146:ILE:HG21	1.84	0.58
1:D:70:HIS:HE2	2:D:160:KXN:HO3	1.52	0.58
1:E:31:ILE:CD1	1:E:143:LEU:HD11	2.33	0.58
1:C:16:PRO:HD3	1:C:112:SER:OG	2.03	0.58
1:E:65:TYR:O	1:E:66:SER:OG	2.13	0.57
1:D:71:LYS:HB2	1:D:87:ILE:CD1	2.34	0.57
1:C:153:ALA:HB1	1:D:152:LEU:HD12	1.85	0.57
1:E:80:PHE:HB3	1:E:105:LEU:HB2	1.87	0.57
1:A:127:GLU:O	1:A:128:ILE:HG13	2.04	0.56
1:B:154:HIS:HB3	1:B:157:GLU:HG3	1.87	0.56
1:E:76:ASP:OD2	1:E:79:ASN:HB2	2.04	0.56
1:D:73:ASP:OD2	1:D:85:SER:OG	2.23	0.56
1:C:92:ILE:HD13	1:C:98:LYS:HA	1.86	0.56
1:C:63:SER:HB2	1:C:66:SER:HB2	1.88	0.56
1:A:81:VAL:HG22	1:A:104:LYS:HG3	1.87	0.56
1:B:34:ILE:O	1:B:34:ILE:HG22	2.06	0.56
1:E:92:ILE:O	1:E:92:ILE:CD1	2.54	0.55
1:A:31:ILE:N	1:A:32:PRO:HD2	2.21	0.55
1:D:14:ILE:HG13	1:D:151:LEU:HD12	1.88	0.55
1:B:34:ILE:HD11	1:B:150:HIS:CE1	2.41	0.55
1:D:45:ILE:O	1:D:46:GLU:HB3	2.05	0.55
1:B:34:ILE:CD1	1:B:150:HIS:CG	2.90	0.55
1:A:31:ILE:HB	1:A:32:PRO:HD3	1.89	0.55
1:B:86:ILE:O	1:B:92:ILE:HD11	2.07	0.55
1:C:31:ILE:N	1:C:32:PRO:CD	2.70	0.55
1:D:70:HIS:NE2	2:D:160:KXN:O3	2.40	0.55
1:B:34:ILE:HD13	1:B:150:HIS:CG	2.43	0.54
1:D:88:GLU:N	1:D:92:ILE:HD12	2.22	0.54
1:E:25:LEU:HD21	1:E:77:LYS:HZ2	1.72	0.54
1:E:139:ARG:NH2	2:E:160:KXN:O71	2.40	0.53
1:E:92:ILE:O	1:E:92:ILE:CG1	2.57	0.53
1:E:25:LEU:HD21	1:E:77:LYS:NZ	2.24	0.53
1:D:87:ILE:C	1:D:92:ILE:HD12	2.34	0.53
1:E:13:VAL:O	1:E:13:VAL:HG23	2.08	0.53
1:C:31:ILE:HB	1:C:32:PRO:HD3	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:73:ASP:OD2	1:B:85:SER:OG	2.25	0.52
1:E:157:GLU:O	1:E:158:TYR:HB2	2.10	0.51
1:E:16:PRO:N	1:E:17:PRO:HD2	2.25	0.51
1:C:64:GLU:C	1:C:66:SER:H	2.19	0.51
1:E:99:ILE:HD13	1:E:120:TYR:CD2	2.46	0.51
1:A:16:PRO:N	1:A:17:PRO:CD	2.74	0.50
1:E:16:PRO:CD	1:E:112:SER:OG	2.59	0.50
1:B:86:ILE:O	1:B:92:ILE:CD1	2.59	0.50
1:C:85:SER:HB3	1:C:100:SER:OG	2.11	0.50
1:A:109:GLY:C	1:A:111:GLY:H	2.19	0.50
1:A:45:ILE:HG22	1:A:46:GLU:HB2	1.92	0.50
1:C:139:ARG:HD2	2:C:160:KXN:C6	2.42	0.50
1:B:92:ILE:CD1	1:B:98:LYS:HA	2.42	0.49
1:B:122:THR:HG21	1:B:126:VAL:HG13	1.94	0.49
1:C:34:ILE:HD12	1:C:146:ILE:CG2	2.43	0.49
1:A:25:LEU:HD12	1:A:25:LEU:N	2.28	0.48
1:D:14:ILE:CG2	1:D:18:LYS:HB3	2.43	0.48
1:A:37:GLN:OE1	1:A:37:GLN:N	2.34	0.48
1:D:71:LYS:HB2	1:D:87:ILE:HD12	1.94	0.48
1:E:100:SER:HB2	1:E:119:HIS:HB2	1.95	0.48
1:B:67:TYR:N	1:B:67:TYR:CD1	2.81	0.48
1:D:31:ILE:HB	1:D:32:PRO:CD	2.43	0.48
1:C:109:GLY:O	1:C:111:GLY:N	2.47	0.47
1:B:64:GLU:C	1:B:65:TYR:CD1	2.92	0.47
1:D:30:LEU:HD11	1:D:34:ILE:CD1	2.43	0.47
1:D:31:ILE:N	1:D:32:PRO:CD	2.77	0.47
1:C:31:ILE:N	1:C:32:PRO:HD2	2.29	0.47
1:E:36:PRO:O	1:E:60:GLY:O	2.33	0.47
1:A:85:SER:HB3	1:A:100:SER:OG	2.14	0.47
1:E:16:PRO:HD3	1:E:112:SER:HG	1.76	0.47
1:C:34:ILE:HD12	1:C:146:ILE:HG22	1.97	0.46
2:E:161:KXN:C4	2:E:161:KXN:C96	2.76	0.46
1:A:35:ALA:N	1:A:36:PRO:HD3	2.30	0.46
1:D:23:PHE:O	1:D:27:ALA:HB2	2.15	0.46
1:B:46:GLU:HG2	1:B:47:GLY:H	1.81	0.46
1:B:92:ILE:HD13	1:B:98:LYS:HA	1.97	0.46
1:E:66:SER:OG	1:E:67:TYR:N	2.49	0.46
1:B:50:GLY:O	1:B:51:VAL:C	2.58	0.46
1:A:6:TYR:OH	1:A:137:LYS:HD2	2.17	0.45
1:B:30:LEU:HD11	1:B:34:ILE:HD12	1.98	0.45
1:B:79:ASN:O	1:B:80:PHE:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4:PHE:CZ	1:E:2:GLY:HA3	2.51	0.45
1:C:81:VAL:HG22	1:C:104:LYS:HD3	1.99	0.45
1:A:18:LYS:HG3	1:A:158:TYR:O	2.16	0.45
1:E:69:LYS:NZ	1:E:88:GLU:OE1	2.47	0.45
1:A:28:ASP:HA	3:A:2001:HOH:O	2.16	0.44
1:D:47:GLY:HA3	1:D:53:THR:HA	1.99	0.44
1:C:64:GLU:C	1:C:66:SER:N	2.74	0.44
1:E:45:ILE:HG22	1:E:46:GLU:HG3	1.99	0.44
1:E:69:LYS:HB2	1:E:88:GLU:HB3	2.00	0.43
1:C:16:PRO:HB2	1:C:17:PRO:HD3	2.00	0.43
1:C:16:PRO:CD	1:C:112:SER:OG	2.66	0.43
1:E:135:ALA:O	1:E:139:ARG:HG2	2.18	0.43
1:C:126:VAL:O	1:E:127:GLU:HA	2.18	0.43
1:D:71:LYS:HB2	1:D:87:ILE:HD11	2.00	0.42
1:C:60:GLY:O	1:C:63:SER:O	2.38	0.42
1:C:19:LEU:HA	1:C:19:LEU:HD12	1.83	0.42
1:B:44:ILE:CG2	1:B:46:GLU:O	2.68	0.42
1:A:15:PRO:HB2	1:A:17:PRO:HD2	2.01	0.42
1:C:53:THR:HG22	1:C:54:ILE:N	2.34	0.42
1:E:87:ILE:HG21	1:E:87:ILE:HD13	1.56	0.42
1:A:155:PRO:HB2	1:D:152:LEU:HD13	2.02	0.42
1:D:30:LEU:C	1:D:30:LEU:CD1	2.93	0.42
1:A:86:ILE:HG22	1:A:92:ILE:HD11	2.02	0.42
1:B:53:THR:HG22	1:B:54:ILE:N	2.35	0.42
1:C:2:GLY:HA3	1:E:4:PHE:CE1	2.54	0.42
1:C:30:LEU:HD12	1:C:30:LEU:O	2.20	0.41
1:A:32:PRO:HA	1:A:39:VAL:O	2.20	0.41
1:B:19:LEU:HA	1:B:19:LEU:HD12	1.84	0.41
1:B:57:ILE:HD13	1:B:70:HIS:CE1	2.55	0.41
1:E:2:GLY:O	1:E:3:VAL:HG23	2.21	0.41
1:D:76:ASP:O	1:D:78:ASP:N	2.53	0.41
1:B:154:HIS:N	1:B:155:PRO:HD3	2.35	0.41
1:E:60:GLY:HA2	1:E:62:GLY:H	1.84	0.41
1:A:86:ILE:HG22	1:A:92:ILE:CD1	2.50	0.41
1:B:154:HIS:N	1:B:155:PRO:CD	2.83	0.41
1:D:14:ILE:HG22	1:D:18:LYS:HB3	2.03	0.41
1:D:80:PHE:HB3	1:D:105:LEU:HB2	2.03	0.41
1:D:139:ARG:HD2	2:D:160:KXN:C7	2.51	0.41
1:E:16:PRO:N	1:E:17:PRO:CD	2.84	0.41
1:E:134:LYS:O	1:E:135:ALA:C	2.63	0.41
1:C:92:ILE:CD1	1:C:98:LYS:HA	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:50:GLY:O	1:D:51:VAL:C	2.64	0.41
1:D:134:LYS:O	1:D:135:ALA:C	2.63	0.41
1:B:34:ILE:HD11	1:B:150:HIS:CG	2.56	0.40
1:B:65:TYR:CD1	1:B:65:TYR:N	2.89	0.40
1:C:46:GLU:O	1:C:46:GLU:HG3	2.20	0.40
1:A:28:ASP:OD2	1:A:55:LYS:HE2	2.21	0.40
1:A:31:ILE:O	1:A:35:ALA:N	2.52	0.40
1:D:86:ILE:HD13	1:D:86:ILE:HG21	1.92	0.40
1:E:60:GLY:HA3	1:E:61:GLU:HA	1.85	0.40
1:A:23:PHE:O	1:A:23:PHE:CG	2.73	0.40
1:B:34:ILE:HD13	1:B:34:ILE:HG21	1.86	0.40
1:E:40:LYS:NZ	1:E:61:GLU:OE1	2.47	0.40
1:E:69:LYS:HE2	1:E:88:GLU:OE1	2.21	0.40
1:A:89:GLY:O	1:A:90:ASP:C	2.63	0.40
1:D:70:HIS:CE1	2:D:160:KXN:O3	2.74	0.40
1:B:14:ILE:CG2	1:B:18:LYS:HB3	2.51	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	159/161 (99%)	148 (93%)	11 (7%)	0	100	100
1	B	159/161 (99%)	148 (93%)	10 (6%)	1 (1%)	21	56
1	C	159/161 (99%)	146 (92%)	12 (8%)	1 (1%)	21	56
1	D	152/161 (94%)	139 (91%)	12 (8%)	1 (1%)	18	53
1	E	159/161 (99%)	143 (90%)	15 (9%)	1 (1%)	21	56
All	All	788/805 (98%)	724 (92%)	60 (8%)	4 (0%)	24	60

