



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:12 PM UTC

PDB ID : 4MOJ / pdb_00004moj
Title : Pyranose 2-oxidase H450G/V546C double mutant with 2-fluorinated glucose
Authors : Tan, T.C.; Spadiut, O.; Gandini, R.; Haltrich, D.; Divne, C.
Deposited on : 2013-09-12
Resolution : 2.00 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

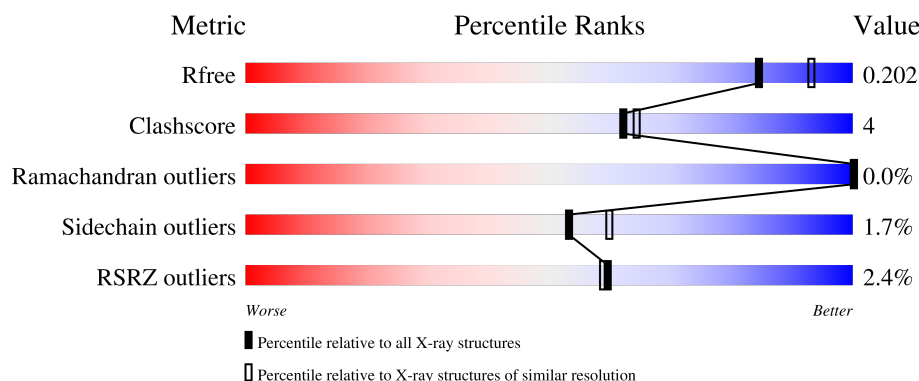
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	633	
1	B	633	
1	C	633	
1	D	633	

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
5	MES	D	804	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 20415 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 Pyranose 2-oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	576	Total	C	N	O	S	0	0	0
			4535	2862	775	872	26			
1	B	576	Total	C	N	O	S	0	1	0
			4541	2866	776	873	26			
1	C	574	Total	C	N	O	S	0	0	0
			4519	2853	773	868	25			
1	D	575	Total	C	N	O	S	0	0	0
			4526	2857	774	870	25			

There are 56 discrepancies between the modelled and reference sequences:

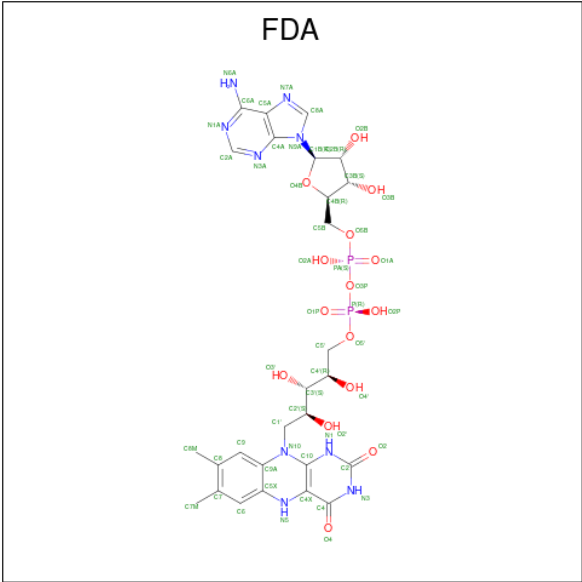
Chain	Residue	Modelled	Actual	Comment	Reference
A	2	ALA	SER	cloning artifact	UNP Q7ZA32
A	450	GLY	HIS	engineered mutation	UNP Q7ZA32
A	546	CYS	VAL	engineered mutation	UNP Q7ZA32
A	623	ALA	-	expression tag	UNP Q7ZA32
A	624	ALA	-	expression tag	UNP Q7ZA32
A	625	ALA	-	expression tag	UNP Q7ZA32
A	626	LEU	-	expression tag	UNP Q7ZA32
A	627	GLU	-	expression tag	UNP Q7ZA32
A	628	HIS	-	expression tag	UNP Q7ZA32
A	629	HIS	-	expression tag	UNP Q7ZA32
A	630	HIS	-	expression tag	UNP Q7ZA32
A	631	HIS	-	expression tag	UNP Q7ZA32
A	632	HIS	-	expression tag	UNP Q7ZA32
A	633	HIS	-	expression tag	UNP Q7ZA32
B	2	ALA	SER	cloning artifact	UNP Q7ZA32
B	450	GLY	HIS	engineered mutation	UNP Q7ZA32
B	546	CYS	VAL	engineered mutation	UNP Q7ZA32
B	623	ALA	-	expression tag	UNP Q7ZA32
B	624	ALA	-	expression tag	UNP Q7ZA32
B	625	ALA	-	expression tag	UNP Q7ZA32
B	626	LEU	-	expression tag	UNP Q7ZA32

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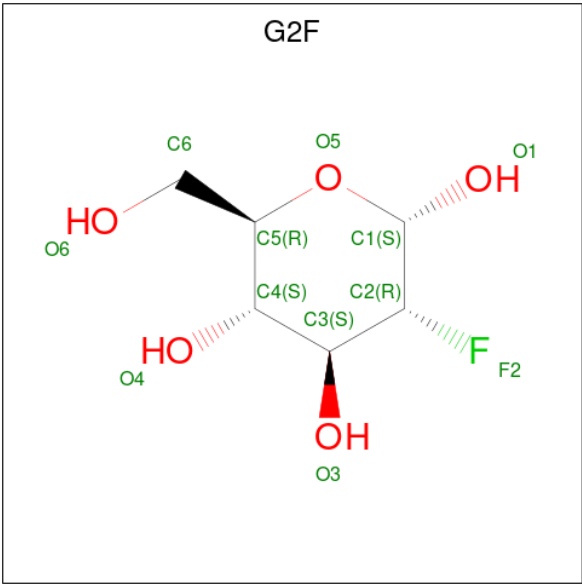
Chain	Residue	Modelled	Actual	Comment	Reference
B	627	GLU	-	expression tag	UNP Q7ZA32
B	628	HIS	-	expression tag	UNP Q7ZA32
B	629	HIS	-	expression tag	UNP Q7ZA32
B	630	HIS	-	expression tag	UNP Q7ZA32
B	631	HIS	-	expression tag	UNP Q7ZA32
B	632	HIS	-	expression tag	UNP Q7ZA32
B	633	HIS	-	expression tag	UNP Q7ZA32
C	2	ALA	SER	cloning artifact	UNP Q7ZA32
C	450	GLY	HIS	engineered mutation	UNP Q7ZA32
C	546	CYS	VAL	engineered mutation	UNP Q7ZA32
C	623	ALA	-	expression tag	UNP Q7ZA32
C	624	ALA	-	expression tag	UNP Q7ZA32
C	625	ALA	-	expression tag	UNP Q7ZA32
C	626	LEU	-	expression tag	UNP Q7ZA32
C	627	GLU	-	expression tag	UNP Q7ZA32
C	628	HIS	-	expression tag	UNP Q7ZA32
C	629	HIS	-	expression tag	UNP Q7ZA32
C	630	HIS	-	expression tag	UNP Q7ZA32
C	631	HIS	-	expression tag	UNP Q7ZA32
C	632	HIS	-	expression tag	UNP Q7ZA32
C	633	HIS	-	expression tag	UNP Q7ZA32
D	2	ALA	SER	cloning artifact	UNP Q7ZA32
D	450	GLY	HIS	engineered mutation	UNP Q7ZA32
D	546	CYS	VAL	engineered mutation	UNP Q7ZA32
D	623	ALA	-	expression tag	UNP Q7ZA32
D	624	ALA	-	expression tag	UNP Q7ZA32
D	625	ALA	-	expression tag	UNP Q7ZA32
D	626	LEU	-	expression tag	UNP Q7ZA32
D	627	GLU	-	expression tag	UNP Q7ZA32
D	628	HIS	-	expression tag	UNP Q7ZA32
D	629	HIS	-	expression tag	UNP Q7ZA32
D	630	HIS	-	expression tag	UNP Q7ZA32
D	631	HIS	-	expression tag	UNP Q7ZA32
D	632	HIS	-	expression tag	UNP Q7ZA32
D	633	HIS	-	expression tag	UNP Q7ZA32

- Molecule 2 is DIHYDROFLAVINE-ADENINE DINUCLEOTIDE (CCD ID: FDA) (formula: $C_{27}H_{35}N_9O_{15}P_2$).



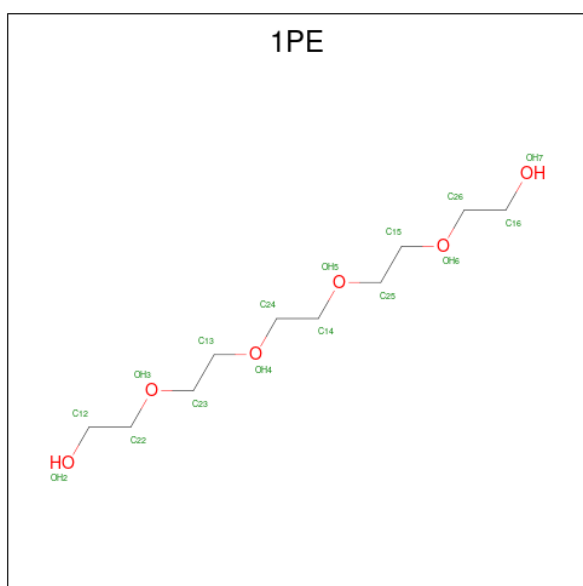
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
2	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 3 is 2-deoxy-2-fluoro-alpha-D-glucopyranose (CCD ID: G2F) (formula: C₆H₁₁FO₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	F	O	0	0
			12	6	1	5		
3	B	1	Total	C	F	O	0	0
			12	6	1	5		
3	C	1	Total	C	F	O	0	0
			12	6	1	5		
3	D	1	Total	C	F	O	0	0
			12	6	1	5		

- Molecule 4 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			12	8	4		
4	B	1	Total	C	O	0	0
			16	10	6		
4	C	1	Total	C	O	0	0
			16	10	6		
4	D	1	Total	C	O	0	0
			16	10	6		

- Molecule 5 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (CCD ID: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
5	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
5	D	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
5	D	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