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	47	GLY
1	D	77	LYS
1	C	36	PRO
1	E	93	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	132/132 (100%)	121 (92%)	11 (8%)	10	37
1	B	132/132 (100%)	130 (98%)	2 (2%)	57	80
1	C	132/132 (100%)	123 (93%)	9 (7%)	14	45
1	D	128/132 (97%)	116 (91%)	12 (9%)	8	32
1	E	132/132 (100%)	123 (93%)	9 (7%)	14	45
All	All	656/660 (99%)	613 (93%)	43 (7%)	15	46

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	PRO
1	A	19	LEU
1	A	54	ILE
1	A	75	ILE
1	A	87	ILE
1	A	102	GLU
1	A	103	ILE
1	A	128	ILE
1	A	137	LYS
1	A	139	ARG
1	A	145	LYS
1	B	54	ILE
1	B	83	SER
1	C	7	GLU
1	C	37	GLN
1	C	54	ILE

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Mol	Chain	Res	Type
1	C	59	LEU
1	C	81	VAL
1	C	98	LYS
1	C	113	ILE
1	C	115	LYS
1	C	131	GLU
1	D	9	GLU
1	D	14	ILE
1	D	31	ILE
1	D	44	ILE
1	D	45	ILE
1	D	56	LYS
1	D	81	VAL
1	D	85	SER
1	D	87	ILE
1	D	96	ILE
1	D	146	ILE
1	D	152	LEU
1	E	5	THR
1	E	13	VAL
1	E	25	LEU
1	E	34	ILE
1	E	54	ILE
1	E	92	ILE
1	E	99	ILE
1	E	105	LEU
1	E	131	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	150	HIS
1	C	159	ASN
1	D	58	HIS

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](#)

6 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$
2	KXN	C	160	-	23,23,23	3.50	7 (30%)	34,34,34	2.18	12 (35%)
2	KXN	A	160	-	23,23,23	3.58	5 (21%)	34,34,34	2.65	21 (61%)
2	KXN	D	160	-	23,23,23	3.28	7 (30%)	34,34,34	2.58	15 (44%)
2	KXN	E	161	-	23,23,23	5.51	12 (52%)	34,34,34	4.62	19 (55%)
2	KXN	E	160	-	23,23,23	3.03	11 (47%)	34,34,34	1.86	9 (26%)
2	KXN	B	160	-	23,23,23	3.71	7 (30%)	34,34,34	2.65	17 (50%)

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	KXN	C	160	-	-	0/4/16/16	0/3/3/3
2	KXN	A	160	-	-	0/4/16/16	0/3/3/3
2	KXN	D	160	-	-	2/4/16/16	0/3/3/3
2	KXN	E	161	-	-	1/4/16/16	0/3/3/3
2	KXN	E	160	-	-	4/4/16/16	0/3/3/3
2	KXN	B	160	-	-	2/4/16/16	0/3/3/3

All (49) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	161	KXN	C91-C2	-15.54	1.24	1.51
2	B	160	KXN	C3-C2	11.25	1.70	1.52
2	E	161	KXN	C3-C2	-11.17	1.34	1.52
2	E	161	KXN	O1-C2	10.86	1.61	1.45
2	A	160	KXN	C91-C2	-10.11	1.33	1.51
2	C	160	KXN	C91-C2	-9.55	1.34	1.51
2	D	160	KXN	C3-C2	9.47	1.68	1.52
2	C	160	KXN	C3-C2	8.65	1.66	1.52
2	A	160	KXN	C3-C2	8.57	1.66	1.52
2	A	160	KXN	C4-C10	-8.07	1.39	1.51
2	E	161	KXN	C4-C10	-7.92	1.39	1.51
2	E	160	KXN	C4-C10	-7.85	1.39	1.51
2	D	160	KXN	C4-C10	-7.80	1.39	1.51
2	B	160	KXN	C4-C10	-7.42	1.40	1.51
2	C	160	KXN	C4-C10	-7.12	1.40	1.51
2	E	161	KXN	C93-C94	7.10	1.52	1.40
2	B	160	KXN	C91-C2	-6.85	1.39	1.51
2	E	160	KXN	C91-C2	-6.78	1.39	1.51
2	D	160	KXN	C91-C2	-6.52	1.40	1.51
2	B	160	KXN	C4-C3	-6.45	1.42	1.52
2	E	161	KXN	C9-C10	-5.61	1.31	1.40
2	E	160	KXN	C4-C3	-5.07	1.44	1.52
2	A	160	KXN	C4-C3	-5.03	1.44	1.52
2	C	160	KXN	O1-C2	-4.92	1.37	1.45
2	D	160	KXN	C4-C3	-4.79	1.45	1.52
2	C	160	KXN	O3-C3	4.16	1.52	1.43
2	E	160	KXN	O1-C2	-4.00	1.39	1.45
2	E	161	KXN	C6-C7	-3.91	1.33	1.39
2	A	160	KXN	O1-C2	-3.87	1.39	1.45
2	B	160	KXN	O3-C3	3.51	1.50	1.43
2	E	161	KXN	C92-C93	-3.40	1.34	1.38
2	C	160	KXN	C4-C3	-3.31	1.47	1.52
2	E	161	KXN	O3-C3	-3.27	1.36	1.43
2	E	160	KXN	C6-C5	-3.12	1.34	1.38
2	E	160	KXN	C3-C2	2.91	1.57	1.52
2	B	160	KXN	C92-C93	-2.84	1.34	1.38
2	E	161	KXN	O93-C93	2.77	1.41	1.36
2	D	160	KXN	C9-C10	2.76	1.44	1.40
2	E	161	KXN	O71-C7	-2.61	1.31	1.37
2	D	160	KXN	O1-C2	-2.61	1.41	1.45
2	E	160	KXN	O51-C5	-2.60	1.31	1.36
2	E	161	KXN	C6-C5	-2.55	1.35	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	160	KXN	C9-C10	2.41	1.44	1.40
2	E	160	KXN	C8-C9	-2.40	1.34	1.38
2	D	160	KXN	C93-C94	2.33	1.44	1.40
2	E	160	KXN	O94-C94	-2.24	1.31	1.36
2	E	160	KXN	C8-C7	-2.17	1.35	1.39
2	C	160	KXN	C9-C10	2.15	1.43	1.40
2	E	160	KXN	C5-C10	-2.01	1.36	1.40

All (93) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	161	KXN	C96-C91-C92	10.88	131.35	118.74
2	E	161	KXN	O1-C2-C91	-10.83	84.36	107.44
2	E	161	KXN	C93-C92-C91	-8.05	111.75	120.49
2	E	161	KXN	O1-C9-C10	-7.41	109.70	122.20
2	E	161	KXN	C91-C2-C3	-7.19	100.02	114.23
2	E	161	KXN	O1-C9-C8	6.88	128.04	116.29
2	E	161	KXN	O94-C94-C95	-6.17	102.82	119.36
2	B	160	KXN	O3-C3-C2	6.10	121.42	110.33
2	E	161	KXN	C95-C96-C91	-5.87	115.32	121.18
2	E	161	KXN	O94-C94-C93	5.81	133.95	118.42
2	C	160	KXN	O3-C3-C2	5.80	120.89	110.33
2	E	161	KXN	O93-C93-C94	5.79	133.90	118.42
2	D	160	KXN	O1-C2-C91	5.76	119.71	107.44
2	A	160	KXN	O1-C2-C3	-5.18	101.05	109.96
2	E	161	KXN	C10-C4-C3	4.96	122.70	111.18
2	E	161	KXN	O93-C93-C92	-4.92	106.18	119.45
2	A	160	KXN	C93-C92-C91	-4.91	115.16	120.49
2	E	160	KXN	C95-C94-C93	4.91	124.90	119.66
2	A	160	KXN	C96-C91-C92	4.88	124.39	118.74
2	C	160	KXN	C96-C91-C92	4.67	124.15	118.74
2	B	160	KXN	C4-C10-C9	4.50	128.40	121.01
2	D	160	KXN	C4-C10-C9	4.49	128.37	121.01
2	D	160	KXN	C96-C95-C94	-4.46	116.03	120.50
2	B	160	KXN	O3-C3-C4	-4.43	99.35	109.60
2	B	160	KXN	C96-C91-C92	4.36	123.79	118.74
2	B	160	KXN	C96-C95-C94	-4.29	116.20	120.50
2	D	160	KXN	O1-C2-C3	4.24	117.26	109.96
2	B	160	KXN	C4-C10-C5	-4.22	111.54	120.81
2	C	160	KXN	C9-O1-C2	-4.21	107.47	116.40
2	D	160	KXN	C93-C92-C91	-4.12	116.01	120.49
2	E	161	KXN	C96-C91-C2	-4.10	112.97	120.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	160	KXN	C96-C95-C94	-4.09	116.41	120.50
2	D	160	KXN	C4-C10-C5	-4.07	111.88	120.81
2	D	160	KXN	C96-C91-C92	3.97	123.34	118.74
2	D	160	KXN	O3-C3-C2	3.86	117.34	110.33
2	A	160	KXN	O3-C3-C2	3.82	117.28	110.33
2	A	160	KXN	O3-C3-C4	-3.72	101.00	109.60
2	D	160	KXN	O3-C3-C4	-3.71	101.02	109.60
2	B	160	KXN	C5-C6-C7	-3.64	116.31	119.67
2	E	160	KXN	C9-O1-C2	-3.61	108.74	116.40
2	B	160	KXN	C95-C94-C93	3.48	123.37	119.66
2	B	160	KXN	O1-C2-C3	3.40	115.81	109.96
2	C	160	KXN	C4-C10-C9	3.37	126.54	121.01
2	E	160	KXN	C96-C91-C92	3.34	122.61	118.74
2	E	161	KXN	C95-C94-C93	3.33	123.21	119.66
2	C	160	KXN	C93-C92-C91	-3.25	116.96	120.49
2	A	160	KXN	C4-C10-C5	-3.19	113.80	120.81
2	C	160	KXN	C96-C95-C94	-3.16	117.33	120.50
2	B	160	KXN	C9-O1-C2	-3.11	109.80	116.40
2	A	160	KXN	C91-C2-C3	-3.06	108.19	114.23
2	E	160	KXN	C92-C93-C94	-3.03	117.08	119.89
2	D	160	KXN	C4-C3-C2	2.92	113.19	109.27
2	E	161	KXN	C4-C3-C2	-2.90	105.37	109.27
2	A	160	KXN	O93-C93-C94	-2.86	110.79	118.42
2	D	160	KXN	C91-C2-C3	-2.83	108.65	114.23
2	E	161	KXN	C4-C10-C5	2.82	126.99	120.81
2	A	160	KXN	C5-C10-C9	2.82	120.69	117.08
2	E	160	KXN	C95-C96-C91	-2.81	118.38	121.18
2	A	160	KXN	C92-C93-C94	2.76	122.44	119.89
2	A	160	KXN	C4-C10-C9	2.74	125.51	121.01
2	A	160	KXN	C9-O1-C2	-2.74	110.58	116.40
2	B	160	KXN	C6-C7-C8	2.72	124.20	120.47
2	A	160	KXN	O93-C93-C92	2.71	126.77	119.45
2	A	160	KXN	C92-C91-C2	-2.69	113.95	119.88
2	E	161	KXN	C92-C91-C2	-2.67	113.98	119.88
2	C	160	KXN	C4-C10-C5	-2.66	114.96	120.81
2	C	160	KXN	C95-C94-C93	2.62	122.45	119.66
2	E	161	KXN	C4-C10-C9	-2.61	116.72	121.01
2	E	161	KXN	C96-C95-C94	-2.54	117.96	120.50
2	D	160	KXN	C5-C6-C7	-2.53	117.33	119.67
2	A	160	KXN	O94-C94-C95	2.50	126.07	119.36
2	A	160	KXN	C8-C9-C10	-2.47	119.30	122.06
2	E	160	KXN	C4-C3-C2	2.45	112.56	109.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	160	KXN	O94-C94-C93	-2.43	111.95	118.42
2	B	160	KXN	C95-C96-C91	-2.39	118.80	121.18
2	C	160	KXN	C95-C96-C91	-2.37	118.82	121.18
2	D	160	KXN	C8-C9-C10	-2.34	119.44	122.06
2	E	160	KXN	C96-C95-C94	-2.34	118.16	120.50
2	B	160	KXN	C5-C10-C9	2.32	120.06	117.08
2	A	160	KXN	O1-C2-C91	2.32	112.38	107.44
2	C	160	KXN	O94-C94-C93	-2.27	112.37	118.42
2	E	160	KXN	C4-C10-C9	2.26	124.72	121.01
2	E	160	KXN	O1-C2-C3	-2.25	106.09	109.96
2	A	160	KXN	C4-C3-C2	2.22	112.24	109.27
2	B	160	KXN	C93-C92-C91	-2.21	118.09	120.49
2	B	160	KXN	O51-C5-C6	2.19	125.37	119.45
2	A	160	KXN	C95-C94-C93	2.18	121.98	119.66
2	C	160	KXN	O94-C94-C95	2.17	125.17	119.36
2	C	160	KXN	O3-C3-C4	-2.14	104.66	109.60
2	B	160	KXN	C8-C9-C10	-2.13	119.68	122.06
2	D	160	KXN	C6-C7-C8	2.11	123.38	120.47
2	B	160	KXN	O51-C5-C10	-2.09	112.95	117.81
2	D	160	KXN	C5-C10-C9	2.08	119.74	117.08