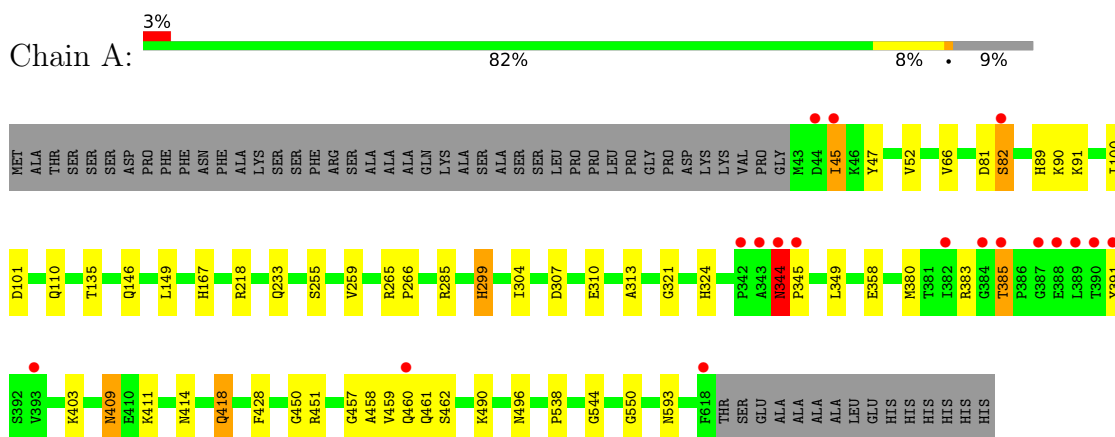
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	466	Total	O	0	0
			466	466		
6	B	561	Total	O	0	0
			561	561		
6	C	378	Total	O	0	0
			378	378		
6	D	521	Total	O	0	0
			521	521		

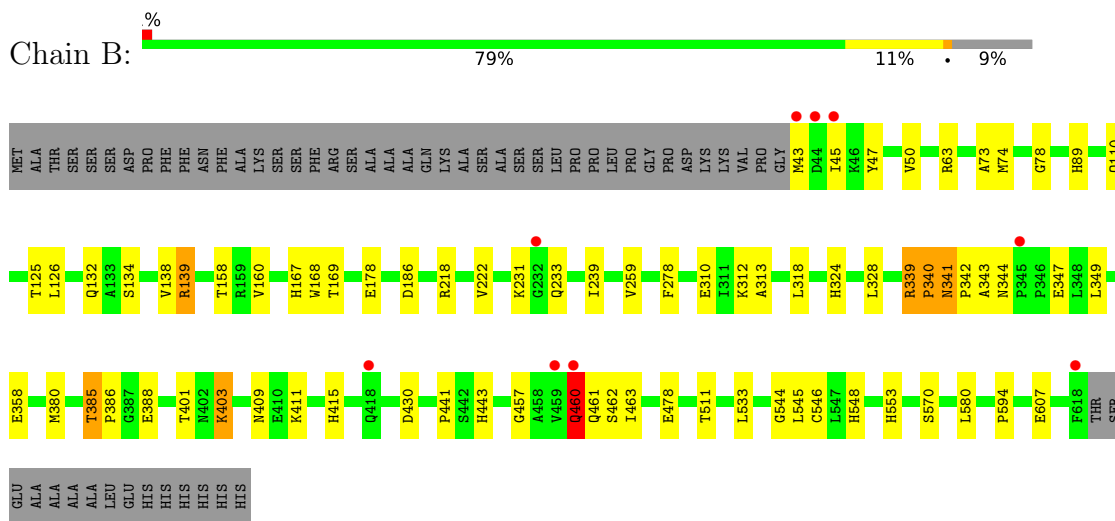
3 Residue-property plots [i](#)

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.

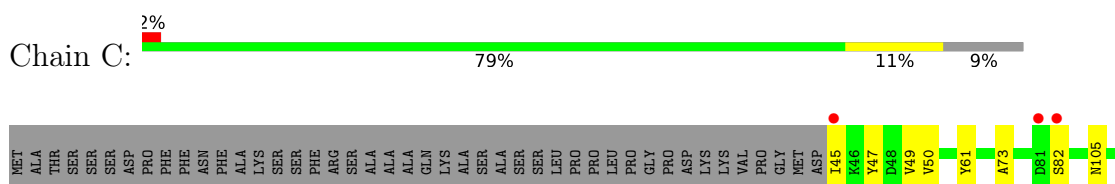
• Molecule 1: Pyranose 2-oxidase

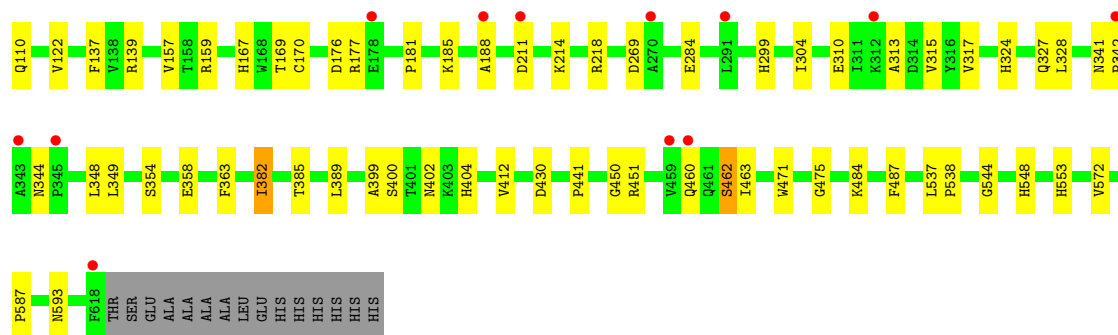


• Molecule 1: Pyranose 2-oxidase

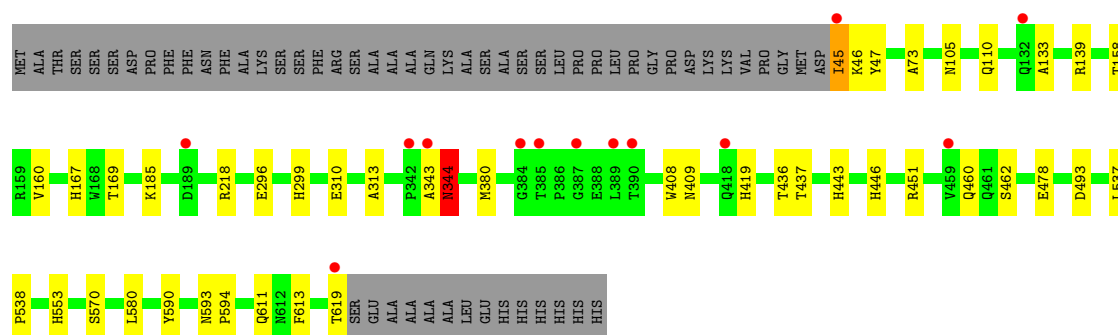
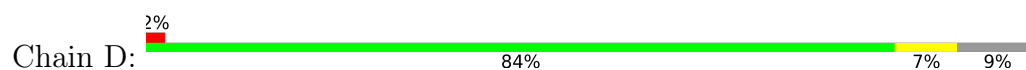


• Molecule 1: Pyranose 2-oxidase





● Molecule 1: Pyranose 2-oxidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	100.08Å 102.52Å 137.34Å 90.00° 90.92° 90.00°	Depositor
Resolution (Å)	50.00 – 2.00 50.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (50.00-2.00) 99.8 (50.00-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.24 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.172 , 0.222 (Not available) , 0.202	Depositor DCC
R_{free} test set	3747 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å ²)	21.0	Xtriage
Anisotropy	0.056	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 49.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.014 for -k,-h,-l 0.015 for k,h,-l 0.024 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	20415	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.60% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 1PE, MES, FDA, G2F

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	1.35	15/4650 (0.3%)	1.16	14/6321 (0.2%)
1	B	1.37	16/4659 (0.3%)	1.18	12/6333 (0.2%)
1	C	1.17	6/4634 (0.1%)	1.09	1/6300 (0.0%)
1	D	1.25	8/4641 (0.2%)	1.12	4/6310 (0.1%)
All	All	1.29	45/18584 (0.2%)	1.14	31/25264 (0.1%)

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	B	0	1
1	D	0	1
All	All	0	3

All (45) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	349	LEU	C-O	-11.07	1.18	1.23
1	A	82	SER	N-CA	8.56	1.56	1.46
1	B	78	GLY	C-O	7.64	1.30	1.23
1	A	345	PRO	C-O	-7.45	1.18	1.25
1	B	548	HIS	ND1-CE1	7.39	1.40	1.32
1	A	299	HIS	CE1-NE2	6.53	1.39	1.32
1	B	443	HIS	CG-CD2	6.35	1.42	1.35
1	B	553	HIS	CG-CD2	6.32	1.42	1.35
1	A	385	THR	CA-C	6.25	1.59	1.53
1	A	324	HIS	ND1-CE1	6.23	1.38	1.32
1	B	457	GLY	N-CA	6.10	1.50	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	89	HIS	CD2-NE2	-5.92	1.31	1.37
1	A	89	HIS	CG-CD2	5.81	1.42	1.35
1	B	89	HIS	CE1-NE2	5.71	1.38	1.32
1	B	74	MET	CA-C	-5.70	1.45	1.52
1	B	125	THR	CA-C	5.70	1.60	1.52
1	B	318	LEU	C-O	-5.58	1.17	1.24
1	D	553	HIS	CG-CD2	5.54	1.42	1.35
1	A	66	VAL	C-O	5.54	1.30	1.24
1	A	255	SER	C-O	-5.52	1.18	1.24
1	B	222	VAL	C-O	-5.52	1.18	1.24
1	A	52	VAL	N-CA	-5.50	1.39	1.46
1	D	446	HIS	CE1-NE2	5.50	1.38	1.32
1	A	321	GLY	N-CA	5.46	1.50	1.45
1	D	553	HIS	CE1-NE2	5.45	1.38	1.32
1	A	82	SER	CB-OG	5.43	1.53	1.42
1	C	441	PRO	C-O	-5.39	1.17	1.24
1	C	475	GLY	N-CA	5.37	1.52	1.44
1	C	404	HIS	CG-CD2	5.26	1.41	1.35
1	D	443	HIS	CG-CD2	5.26	1.41	1.35
1	D	611	GLN	C-O	-5.25	1.17	1.24
1	A	428	PHE	C-O	-5.20	1.17	1.24
1	C	122	VAL	C-O	-5.20	1.18	1.24
1	B	553	HIS	ND1-CE1	5.17	1.37	1.32
1	D	419	HIS	CG-ND1	-5.17	1.32	1.38
1	C	548	HIS	CG-CD2	5.14	1.41	1.35
1	B	415	HIS	CE1-NE2	5.14	1.37	1.32
1	D	478	GLU	CD-OE2	5.10	1.35	1.25
1	B	134	SER	CA-C	-5.09	1.45	1.52
1	C	553	HIS	CG-CD2	5.08	1.41	1.35
1	A	458	ALA	N-CA	5.08	1.52	1.46
1	D	446	HIS	CG-CD2	5.07	1.41	1.35
1	B	401	THR	CA-C	5.05	1.59	1.52
1	A	457	GLY	N-CA	5.05	1.50	1.45
1	A	550	GLY	CA-C	-5.04	1.47	1.52

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	82	SER	CA-CB-OG	8.89	128.89	111.10
1	A	349	LEU	CA-C-N	-7.79	111.77	119.87
1	A	349	LEU	C-N-CA	-7.79	111.77	119.87
1	C	412	VAL	N-CA-C	-7.67	102.97	110.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	324	HIS	N-CA-C	7.10	121.69	112.89
1	D	344	ASN	CA-C-N	-7.06	113.11	120.38
1	D	344	ASN	C-N-CA	-7.06	113.11	120.38
1	A	344	ASN	CA-C-N	7.06	124.81	119.66
1	A	344	ASN	C-N-CA	7.06	124.81	119.66
1	A	321	GLY	N-CA-C	-6.36	105.56	112.04
1	A	409	ASN	N-CA-C	6.33	118.18	111.28
1	B	139	ARG	NE-CZ-NH2	-6.01	113.79	119.20
1	B	546	CYS	N-CA-C	5.92	118.49	111.33
1	B	239	ILE	N-CA-C	-5.82	102.61	108.96
1	B	411	LYS	N-CA-C	-5.80	105.04	111.36
1	A	304	ILE	CB-CA-C	-5.72	104.42	111.92
1	B	168	TRP	N-CA-C	5.72	117.71	110.33
1	A	345	PRO	CA-C-N	-5.60	114.82	120.31
1	A	345	PRO	C-N-CA	-5.60	114.82	120.31
1	B	233	GLN	N-CA-C	-5.58	106.41	113.43
1	A	259	VAL	N-CA-C	-5.57	105.29	110.53
1	B	546	CYS	CA-CB-SG	-5.53	101.67	114.40
1	A	307	ASP	N-CA-C	5.50	118.63	110.48
1	D	613	PHE	N-CA-C	-5.50	100.80	109.50
1	B	339	ARG	CA-C-N	-5.39	114.40	119.90
1	B	339	ARG	C-N-CA	-5.39	114.40	119.90
1	B	385	THR	CB-CA-C	5.37	116.66	109.42
1	D	139	ARG	NE-CZ-NH2	-5.35	114.39	119.20
1	A	345	PRO	CB-CA-C	-5.24	106.46	111.39
1	B	594	PRO	N-CA-C	5.11	121.17	114.27
1	A	146	GLN	N-CA-C	5.03	116.94	109.25

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	81	ASP	Peptide
1	B	138	VAL	Peptide
1	D	436	THR	Peptide

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	4535	0	4380	32	0
1	B	4541	0	4388	40	0
1	C	4519	0	4367	47	0
1	D	4526	0	4374	25	0
2	A	53	0	30	0	0
2	B	53	0	30	2	0
2	C	53	0	29	2	0
2	D	53	0	30	2	0
3	A	12	0	11	0	0
3	B	12	0	11	1	0
3	C	12	0	11	1	0
3	D	12	0	11	1	0
4	A	12	0	14	0	0
4	B	16	0	22	0	0
4	C	16	0	22	0	0
4	D	16	0	22	4	0
5	A	12	0	13	0	0
5	B	12	0	13	1	0
5	D	24	0	26	10	0
6	A	466	0	0	8	0
6	B	561	0	0	6	0
6	C	378	0	0	6	0
6	D	521	0	0	4	0
All	All	20415	0	17804	148	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (148) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:299:HIS:CE1	1:D:310:GLU:HG2	1.91	1.06
1:A:45:ILE:H	1:A:45:ILE:HD12	1.15	1.05
1:B:460[B]:GLN:NE2	1:B:463:ILE:H	1.68	0.89
1:B:460[B]:GLN:HE22	1:B:463:ILE:H	0.93	0.89
1:C:110:GLN:HE21	1:C:167:HIS:HD1	1.20	0.89
1:D:343:ALA:C	1:D:344:ASN:HD22	1.84	0.86
1:B:385:THR:HG23	1:B:388:GLU:OE1	1.76	0.85
1:B:110:GLN:HE21	1:B:167:HIS:HD1	1.26	0.84
1:A:414:ASN:O	1:A:418:GLN:HG2	1.80	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:110:GLN:HE21	1:A:167:HIS:HD1	1.29	0.79
1:D:110:GLN:HE21	1:D:167:HIS:HD1	1.30	0.77
1:A:45:ILE:H	1:A:45:ILE:CD1	1.92	0.76
1:B:460[B]:GLN:HE22	1:B:463:ILE:N	1.77	0.76
1:B:45:ILE:HG22	6:B:1277:HOH:O	1.85	0.75
1:A:101:ASP:HB2	6:A:1321:HOH:O	1.88	0.74
1:B:341:ASN:C	1:B:341:ASN:HD22	1.95	0.73
1:D:133:ALA:HB2	5:D:804:MES:O3S	1.89	0.73
1:A:460:GLN:NE2	6:A:1217:HOH:O	2.23	0.71
1:B:385:THR:CG2	1:B:388:GLU:OE1	2.37	0.71
1:A:45:ILE:HD12	1:A:45:ILE:N	1.99	0.69
1:D:45:ILE:HG22	1:D:46:LYS:H	1.57	0.69
1:C:450:GLY:O	1:C:451:ARG:HD2	1.93	0.69
5:D:804:MES:H32	5:D:804:MES:O1S	1.93	0.69
1:C:463:ILE:HD13	5:D:804:MES:H81	1.76	0.67
1:A:462:SER:OG	5:B:701:MES:H61	1.95	0.67
1:B:341:ASN:ND2	6:B:1276:HOH:O	2.29	0.64
1:D:344:ASN:HD22	1:D:344:ASN:N	1.96	0.63
1:C:349:LEU:HD21	1:C:572:VAL:HG13	1.82	0.60
1:B:45:ILE:HA	6:B:1277:HOH:O	2.01	0.60
1:B:607:GLU:HG3	6:B:1246:HOH:O	2.01	0.60
1:A:101:ASP:OD2	1:A:459:VAL:HG21	2.01	0.60
1:C:176:ASP:HB2	6:C:1161:HOH:O	2.01	0.59
1:B:341:ASN:C	1:B:341:ASN:ND2	2.57	0.59
1:B:43:MET:HE2	1:B:278:PHE:CD1	2.38	0.59
1:C:157:VAL:HG21	1:C:324:HIS:HE1	1.68	0.59
1:B:63:ARG:HD2	1:B:259:VAL:O	2.04	0.58
1:C:177:ARG:NH2	1:C:188:ALA:HB1	2.19	0.58
1:C:47:TYR:O	1:C:313:ALA:HA	2.04	0.57
1:A:90:LYS:NZ	1:A:110:GLN:OE1	2.33	0.57
1:C:82:SER:N	6:C:963:HOH:O	2.38	0.56
1:D:47:TYR:CE2	1:D:73:ALA:HB2	2.40	0.56
1:A:135:THR:HG22	4:D:803:1PE:C22	2.36	0.56
1:A:285:ARG:HD2	6:A:1282:HOH:O	2.06	0.56
1:A:538:PRO:HG2	1:C:538:PRO:HG2	1.89	0.55
1:A:135:THR:HG22	4:D:803:1PE:H222	1.90	0.54
1:B:126:LEU:HD12	1:B:132:GLN:HG3	1.90	0.53
1:A:299:HIS:CE1	1:A:310:GLU:HG3	2.43	0.53
1:B:126:LEU:HD12	1:B:132:GLN:CG	2.38	0.53
1:B:380:MET:HE1	1:B:409:ASN:HB3	1.91	0.53
1:D:133:ALA:H	5:D:804:MES:H72	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:ARG:HD2	6:A:1001:HOH:O	2.07	0.53
1:B:310:GLU:OE1	1:B:312:LYS:NZ	2.41	0.53
1:D:133:ALA:HA	6:D:1407:HOH:O	2.08	0.53
1:B:50:VAL:HG13	1:B:313:ALA:HB2	1.90	0.52
1:D:537:LEU:HB3	1:D:538:PRO:HD2	1.92	0.52
2:B:702:FDA:N5	3:B:703:G2F:H3	2.25	0.51
1:C:157:VAL:HG22	6:C:1176:HOH:O	2.11	0.51
1:C:284:GLU:C	1:C:328:LEU:CD1	2.85	0.50
1:A:344:ASN:CG	1:A:344:ASN:O	2.54	0.50
1:C:299:HIS:CD2	1:C:310:GLU:HB3	2.46	0.50
1:C:341:ASN:C	1:C:341:ASN:HD22	2.19	0.50
1:A:459:VAL:HG13	1:A:461:GLN:HE21	1.76	0.50
1:A:380:MET:HE1	1:A:409:ASN:HB3	1.94	0.49
1:C:211:ASP:O	1:C:214:LYS:HG2	2.11	0.49
1:C:49:VAL:HG22	1:C:315:VAL:HB	1.95	0.49
1:B:460[B]:GLN:HG3	1:B:533:LEU:HD21	1.95	0.49
1:A:91:LYS:HD2	1:A:100:ILE:HD11	1.93	0.49
1:B:218:ARG:HG3	1:B:430:ASP:OD2	2.12	0.49
1:C:463:ILE:CD1	5:D:804:MES:H81	2.43	0.49
1:C:105:ASN:HB3	1:D:105:ASN:O	2.13	0.48
1:B:460[B]:GLN:HB2	6:B:1204:HOH:O	2.14	0.48
1:A:149:LEU:HD22	5:D:804:MES:H62	1.94	0.48
1:A:233:GLN:NE2	6:A:1252:HOH:O	2.27	0.48
1:C:358:GLU:HG2	1:C:544:GLY:HA2	1.96	0.48
1:B:342:PRO:HD2	6:B:1276:HOH:O	2.14	0.47
1:C:157:VAL:HG21	1:C:324:HIS:CE1	2.48	0.47
1:B:380:MET:HE1	1:B:409:ASN:CB	2.45	0.47
1:D:47:TYR:CD2	1:D:73:ALA:HB2	2.49	0.47
1:A:450:GLY:O	1:A:451:ARG:HD2	2.14	0.47
1:B:328:LEU:HD23	1:B:328:LEU:C	2.40	0.47
1:B:341:ASN:HD21	1:B:343:ALA:HB3	1.80	0.47
1:C:167:HIS:CD2	1:C:167:HIS:C	2.93	0.46
1:D:380:MET:HE1	1:D:409:ASN:HB3	1.97	0.46
1:C:382:ILE:HD13	6:C:1038:HOH:O	2.15	0.46
1:B:460[A]:GLN:HG3	1:B:461:GLN:N	2.31	0.46
1:C:159:ARG:HA	2:C:801:FDA:O2B	2.16	0.46
1:D:570:SER:HB3	1:D:580:LEU:O	2.16	0.46
1:B:570:SER:HB3	1:B:580:LEU:O	2.16	0.46
1:B:169:THR:HB	2:B:702:FDA:O4	2.16	0.46
2:D:801:FDA:N5	3:D:802:G2F:H3	2.30	0.46
1:B:545:LEU:HD12	1:B:545:LEU:HA	1.72	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:342:PRO:C	1:C:344:ASN:H	2.24	0.46
1:A:265:ARG:HA	1:A:266:PRO:C	2.42	0.45
1:B:385:THR:HA	1:B:386:PRO:HD3	1.85	0.45
1:D:158:THR:HG22	1:D:160:VAL:HG22	1.99	0.45
1:C:389:LEU:HD12	1:C:389:LEU:HA	1.72	0.45
1:C:137:PHE:CE2	1:C:139:ARG:HG3	2.52	0.44
1:C:284:GLU:O	1:C:328:LEU:CD1	2.65	0.44
1:C:463:ILE:CD1	5:D:804:MES:C8	2.95	0.44
1:C:399:ALA:HB3	1:C:402:ASN:CG	2.43	0.43
1:D:169:THR:HB	2:D:801:FDA:O4	2.18	0.43
1:A:47:TYR:O	1:A:313:ALA:HA	2.18	0.43
1:C:47:TYR:CE2	1:C:73:ALA:HB2	2.53	0.43
5:D:805:MES:H51	5:D:805:MES:H82	1.86	0.43
1:C:218:ARG:HG3	1:C:430:ASP:OD2	2.18	0.43
1:C:463:ILE:HD12	5:D:804:MES:H82	2.00	0.43
1:D:47:TYR:O	1:D:313:ALA:HA	2.18	0.43
2:C:801:FDA:N5	3:C:802:G2F:H3	2.33	0.43
1:D:45:ILE:HG22	1:D:46:LYS:N	2.28	0.43
1:A:299:HIS:CE1	1:A:310:GLU:CG	3.01	0.43
1:B:403:LYS:HD2	1:B:403:LYS:N	2.33	0.43
1:C:341:ASN:C	1:C:341:ASN:ND2	2.77	0.43
1:C:284:GLU:O	1:C:328:LEU:HD12	2.19	0.43
1:C:460:GLN:NE2	1:C:462:SER:HB2	2.34	0.43
1:A:135:THR:HG22	4:D:803:1PE:H221	2.00	0.43
1:B:158:THR:HG22	1:B:160:VAL:HG22	2.01	0.43
1:B:358:GLU:HG2	1:B:544:GLY:HA2	2.01	0.43
1:C:399:ALA:HB3	1:C:402:ASN:OD1	2.19	0.43
1:D:451:ARG:NH2	6:D:1239:HOH:O	2.52	0.43
1:D:493:ASP:HB2	6:D:1382:HOH:O	2.19	0.42
1:A:82:SER:HB2	6:A:1013:HOH:O	2.19	0.42
1:A:383:ARG:O	1:A:391:TYR:HA	2.20	0.42
1:D:437:THR:O	1:D:437:THR:HG23	2.19	0.42
1:D:218:ARG:HD2	6:D:968:HOH:O	2.18	0.42
1:A:358:GLU:HG2	1:A:544:GLY:HA2	2.02	0.42
1:B:47:TYR:CD2	1:B:73:ALA:HB2	2.55	0.42
1:C:50:VAL:HG12	1:C:73:ALA:HB3	2.02	0.42
1:A:411:LYS:HD3	6:A:1275:HOH:O	2.19	0.41
1:C:61:TYR:CG	1:C:317:VAL:HG11	2.55	0.41
4:D:803:1PE:H222	4:D:803:1PE:H132	1.79	0.41
1:B:478:GLU:HG3	1:B:511:THR:OG1	2.19	0.41
1:C:181:PRO:HB3	1:C:587:PRO:HG2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:126:LEU:CD1	1:B:132:GLN:CG	2.99	0.41
1:B:339:ARG:O	1:B:340:PRO:C	2.63	0.41
1:C:327:GLN:HB2	1:C:487:PHE:CE1	2.55	0.41
1:C:363:PHE:HA	1:C:471:TRP:O	2.20	0.41
1:D:133:ALA:HB2	5:D:804:MES:S	2.60	0.41
1:D:408:TRP:CD1	1:D:408:TRP:C	2.98	0.41
1:D:590:TYR:CE2	1:D:594:PRO:HB3	2.56	0.41
1:C:349:LEU:HD21	1:C:572:VAL:CG1	2.49	0.41
1:B:178:GLU:OE1	1:B:441:PRO:HG3	2.21	0.41
1:C:354:SER:OG	1:C:484:LYS:NZ	2.53	0.41
1:A:82:SER:HB3	6:A:1040:HOH:O	2.20	0.41
1:C:348:LEU:HD22	6:C:1269:HOH:O	2.21	0.40
1:B:385:THR:HG21	1:B:388:GLU:OE1	2.21	0.40
1:C:169:THR:O	1:C:170:CYS:HB2	2.22	0.40
1:C:537:LEU:HB3	1:C:538:PRO:HD2	2.04	0.40
1:C:304:ILE:HG12	6:C:1134:HOH:O	2.21	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	574/633 (91%)	559 (97%)	15 (3%)	0	100	100
1	B	575/633 (91%)	555 (96%)	18 (3%)	2 (0%)	36	35
1	C	572/633 (90%)	554 (97%)	18 (3%)	0	100	100
1	D	573/633 (90%)	553 (96%)	20 (4%)	0	100	100
All	All	2294/2532 (91%)	2221 (97%)	71 (3%)	2 (0%)	100	46