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	160	KXN	C3-C2-C91-C96
2	E	160	KXN	C3-C2-C91-C92
2	B	160	KXN	O1-C2-C91-C92
2	D	160	KXN	O1-C2-C91-C96
2	E	160	KXN	O1-C2-C91-C92
2	B	160	KXN	O1-C2-C91-C96
2	E	160	KXN	O1-C2-C91-C96
2	D	160	KXN	O1-C2-C91-C92
2	E	161	KXN	C3-C2-C91-C92

There are no ring outliers.

6 monomers are involved in 12 short contacts:

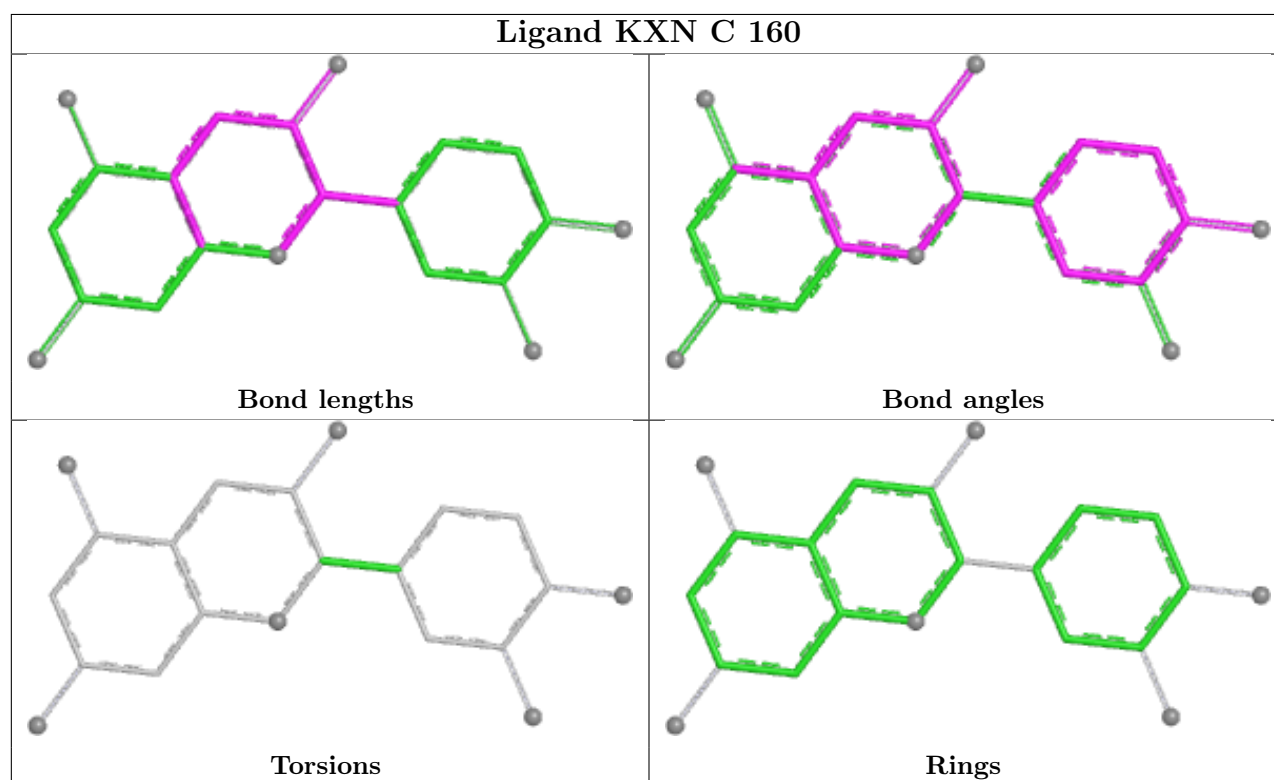
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	160	KXN	1	0
2	A	160	KXN	1	0