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	460[A]	GLN
1	B	460[B]	GLN

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	503/547 (92%)	495 (98%)	8 (2%)	55	62
1	B	504/547 (92%)	493 (98%)	11 (2%)	45	50
1	C	501/547 (92%)	493 (98%)	8 (2%)	55	62
1	D	502/547 (92%)	494 (98%)	8 (2%)	55	62
All	All	2010/2188 (92%)	1975 (98%)	35 (2%)	53	60

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	ILE
1	A	344	ASN
1	A	385	THR
1	A	403	LYS
1	A	418	GLN
1	A	490	LYS
1	A	496	ASN
1	A	593	ASN
1	B	139	ARG
1	B	186	ASP
1	B	231	LYS
1	B	340	PRO
1	B	341	ASN
1	B	344	ASN
1	B	347	GLU
1	B	403	LYS
1	B	460[A]	GLN
1	B	460[B]	GLN
1	B	462	SER
1	C	45	ILE

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Mol	Chain	Res	Type
1	C	185	LYS
1	C	269	ASP
1	C	382	ILE
1	C	385	THR
1	C	400	SER
1	C	462	SER
1	C	593	ASN
1	D	45	ILE
1	D	185	LYS
1	D	296	GLU
1	D	344	ASN
1	D	460	GLN
1	D	462	SER
1	D	593	ASN
1	D	619	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	105	ASN
1	A	132	GLN
1	A	263	GLN
1	A	276	ASN
1	A	299	HIS
1	A	341	ASN
1	A	419	HIS
1	A	461	GLN
1	B	105	ASN
1	B	257	ASN
1	B	263	GLN
1	B	341	ASN
1	B	419	HIS
1	B	611	GLN
1	C	132	GLN
1	C	257	ASN
1	C	263	GLN
1	C	341	ASN
1	C	460	GLN
1	D	105	ASN
1	D	110	GLN
1	D	263	GLN
1	D	299	HIS

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Mol	Chain	Res	Type
1	D	324	HIS
1	D	341	ASN
1	D	344	ASN
1	D	365	GLN
1	D	419	HIS

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](#)

16 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	MES	B	701	-	12,12,12	2.07	3 (25%)	15,16,16	1.96	3 (20%)
5	MES	A	804	-	12,12,12	2.13	1 (8%)	15,16,16	2.01	4 (26%)
4	1PE	A	803	-	11,11,15	0.79	0	10,10,14	0.58	0
5	MES	D	805	-	12,12,12	1.99	2 (16%)	15,16,16	1.67	3 (20%)
2	FDA	B	702	1	57,58,58	1.82	11 (19%)	78,89,89	2.54	28 (35%)
2	FDA	D	801	1	57,58,58	1.42	10 (17%)	78,89,89	2.42	26 (33%)
4	1PE	B	704	-	15,15,15	0.59	0	14,14,14	0.40	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	FDA	C	801	1	57,58,58	1.50	13 (22%)	78,89,89	2.44	25 (32%)
3	G2F	A	802	-	12,12,12	1.47	3 (25%)	16,17,17	4.09	6 (37%)
3	G2F	B	703	-	12,12,12	1.56	3 (25%)	16,17,17	3.65	11 (68%)
3	G2F	D	802	-	12,12,12	1.15	1 (8%)	16,17,17	3.91	9 (56%)
4	1PE	D	803	-	15,15,15	0.64	0	14,14,14	0.31	0
3	G2F	C	802	-	12,12,12	1.40	1 (8%)	16,17,17	3.94	8 (50%)
2	FDA	A	801	1	57,58,58	1.50	7 (12%)	78,89,89	2.60	26 (33%)
5	MES	D	804	-	12,12,12	2.45	6 (50%)	15,16,16	2.94	4 (26%)
4	1PE	C	803	-	15,15,15	0.56	0	14,14,14	0.19	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	MES	B	701	-	-	0/6/14/14	0/1/1/1
5	MES	A	804	-	-	1/6/14/14	0/1/1/1
4	1PE	A	803	-	-	3/9/9/13	-
5	MES	D	805	-	-	0/6/14/14	0/1/1/1
2	FDA	B	702	1	-	0/34/50/50	0/6/6/6
2	FDA	D	801	1	-	1/34/50/50	0/6/6/6
4	1PE	B	704	-	-	2/13/13/13	-
2	FDA	C	801	1	-	4/34/50/50	0/6/6/6
3	G2F	A	802	-	-	1/2/22/22	0/1/1/1
3	G2F	B	703	-	-	2/2/22/22	0/1/1/1
3	G2F	D	802	-	-	1/2/22/22	0/1/1/1
4	1PE	D	803	-	-	5/13/13/13	-
3	G2F	C	802	-	-	0/2/22/22	0/1/1/1
2	FDA	A	801	1	-	3/34/50/50	0/6/6/6
5	MES	D	804	-	-	4/6/14/14	0/1/1/1
4	1PE	C	803	-	-	4/13/13/13	-

All (61) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	702	FDA	PA-O3P	6.93	1.67	1.59
5	A	804	MES	C8-S	-6.85	1.68	1.77
5	D	805	MES	C8-S	-5.87	1.69	1.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	701	MES	C8-S	-5.67	1.69	1.77
5	D	804	MES	C8-S	-4.67	1.71	1.77
2	B	702	FDA	C5'-C4'	4.35	1.57	1.51
2	B	702	FDA	C9-C8	4.13	1.45	1.39
2	A	801	FDA	C2-N1	-4.12	1.30	1.37
3	C	802	G2F	C2-C3	-4.06	1.48	1.52
2	A	801	FDA	PA-O3P	3.86	1.63	1.59
2	C	801	FDA	C8A-N9A	-3.78	1.31	1.37
2	B	702	FDA	C8A-N9A	-3.67	1.31	1.37
2	D	801	FDA	C2-N1	-3.62	1.31	1.37
5	D	804	MES	C7-C8	3.59	1.61	1.52
2	D	801	FDA	O4B-C4B	-3.56	1.37	1.45
2	A	801	FDA	C4-N3	-3.45	1.32	1.38
2	B	702	FDA	P-O3P	3.42	1.63	1.59
2	D	801	FDA	C9-C8	3.04	1.43	1.39
5	D	804	MES	C3-N4	3.02	1.55	1.46
2	D	801	FDA	C8A-N9A	-3.02	1.32	1.37
2	A	801	FDA	O4B-C4B	-2.94	1.38	1.45
5	D	804	MES	C7-N4	2.91	1.54	1.47
2	B	702	FDA	C2A-N3A	2.85	1.39	1.33
2	C	801	FDA	C9-C8	2.81	1.43	1.39
2	A	801	FDA	C5X-N5	-2.78	1.35	1.39
2	A	801	FDA	C4X-C4	2.74	1.50	1.41
2	C	801	FDA	O4B-C4B	-2.73	1.38	1.45
2	D	801	FDA	C5X-N5	-2.72	1.35	1.39
3	B	703	G2F	O1-C1	2.70	1.48	1.39
3	A	802	G2F	C2-C3	-2.60	1.50	1.52
2	B	702	FDA	C2A-N1A	2.55	1.38	1.33
3	B	703	G2F	F2-C2	-2.53	1.35	1.40
2	C	801	FDA	C8A-N7A	2.51	1.36	1.31
2	B	702	FDA	O4B-C4B	-2.51	1.39	1.45
2	B	702	FDA	C8M-C8	2.49	1.55	1.51
2	C	801	FDA	C6-C5X	2.47	1.43	1.39
2	B	702	FDA	C2-N3	-2.45	1.33	1.37
2	C	801	FDA	PA-O3P	2.43	1.62	1.59
5	D	804	MES	O1S-S	2.41	1.51	1.45
3	D	802	G2F	F2-C2	-2.38	1.35	1.40
2	A	801	FDA	C5A-C4A	-2.38	1.34	1.39
2	C	801	FDA	P-O3P	2.31	1.62	1.59
2	D	801	FDA	C6-C5X	2.29	1.43	1.39
2	B	702	FDA	C8A-N7A	2.29	1.36	1.31
3	A	802	G2F	C4-C5	2.27	1.57	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	801	FDA	O3B-C3B	-2.25	1.37	1.43
2	D	801	FDA	C2B-C1B	-2.23	1.46	1.53
3	B	703	G2F	O4-C4	-2.19	1.37	1.43
2	C	801	FDA	O4'-C4'	-2.16	1.38	1.43
3	A	802	G2F	C4-C3	2.16	1.57	1.52
5	D	805	MES	C3-N4	2.14	1.52	1.46
2	C	801	FDA	C2B-C3B	-2.13	1.47	1.53
5	D	804	MES	C5-N4	2.12	1.52	1.46
2	D	801	FDA	C4X-C4	2.12	1.48	1.41
5	B	701	MES	C3-N4	2.09	1.52	1.46
2	D	801	FDA	O2B-C2B	-2.09	1.37	1.43
2	D	801	FDA	C8A-N7A	2.08	1.35	1.31
2	C	801	FDA	C4-N3	-2.05	1.35	1.38
2	C	801	FDA	C4X-C4	2.02	1.47	1.41
5	B	701	MES	C5-N4	2.02	1.52	1.46
2	C	801	FDA	C5'-C4'	2.01	1.54	1.51

All (153) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	802	G2F	O5-C1-C2	9.88	122.50	109.75
5	D	804	MES	O2S-S-C8	9.80	121.53	106.73
3	A	802	G2F	F2-C2-C1	9.52	118.48	107.81
3	C	802	G2F	F2-C2-C1	9.21	118.13	107.81
3	D	802	G2F	F2-C2-C3	8.51	116.18	108.81
2	B	702	FDA	C4-N3-C2	8.40	137.94	126.37
3	C	802	G2F	O5-C1-C2	8.36	120.54	109.75
2	A	801	FDA	N3A-C2A-N1A	-7.89	116.65	128.58
2	C	801	FDA	C4A-N9A-C8A	7.62	113.74	105.74
2	A	801	FDA	N9A-C8A-N7A	-7.43	103.39	113.94
3	D	802	G2F	O5-C1-C2	7.26	119.12	109.75
3	B	703	G2F	F2-C2-C1	7.26	115.94	107.81
2	D	801	FDA	C4A-N9A-C8A	7.23	113.33	105.74
2	B	702	FDA	C4A-N9A-C8A	6.99	113.07	105.74
2	A	801	FDA	C4A-N9A-C8A	6.97	113.06	105.74
2	D	801	FDA	N3A-C2A-N1A	-6.64	118.54	128.58
3	B	703	G2F	O5-C1-C2	6.39	118.00	109.75
2	C	801	FDA	N3A-C2A-N1A	-6.39	118.91	128.58
2	C	801	FDA	N9A-C8A-N7A	-6.27	105.04	113.94
2	A	801	FDA	C4-N3-C2	6.27	135.00	126.37
2	D	801	FDA	N9A-C8A-N7A	-6.13	105.24	113.94
2	B	702	FDA	N9A-C8A-N7A	-6.12	105.25	113.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	702	FDA	O4-C4-N3	5.99	131.38	120.11
2	C	801	FDA	O4B-C1B-N9A	5.94	119.50	108.09
2	D	801	FDA	O3B-C3B-C4B	5.85	127.89	111.08
3	A	802	G2F	O1-C1-O5	-5.81	93.16	110.41
2	B	702	FDA	N3A-C2A-N1A	-5.76	119.86	128.58
3	D	802	G2F	C1-O5-C5	5.61	124.50	113.65
2	B	702	FDA	C2B-C1B-N9A	5.45	126.83	113.30
5	B	701	MES	O3S-S-C8	5.44	116.65	106.00
2	D	801	FDA	O4B-C1B-N9A	5.33	118.32	108.09
2	C	801	FDA	O3B-C3B-C4B	5.29	126.27	111.08
2	A	801	FDA	C2B-C1B-N9A	5.23	126.31	113.30
2	A	801	FDA	O4B-C1B-N9A	5.13	117.95	108.09
2	C	801	FDA	O4-C4-N3	-5.03	110.66	120.11
2	C	801	FDA	C2B-C1B-N9A	4.93	125.55	113.30
2	A	801	FDA	C5A-N7A-C8A	4.86	111.09	103.45
2	D	801	FDA	C2B-C1B-N9A	4.81	125.24	113.30
5	D	805	MES	O3S-S-C8	4.70	115.19	106.00
2	A	801	FDA	N3A-C4A-N9A	4.55	134.90	127.17
3	D	802	G2F	C1-C2-C3	4.52	117.43	110.69
3	D	802	G2F	C3-C4-C5	4.49	118.36	110.23
3	C	802	G2F	C1-O5-C5	4.47	122.29	113.65
2	B	702	FDA	N3-C2-N1	-4.45	108.74	115.74
3	C	802	G2F	O3-C3-C4	4.42	120.80	110.38
3	B	703	G2F	C3-C4-C5	4.41	118.22	110.23
3	B	703	G2F	C1-O5-C5	4.37	122.11	113.65
2	A	801	FDA	O3B-C3B-C4B	4.35	123.58	111.08
2	A	801	FDA	C2A-N3A-C4A	4.19	122.06	111.83
3	C	802	G2F	C3-C4-C5	4.18	117.81	110.23
3	B	703	G2F	O1-C1-O5	-4.15	98.09	110.41
2	A	801	FDA	C5A-C4A-N3A	-4.15	121.00	126.72
2	D	801	FDA	C5A-N7A-C8A	4.06	109.84	103.45
2	B	702	FDA	O4-C4-C4X	-4.02	117.56	127.26
2	B	702	FDA	C5A-N7A-C8A	4.00	109.73	103.45
3	B	703	G2F	O5-C5-C4	3.97	116.85	109.70
2	C	801	FDA	O2B-C2B-C3B	3.93	124.42	111.82
3	D	802	G2F	O5-C5-C4	3.90	116.72	109.70
3	B	703	G2F	C1-C2-C3	3.89	116.48	110.69
2	A	801	FDA	O4-C4-N3	3.88	127.41	120.11
3	A	802	G2F	C1-O5-C5	3.85	121.10	113.65
2	D	801	FDA	C5B-C4B-C3B	3.84	129.03	115.21
2	B	702	FDA	O2B-C2B-C3B	3.83	124.08	111.82
2	C	801	FDA	C4-N3-C2	-3.79	121.15	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	702	FDA	O2P-P-O3P	-3.75	97.14	107.27
2	A	801	FDA	O2B-C2B-C3B	3.75	123.83	111.82
2	D	801	FDA	O4B-C4B-C5B	3.62	120.93	109.33
2	D	801	FDA	C2A-N1A-C6A	3.60	124.64	118.73
2	C	801	FDA	O2B-C2B-C1B	3.59	122.46	110.10
2	A	801	FDA	N3-C2-N1	-3.55	110.15	115.74
2	D	801	FDA	O2-C2-N1	-3.54	115.57	121.86
3	D	802	G2F	O3-C3-C4	3.53	118.70	110.38
2	D	801	FDA	N3-C2-N1	3.52	121.27	115.74
2	C	801	FDA	C4X-C4-N3	3.50	121.73	112.13
2	D	801	FDA	O4-C4-C4X	-3.49	118.85	127.26
5	D	804	MES	C2-C3-N4	3.48	115.41	110.12
2	D	801	FDA	O2B-C2B-C3B	3.44	122.84	111.82
3	B	703	G2F	F2-C2-C3	3.37	111.73	108.81
5	A	804	MES	C2-C3-N4	3.35	115.20	110.12
2	B	702	FDA	C1B-N9A-C8A	-3.35	119.67	127.09
2	B	702	FDA	O4B-C4B-C3B	3.32	111.75	105.15
2	A	801	FDA	C1B-N9A-C8A	-3.32	119.73	127.09
2	D	801	FDA	O2B-C2B-C1B	3.31	121.49	110.10
2	D	801	FDA	C4A-C5A-N7A	-3.29	106.82	110.58
2	C	801	FDA	C5A-N7A-C8A	3.24	108.55	103.45
2	C	801	FDA	C4-C4X-N5	3.23	124.64	116.37
2	C	801	FDA	O4B-C4B-C3B	3.21	111.53	105.15
2	D	801	FDA	C2A-N3A-C4A	3.19	119.61	111.83
5	A	804	MES	O1-C2-C3	3.19	118.64	111.77
2	D	801	FDA	N3A-C4A-N9A	3.18	132.58	127.17
2	C	801	FDA	C1B-N9A-C8A	-3.17	120.05	127.09
2	B	702	FDA	O2B-C2B-C1B	3.16	120.98	110.10
2	B	702	FDA	C4A-C5A-N7A	-3.12	107.02	110.58
3	A	802	G2F	F2-C2-C3	-3.10	106.13	108.81
3	C	802	G2F	O5-C5-C4	3.08	115.25	109.70
2	D	801	FDA	C5A-C4A-N3A	-3.08	122.48	126.72
5	A	804	MES	C6-O1-C2	3.07	119.80	109.88
2	C	801	FDA	C2A-N1A-C6A	3.02	123.70	118.73
2	A	801	FDA	C2A-N1A-C6A	3.01	123.67	118.73
5	D	804	MES	O3S-S-O2S	-2.97	103.97	111.40
2	A	801	FDA	O2B-C2B-C1B	2.95	120.26	110.10
2	C	801	FDA	N3A-C4A-N9A	2.93	132.15	127.17
5	A	804	MES	O2S-S-C8	2.92	111.14	106.73
2	B	702	FDA	C5B-C4B-C3B	2.91	125.68	115.21
2	B	702	FDA	O4B-C1B-N9A	2.87	113.60	108.09
2	C	801	FDA	O4B-C4B-C5B	2.86	118.51	109.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	802	G2F	O1-C1-O5	-2.79	102.12	110.41
2	A	801	FDA	O4-C4-C4X	-2.76	120.60	127.26
2	C	801	FDA	C2A-N3A-C4A	2.74	118.52	111.83
2	B	702	FDA	C8M-C8-C7	-2.71	115.22	120.76
3	C	802	G2F	C1-C2-C3	2.71	114.72	110.69
2	B	702	FDA	O4B-C4B-C5B	2.69	117.94	109.33
3	D	802	G2F	C6-C5-C4	2.67	119.59	113.02
3	B	703	G2F	C6-C5-C4	2.64	119.50	113.02
2	C	801	FDA	O4-C4-C4X	-2.63	120.91	127.26
2	D	801	FDA	O4'-C4'-C5'	-2.62	104.20	109.99
5	B	701	MES	O2S-S-O1S	-2.61	105.32	113.82
2	A	801	FDA	C7M-C7-C6	-2.58	115.03	119.57
2	B	702	FDA	N3A-C4A-N9A	2.58	131.55	127.17
2	D	801	FDA	O4'-C4'-C3'	2.57	115.26	109.25
3	B	703	G2F	O3-C3-C4	2.56	116.42	110.38
5	D	804	MES	C7-N4-C3	2.54	118.02	111.24
2	D	801	FDA	O2'-C2'-C3'	2.52	115.14	109.25
2	A	801	FDA	O3P-P-O1P	2.51	118.24	110.70
2	A	801	FDA	O4B-C4B-C5B	2.50	117.33	109.33
2	B	702	FDA	O2A-PA-O3P	2.48	113.97	107.27
2	B	702	FDA	O2-C2-N1	2.44	126.20	121.86
2	B	702	FDA	C4-C4X-N5	2.43	122.59	116.37
2	D	801	FDA	C1B-N9A-C8A	-2.38	121.81	127.09
3	D	802	G2F	O1-C1-O5	-2.35	103.43	110.41
2	C	801	FDA	C5A-C4A-N3A	-2.34	123.50	126.72
2	C	801	FDA	C5B-C4B-C3B	2.33	123.60	115.21
5	D	805	MES	C6-C5-N4	2.32	113.65	110.12
2	B	702	FDA	C2A-N3A-C4A	2.32	117.49	111.83
2	B	702	FDA	C5A-C4A-N3A	-2.26	123.61	126.72
2	A	801	FDA	O2P-P-O3P	-2.25	101.18	107.27
2	A	801	FDA	O4B-C4B-C3B	2.23	109.59	105.15
2	C	801	FDA	O2P-P-O3P	-2.23	101.25	107.27
2	B	702	FDA	O4B-C1B-C2B	2.20	111.33	106.62
2	D	801	FDA	C5X-C9A-N10	-2.17	115.56	118.01
2	C	801	FDA	C9-C9A-C5X	-2.17	116.92	119.95
5	D	805	MES	O3S-S-O2S	-2.15	106.01	111.40
2	A	801	FDA	C5B-C4B-C3B	2.15	122.94	115.21
2	B	702	FDA	C8M-C8-C9	2.13	123.32	119.57
2	A	801	FDA	C1'-N10-C9A	2.08	124.67	120.63
5	B	701	MES	C2-C3-N4	2.06	113.26	110.12
2	D	801	FDA	C9-C9A-N10	2.04	124.60	121.85
3	B	703	G2F	O3-C3-C2	2.03	113.38	109.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	801	FDA	O3P-PA-O1A	-2.03	104.60	110.70
2	A	801	FDA	O2A-PA-O1A	2.01	121.81	112.44
3	A	802	G2F	O4-C4-C3	2.01	115.11	110.38
2	B	702	FDA	C9A-C5X-N5	2.01	121.82	119.37
2	C	801	FDA	C4A-C5A-N7A	-2.00	108.29	110.58