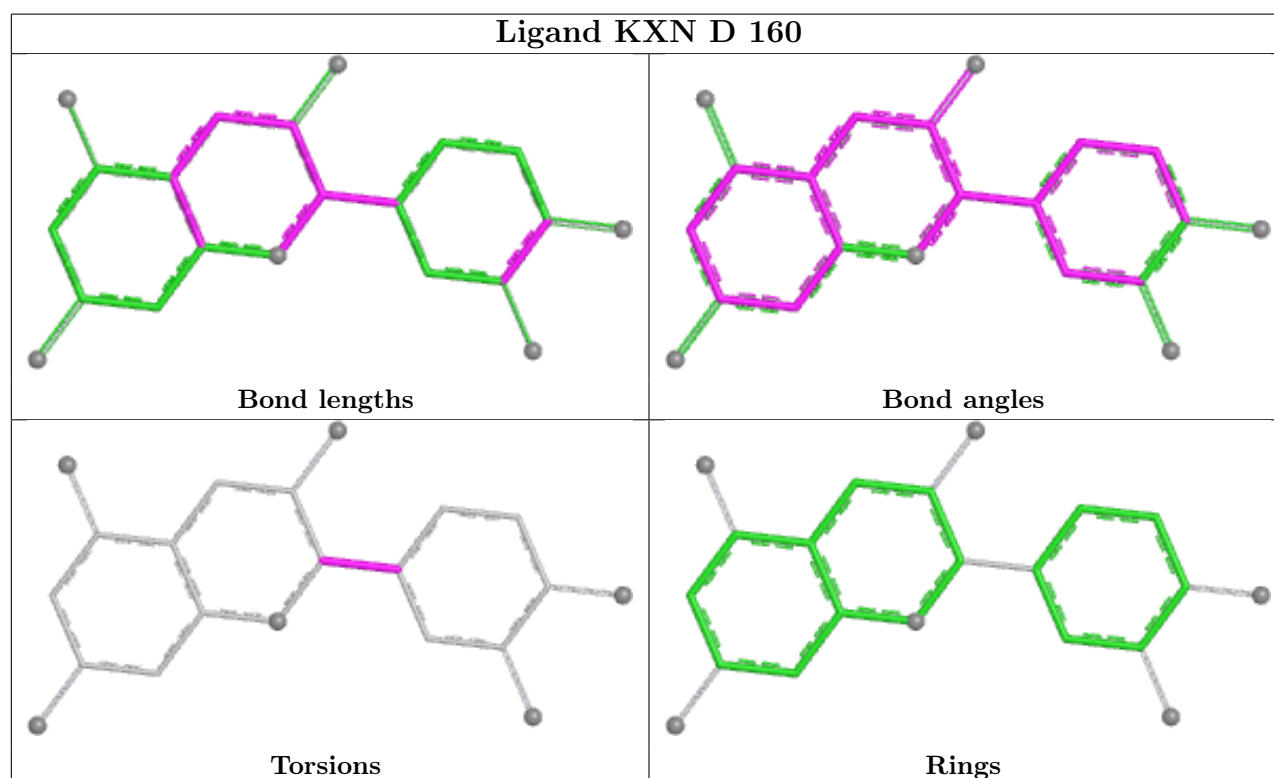
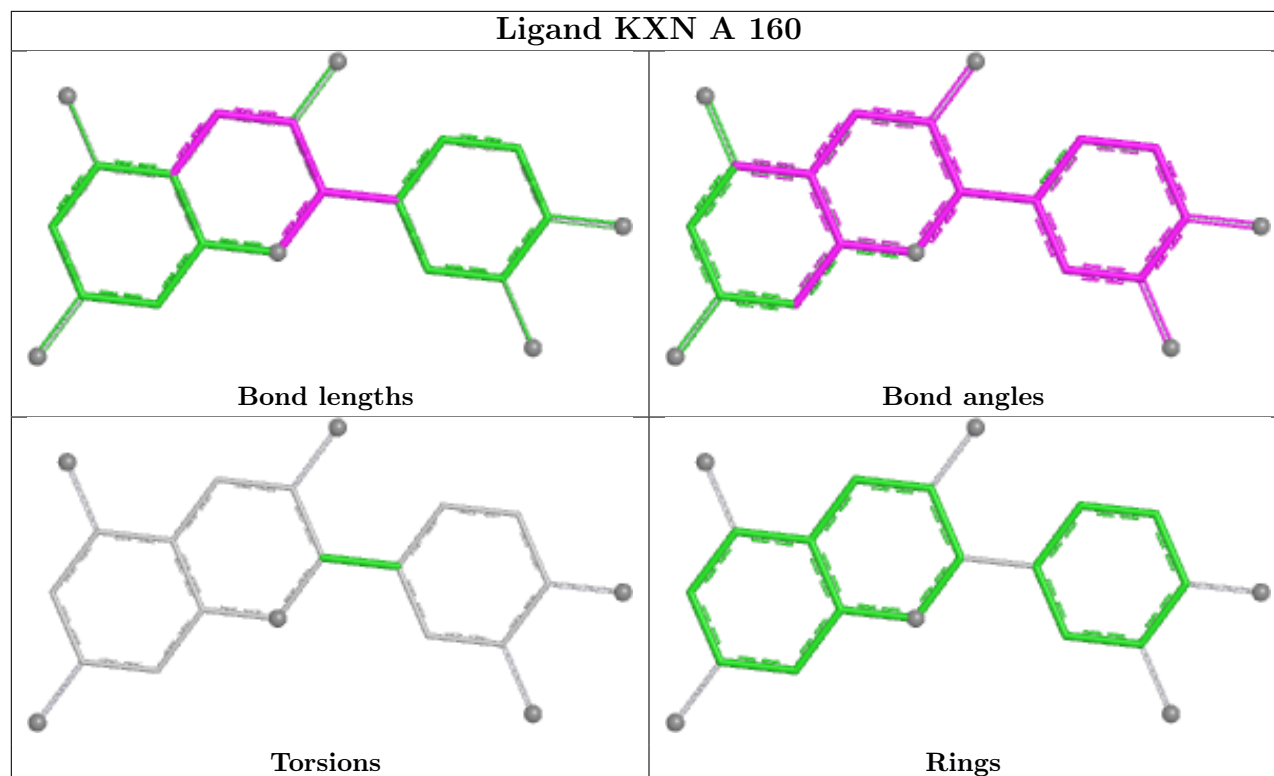
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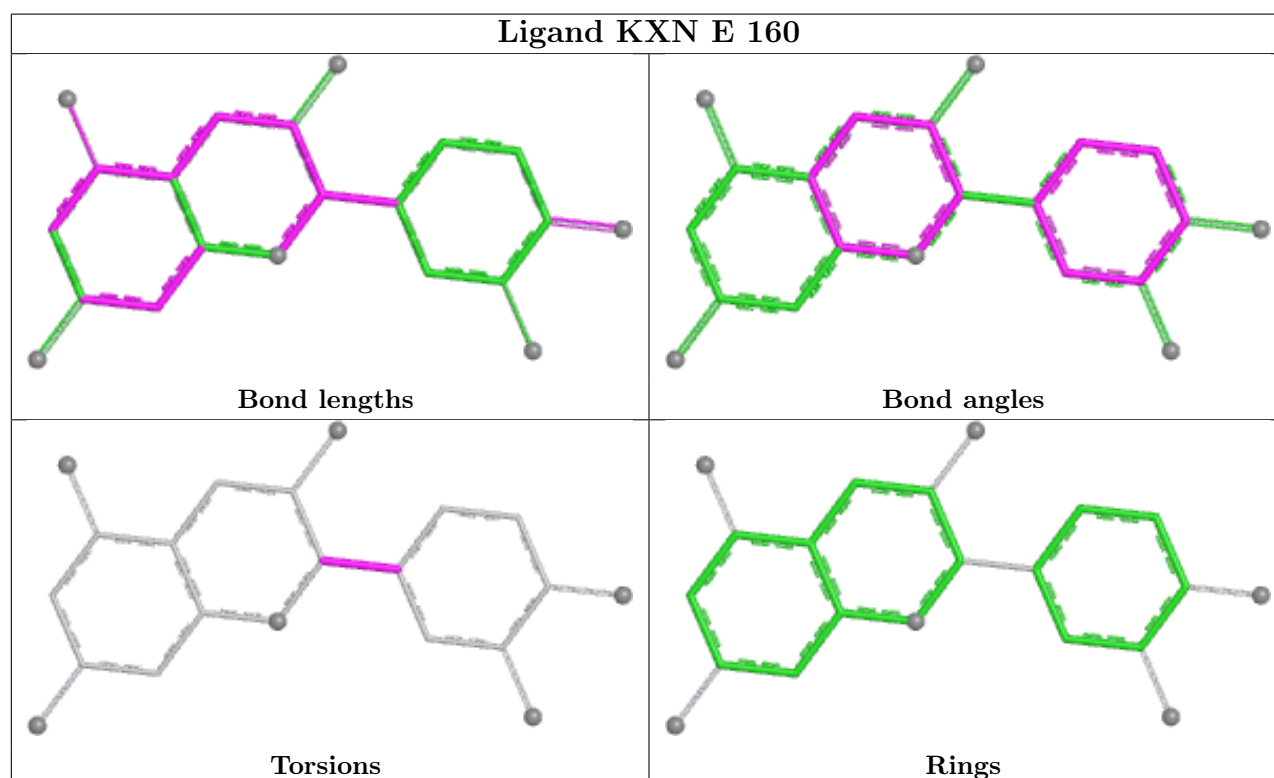
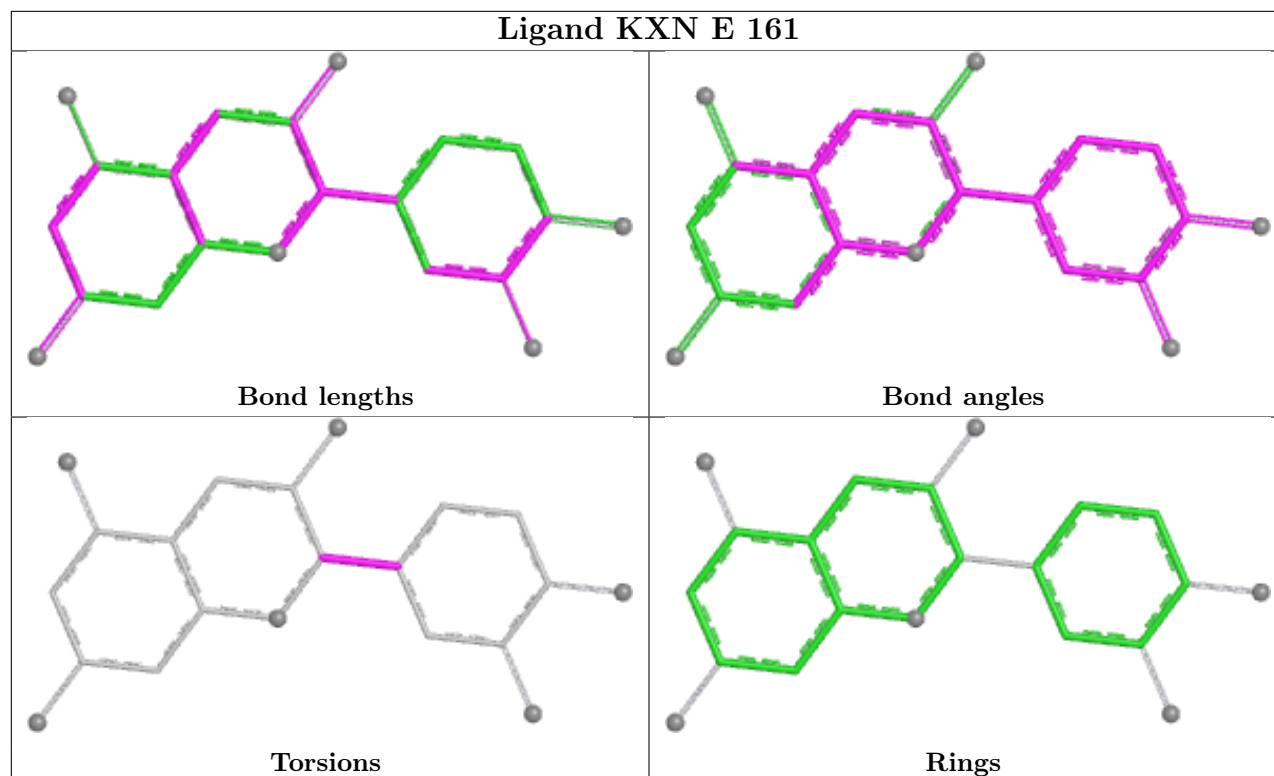
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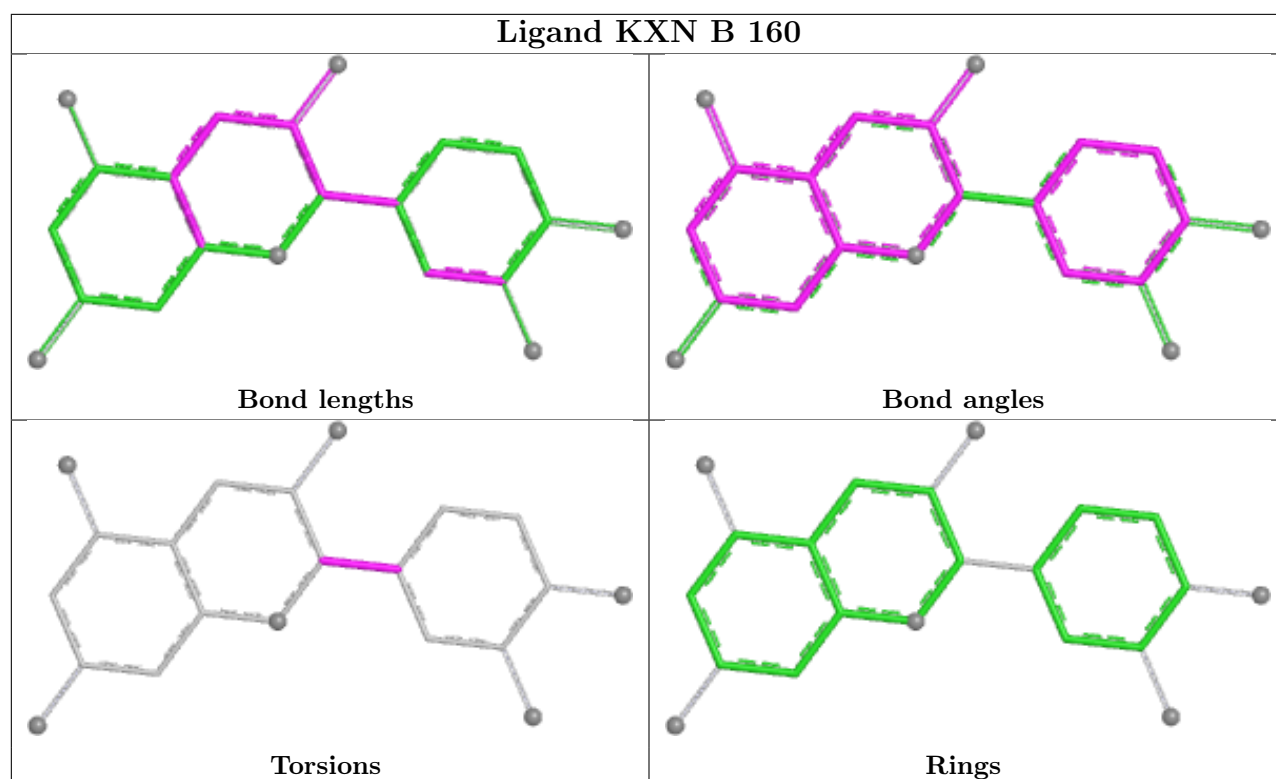
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	160	KXN	5	0
2	E	161	KXN	3	0
2	E	160	KXN	1	0
2	B	160	KXN	1	0