There are no chirality outliers.

All (31) torsion outliers are listed below:

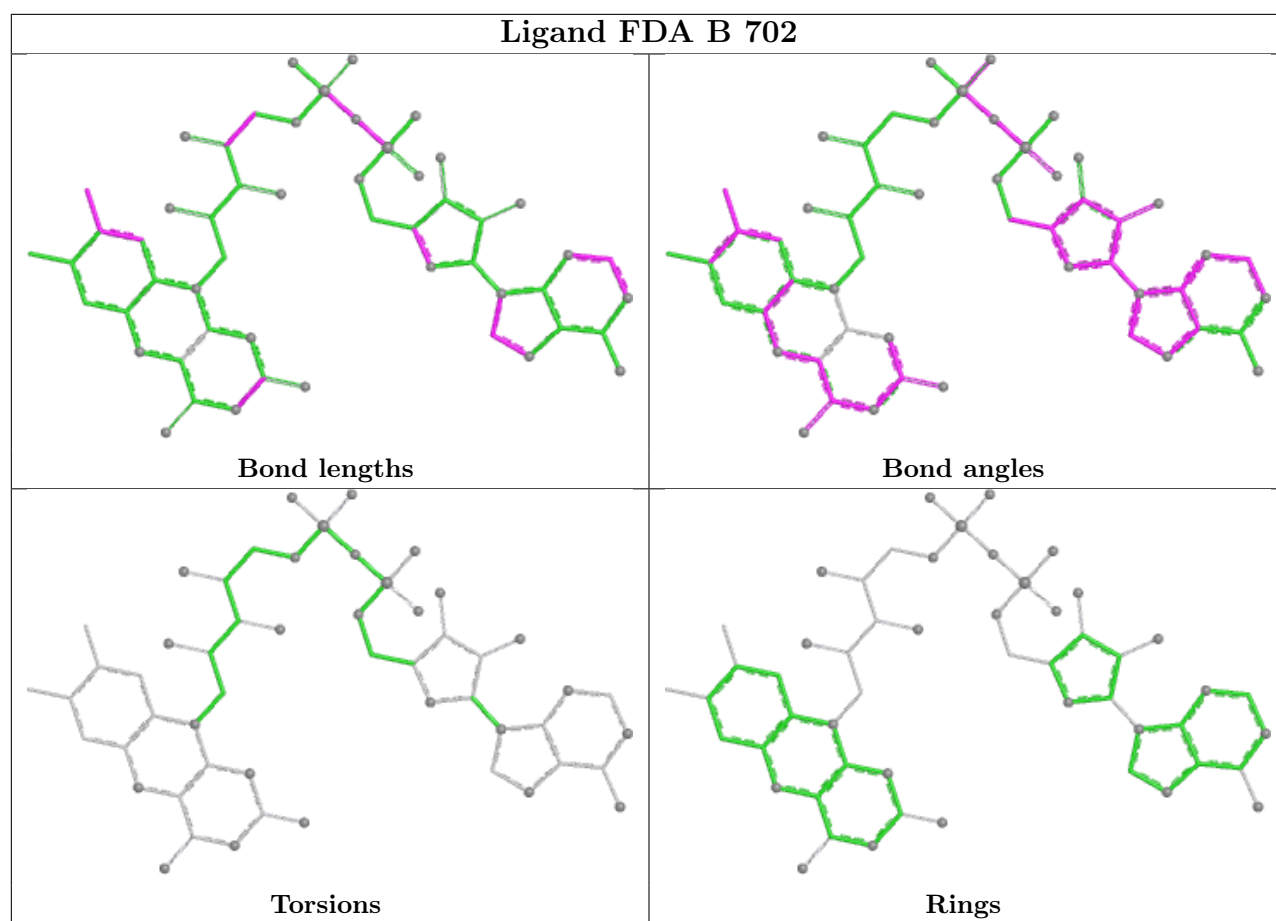
Mol	Chain	Res	Type	Atoms
2	C	801	FDA	PA-O3P-P-O5'
5	D	804	MES	C8-C7-N4-C3
5	D	804	MES	C7-C8-S-O2S
3	B	703	G2F	C4-C5-C6-O6
4	C	803	1PE	OH4-C13-C23-OH3
4	D	803	1PE	OH2-C12-C22-OH3
4	A	803	1PE	OH6-C15-C25-OH5
4	D	803	1PE	C13-C23-OH3-C22
3	D	802	G2F	C4-C5-C6-O6
4	B	704	1PE	OH7-C16-C26-OH6
5	A	804	MES	N4-C7-C8-S
5	D	804	MES	C8-C7-N4-C5
3	A	802	G2F	C4-C5-C6-O6
4	C	803	1PE	OH5-C14-C24-OH4
4	A	803	1PE	C15-C25-OH5-C14
4	D	803	1PE	OH7-C16-C26-OH6
2	D	801	FDA	C3B-C4B-C5B-O5B
4	C	803	1PE	C24-C14-OH5-C25
4	D	803	1PE	OH6-C15-C25-OH5
4	C	803	1PE	C23-C13-OH4-C24
5	D	804	MES	C7-C8-S-O3S
2	A	801	FDA	O4B-C4B-C5B-O5B
4	B	704	1PE	OH5-C14-C24-OH4
4	D	803	1PE	C12-C22-OH3-C23
2	A	801	FDA	PA-O3P-P-O5'
4	A	803	1PE	C24-C14-OH5-C25
3	B	703	G2F	O5-C5-C6-O6
2	C	801	FDA	O4B-C4B-C5B-O5B
2	C	801	FDA	O4B-C1B-N9A-C8A
2	A	801	FDA	P-O3P-PA-O2A
2	C	801	FDA	P-O3P-PA-O2A