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	161/161 (100%)	-0.51	1 (0%) 85 69	42, 60, 100, 121	0
1	B	161/161 (100%)	-0.47	5 (3%) 51 30	37, 62, 120, 142	0
1	C	161/161 (100%)	-0.20	8 (4%) 34 18	45, 77, 129, 185	0
1	D	156/161 (96%)	-0.36	4 (2%) 57 34	50, 72, 115, 134	0
1	E	161/161 (100%)	-0.09	8 (4%) 34 18	49, 76, 115, 151	0
All	All	800/805 (99%)	-0.33	26 (3%) 49 28	37, 71, 118, 185	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	93	GLY	4.8
1	B	67	TYR	4.2
1	E	67	TYR	4.1
1	D	37	GLN	3.7
1	C	65	TYR	3.6
1	C	62	GLY	3.5
1	C	67	TYR	3.4
1	A	-1	ALA	3.3
1	E	60	GLY	3.3
1	C	61	GLU	3.2
1	D	58	HIS	3.2
1	B	61	GLU	3.2
1	E	-1	ALA	3.0
1	E	91	ALA	2.9
1	C	46	GLU	2.9
1	C	-1	ALA	2.8
1	C	43	GLU	2.8
1	D	60	GLY	2.6
1	E	77	LYS	2.5
1	E	95	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	E	158	TYR	2.4
1	B	-1	ALA	2.2
1	C	63	SER	2.2
1	B	65	TYR	2.1
1	B	62	GLY	2.1
1	D	66	SER	2.1