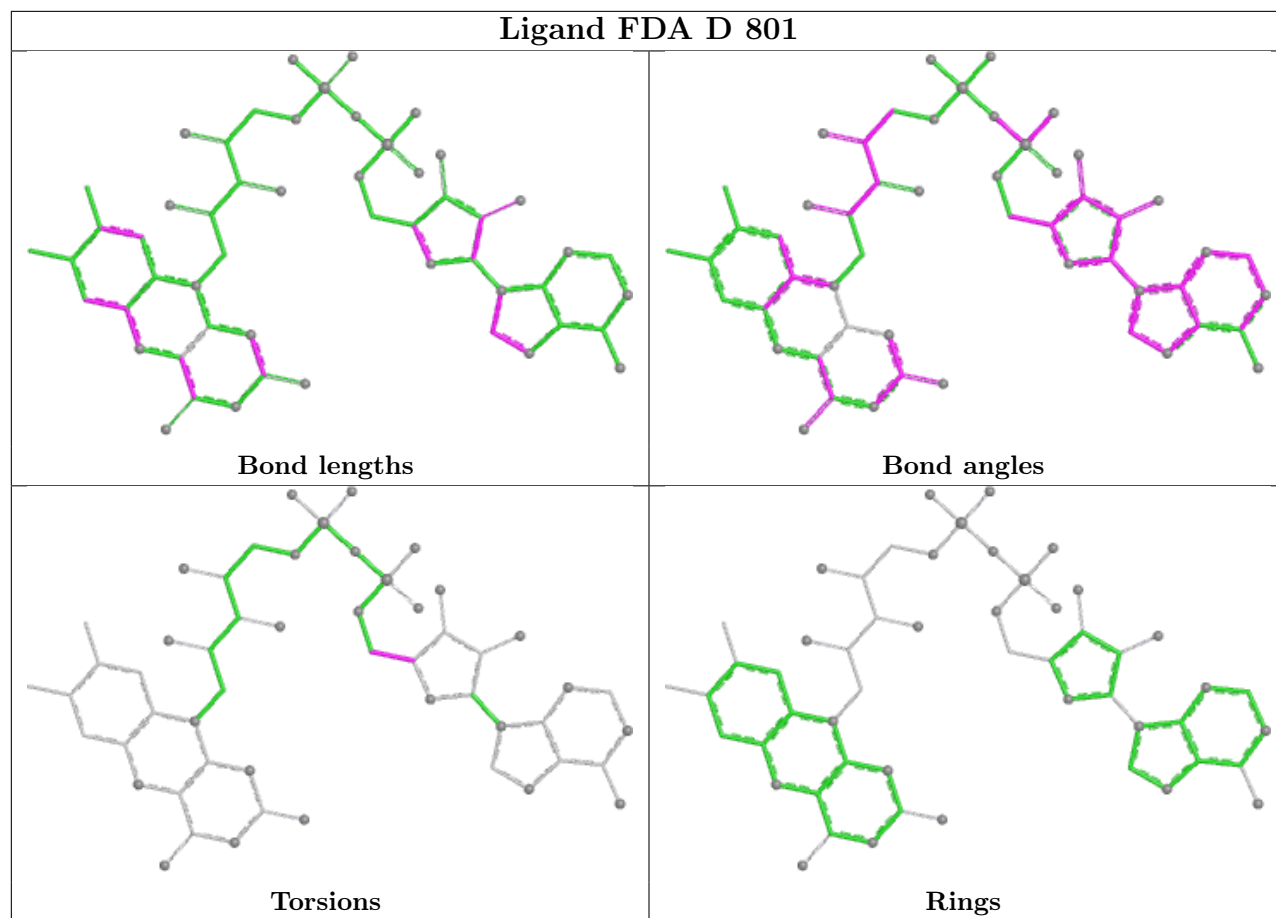
There are no ring outliers.

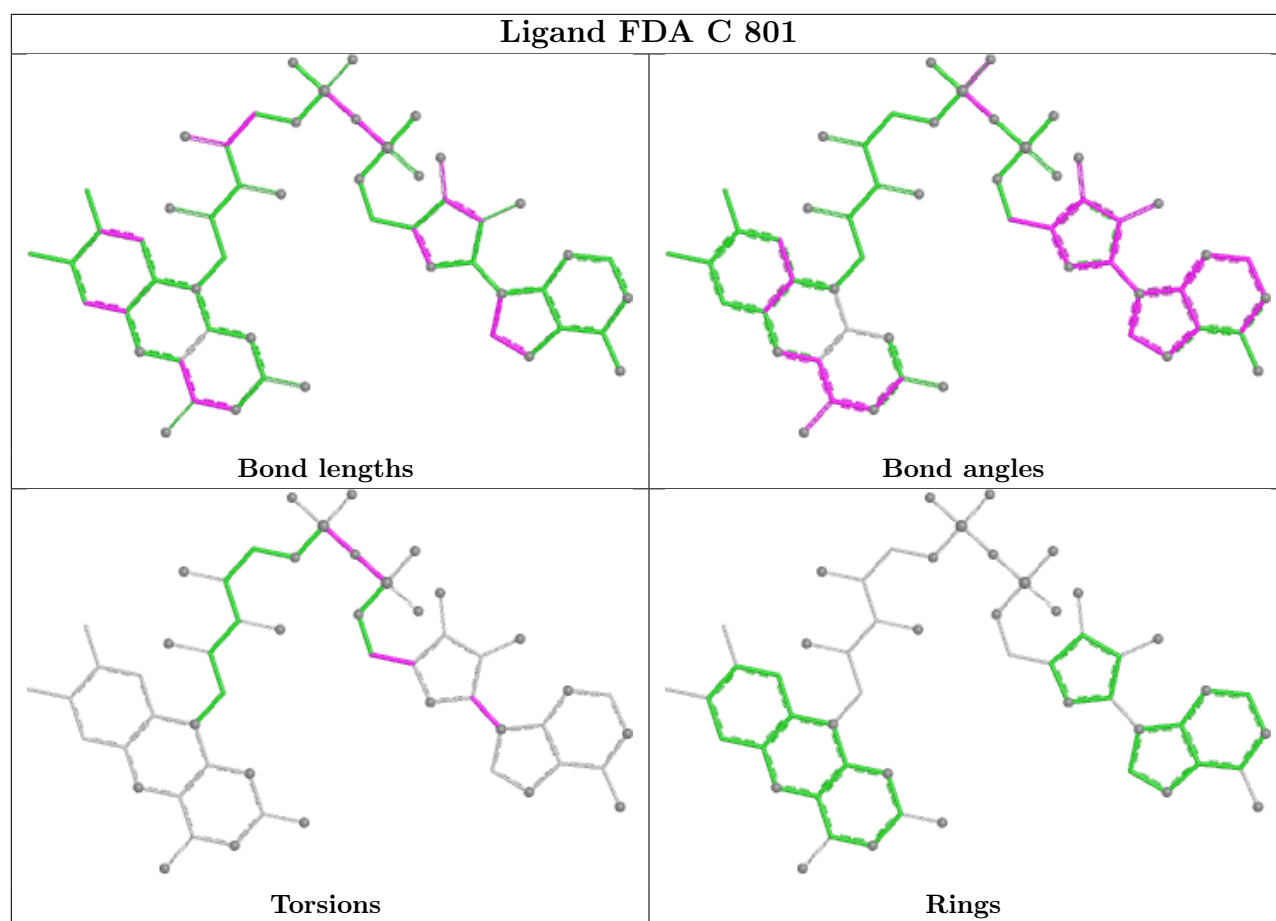
10 monomers are involved in 21 short contacts:

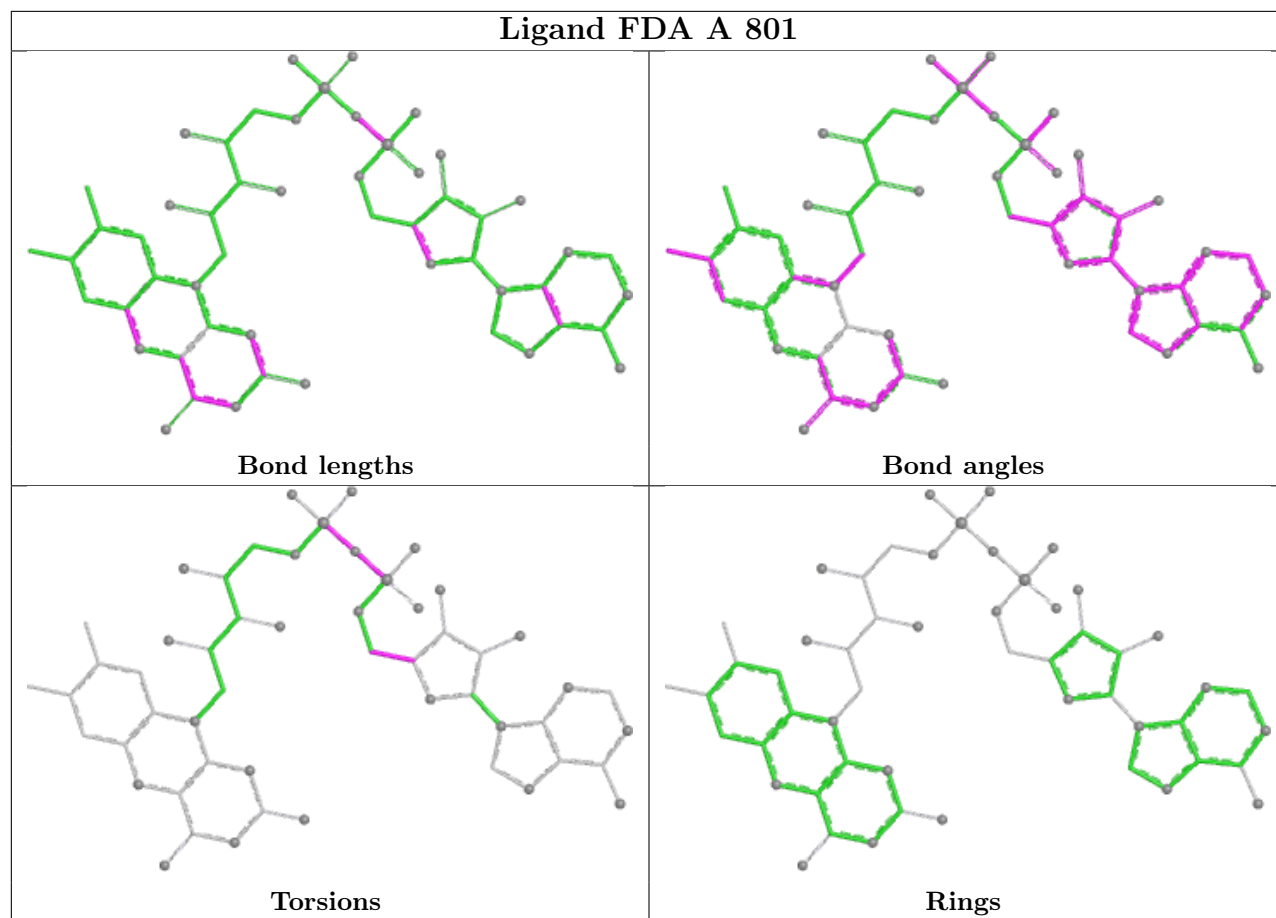
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	701	MES	1	0
5	D	805	MES	1	0
2	B	702	FDA	2	0
2	D	801	FDA	2	0
2	C	801	FDA	2	0
3	B	703	G2F	1	0
3	D	802	G2F	1	0
4	D	803	1PE	4	0
3	C	802	G2F	1	0
5	D	804	MES	9	0

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	576/633 (90%)	-0.19	18 (3%) 51 50	17, 23, 45, 78	0
1	B	576/633 (90%)	-0.31	9 (1%) 70 70	16, 22, 39, 68	1 (0%)
1	C	574/633 (90%)	0.24	15 (2%) 57 56	20, 34, 54, 81	0
1	D	575/633 (90%)	-0.12	13 (2%) 61 60	18, 27, 47, 74	0
All	All	2301/2532 (90%)	-0.10	55 (2%) 59 59	16, 26, 48, 81	1 (0%)

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	45	ILE	5.6
1	B	45	ILE	5.2
1	A	389	LEU	4.8
1	A	45	ILE	4.7
1	A	343	ALA	3.6
1	A	393	VAL	3.5
1	C	460	GLN	3.5
1	A	390	THR	3.5
1	D	45	ILE	3.4
1	D	343	ALA	3.4
1	C	618	PHE	3.4
1	D	389	LEU	3.3
1	A	344	ASN	3.2
1	D	459	VAL	3.1
1	B	618	PHE	3.1
1	A	460	GLN	3.1
1	B	44	ASP	3.1
1	C	343	ALA	2.9
1	C	459	VAL	2.9
1	A	82	SER	2.9
1	A	385	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	44	ASP	2.8
1	C	312	LYS	2.8
1	C	342	PRO	2.7
1	A	342	PRO	2.6
1	C	188	ALA	2.6
1	C	82	SER	2.5
1	D	619	THR	2.5
1	A	388	GLU	2.5
1	D	384	GLY	2.5
1	B	459	VAL	2.4
1	C	81	ASP	2.4
1	D	342	PRO	2.4
1	C	345	PRO	2.4
1	A	382	ILE	2.3
1	A	384	GLY	2.3
1	A	387	GLY	2.3
1	B	232	GLY	2.3
1	A	618	PHE	2.3
1	B	460[A]	GLN	2.2
1	D	418	GLN	2.2
1	C	211	ASP	2.2
1	B	43	MET	2.2
1	A	391	TYR	2.2
1	B	345	PRO	2.2
1	C	270	ALA	2.2
1	C	178	GLU	2.1
1	B	418	GLN	2.1
1	D	132	GLN	2.1
1	D	390	THR	2.1
1	A	345	PRO	2.1
1	D	385	THR	2.1
1	C	291	LEU	2.0
1	D	189	ASP	2.0
1	D	387	GLY	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

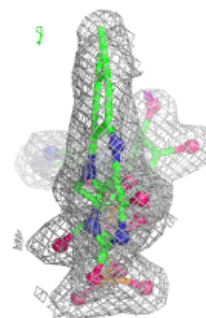
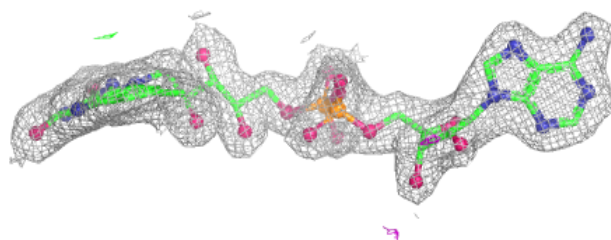
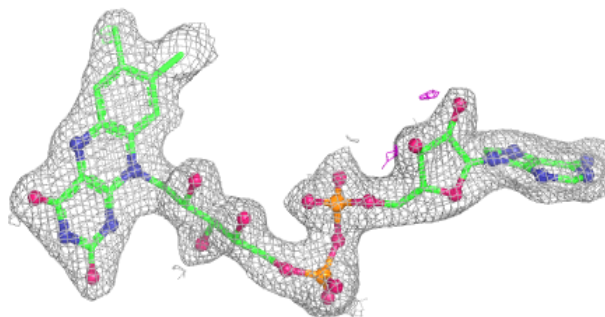
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	MES	A	804	12/12	0.81	0.19	69,76,94,113	0
5	MES	D	804	12/12	0.83	0.18	35,44,54,54	0
4	1PE	C	803	16/16	0.88	0.12	43,47,57,57	0
4	1PE	A	803	12/16	0.89	0.12	30,36,39,40	0
4	1PE	B	704	16/16	0.91	0.10	34,38,52,54	0
4	1PE	D	803	16/16	0.91	0.12	37,40,54,55	0
3	G2F	C	802	12/12	0.92	0.09	31,37,40,43	0
5	MES	B	701	12/12	0.94	0.10	31,37,43,44	0
3	G2F	A	802	12/12	0.94	0.08	24,27,29,29	0
3	G2F	D	802	12/12	0.95	0.08	27,30,31,34	0
3	G2F	B	703	12/12	0.96	0.06	23,25,27,32	0
2	FDA	C	801	53/53	0.97	0.06	23,27,30,32	0
5	MES	D	805	12/12	0.97	0.08	31,33,40,41	0
2	FDA	B	702	53/53	0.98	0.05	13,17,20,21	0
2	FDA	A	801	53/53	0.98	0.05	16,19,20,23	0
2	FDA	D	801	53/53	0.98	0.05	19,22,27,29	0

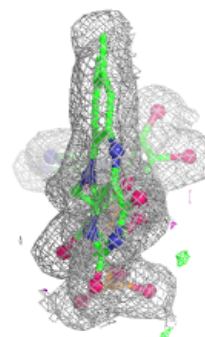
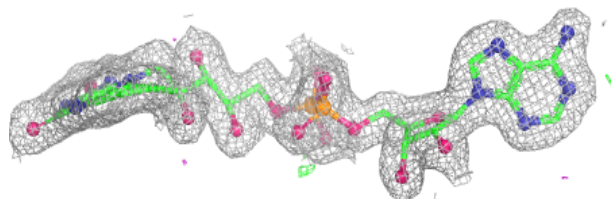
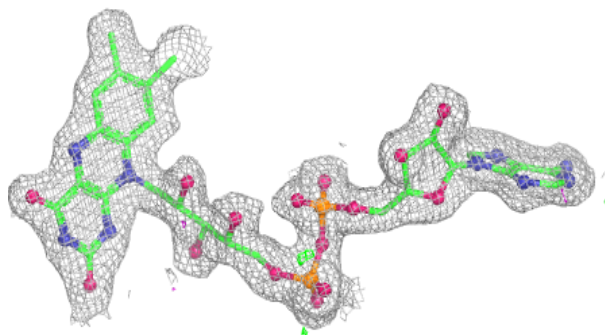
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around FDA C 801:

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

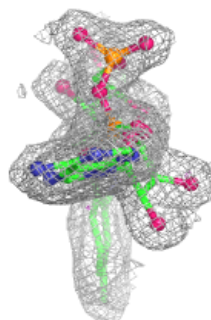
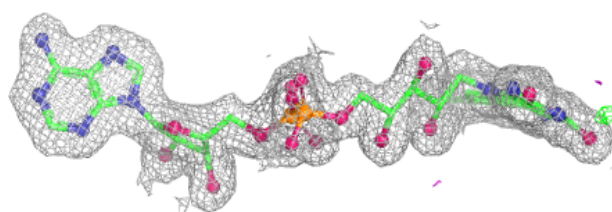
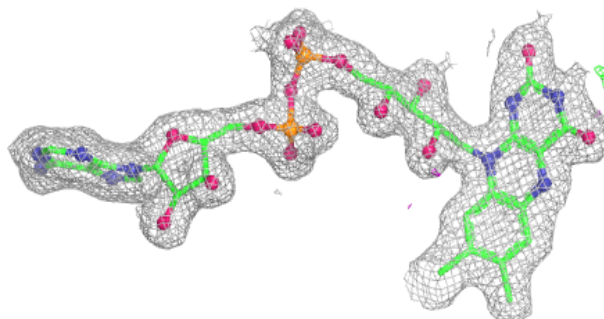
**Electron density around FDA B 702:**

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

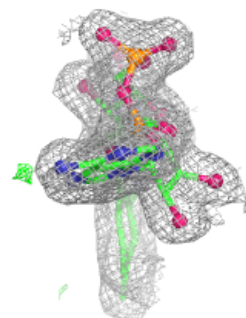
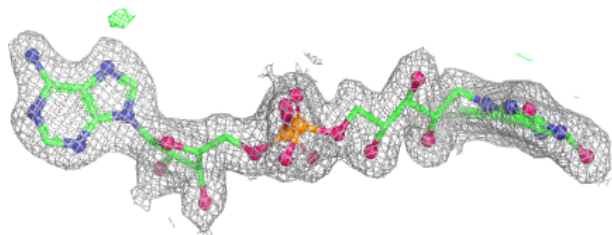
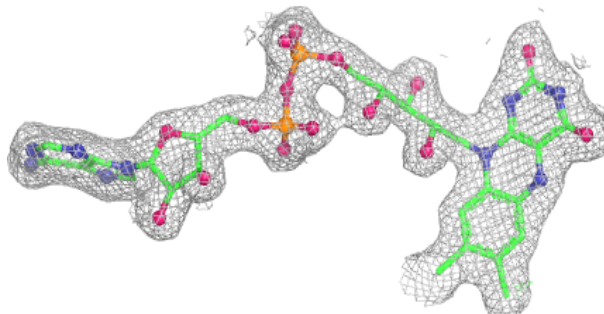


Electron density around FDA A 801:

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

**Electron density around FDA D 801:**

$2mF_o-DF_c$ (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.