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

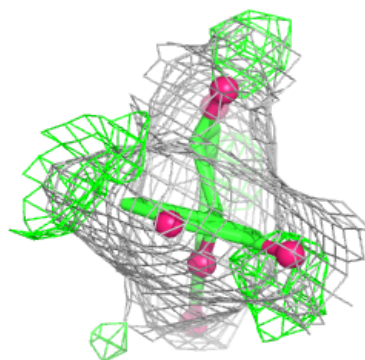
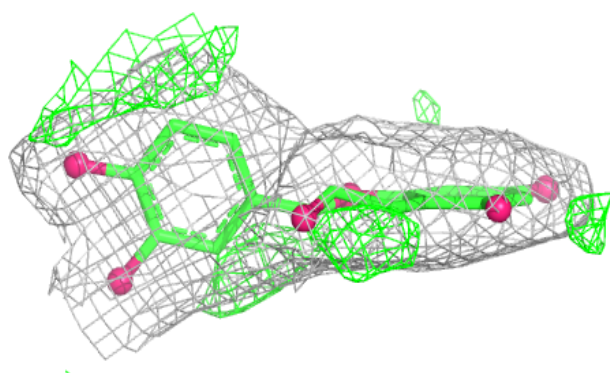
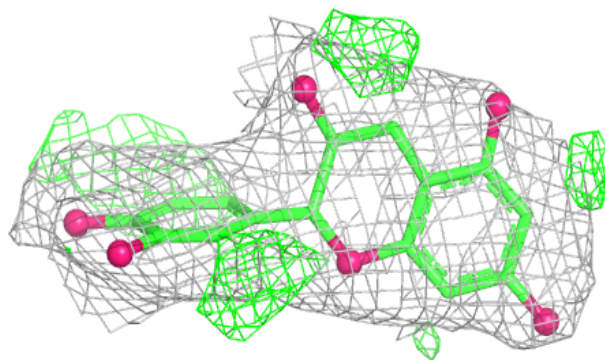
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	KXN	D	160	21/21	0.88	0.14	83,113,130,131	0
2	KXN	E	161	21/21	0.91	0.20	43,77,105,182	0
2	KXN	B	160	21/21	0.92	0.12	60,85,99,109	0
2	KXN	C	160	21/21	0.92	0.12	77,111,135,145	0
2	KXN	A	160	21/21	0.93	0.11	62,85,97,113	0
2	KXN	E	160	21/21	0.96	0.09	66,79,88,91	0

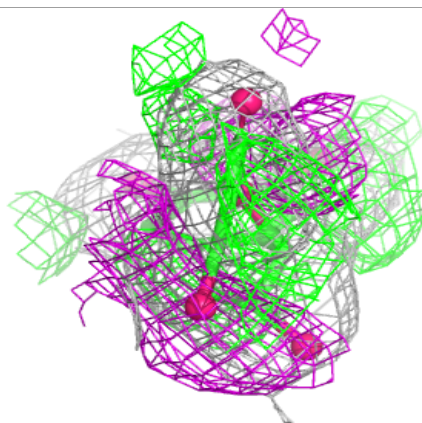
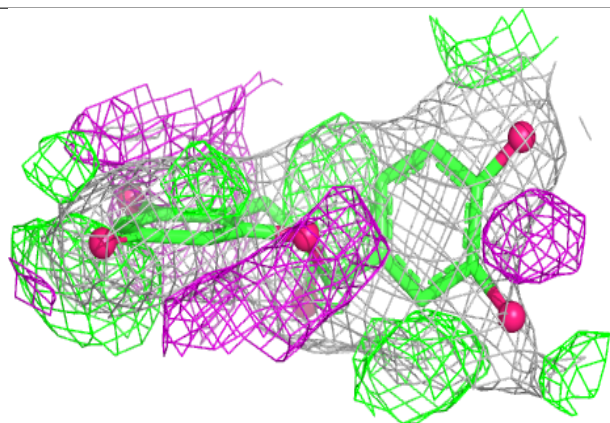
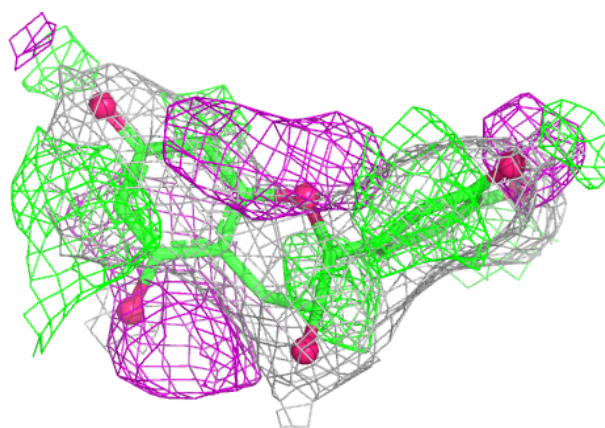
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around KXN D 160:

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

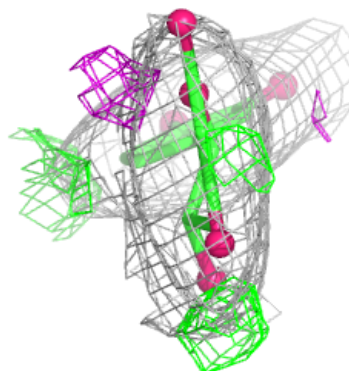
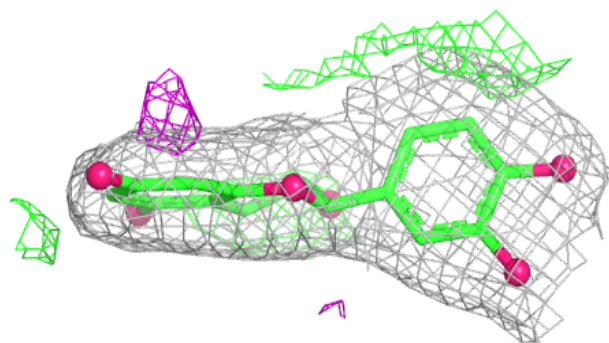
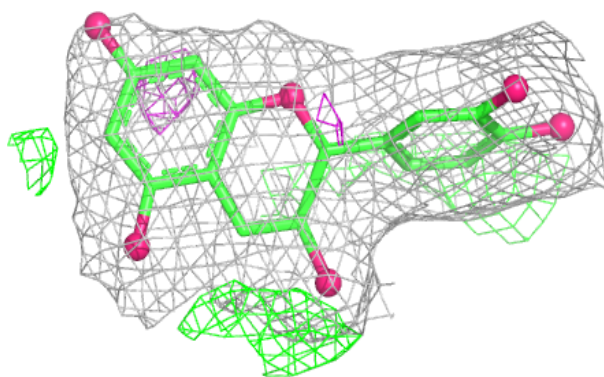
**Electron density around KXN E 161:**

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

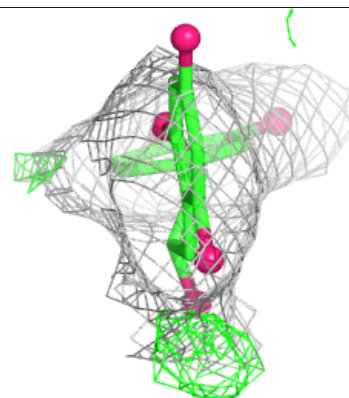
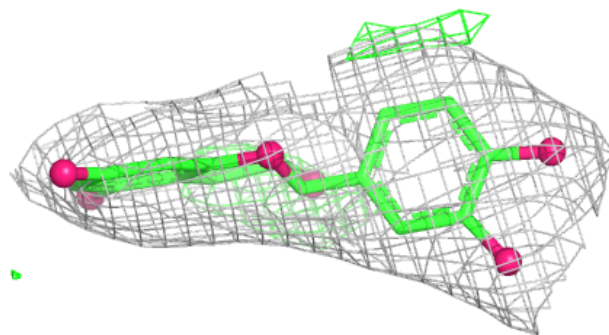
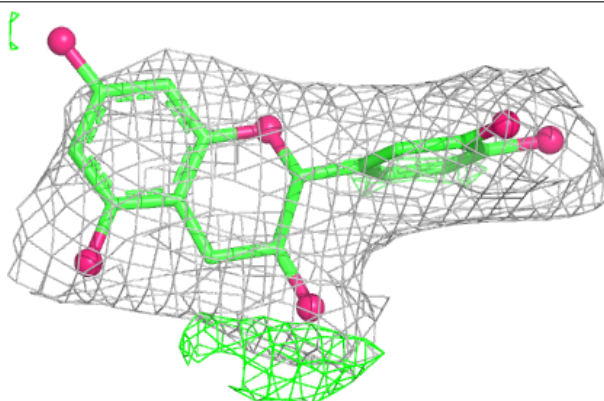


Electron density around KXN B 160:

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

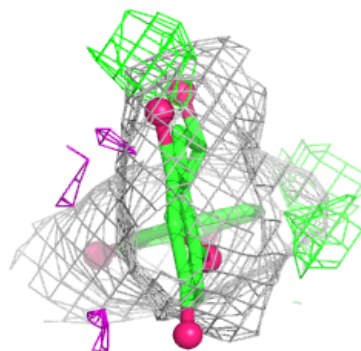
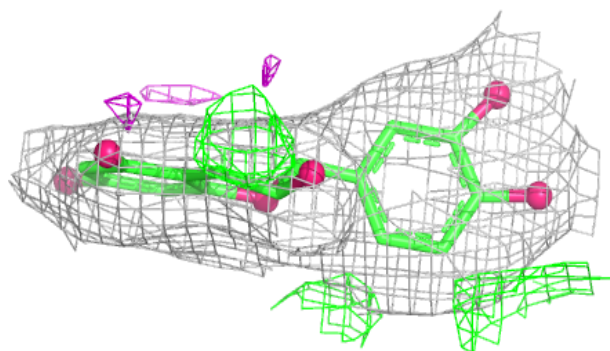
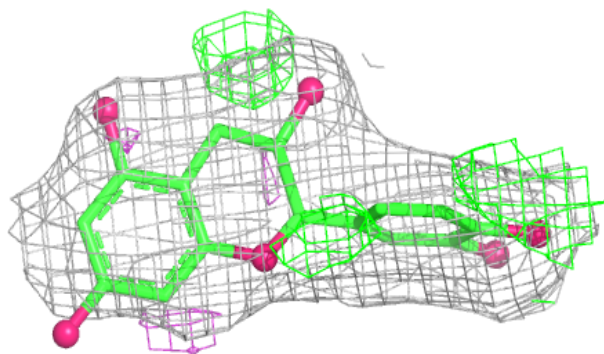
**Electron density around KXN C 160:**

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

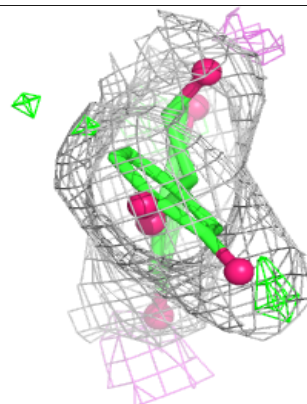
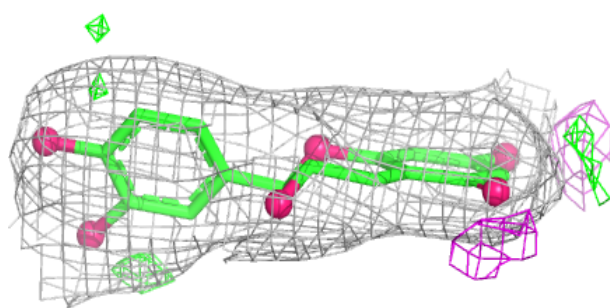
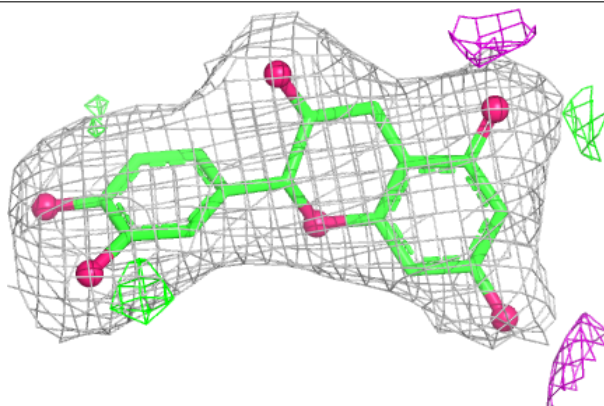


Electron density around KXN A 160:

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

**Electron density around KXN E 160:**

$2mF_o-DF_c$ (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.