



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:42 AM UTC

PDB ID : 1U1C / pdb_00001u1c
Title : Structure of E. coli uridine phosphorylase complexed to 5-benzylacyclouridine (BAU)
Authors : Bu, W.; Settembre, E.C.; Ealick, S.E.
Deposited on : 2004-07-15
Resolution : 2.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

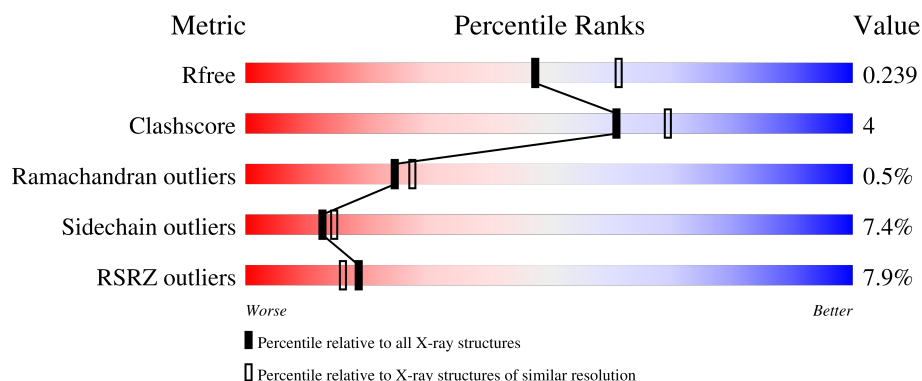
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	256	4% 86% 11% ..
1	B	256	10% 82% 14% ..
1	C	256	11% 81% 15% ..
1	D	256	12% 80% 13% 5%
1	E	256	5% 86% 11% ..

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Mol	Chain	Length	Quality of chain
1	F	256	

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
4	BAU	A	5400	-	X	-	-
4	BAU	B	5011	-	X	-	-
4	BAU	C	5021	-	X	-	-
4	BAU	D	5031	-	X	-	-
4	BAU	E	5041	-	X	-	-
4	BAU	F	5051	-	X	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11925 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 Uridine phosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	253	Total	C	N	O	S	0	0	0
			1895	1186	330	367	12			
1	B	251	Total	C	N	O	S	0	0	0
			1881	1178	328	364	11			
1	C	250	Total	C	N	O	S	0	0	0
			1872	1172	326	363	11			
1	D	242	Total	C	N	O	S	0	0	0
			1810	1135	316	348	11			
1	E	251	Total	C	N	O	S	0	0	0
			1881	1178	328	364	11			
1	F	250	Total	C	N	O	S	0	0	0
			1872	1172	326	363	11			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	cloning artifact	UNP P12758
A	-1	SER	-	cloning artifact	UNP P12758
A	0	HIS	-	cloning artifact	UNP P12758
A	1	MET	-	cloning artifact	UNP P12758
B	-2	GLY	-	cloning artifact	UNP P12758
B	-1	SER	-	cloning artifact	UNP P12758
B	0	HIS	-	cloning artifact	UNP P12758
B	1	MET	-	cloning artifact	UNP P12758
C	-2	GLY	-	cloning artifact	UNP P12758
C	-1	SER	-	cloning artifact	UNP P12758
C	0	HIS	-	cloning artifact	UNP P12758
C	1	MET	-	cloning artifact	UNP P12758
D	-2	GLY	-	cloning artifact	UNP P12758
D	-1	SER	-	cloning artifact	UNP P12758
D	0	HIS	-	cloning artifact	UNP P12758
D	1	MET	-	cloning artifact	UNP P12758
E	-2	GLY	-	cloning artifact	UNP P12758

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-1	SER	-	cloning artifact	UNP P12758
E	0	HIS	-	cloning artifact	UNP P12758
E	1	MET	-	cloning artifact	UNP P12758
F	-2	GLY	-	cloning artifact	UNP P12758
F	-1	SER	-	cloning artifact	UNP P12758
F	0	HIS	-	cloning artifact	UNP P12758
F	1	MET	-	cloning artifact	UNP P12758

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).

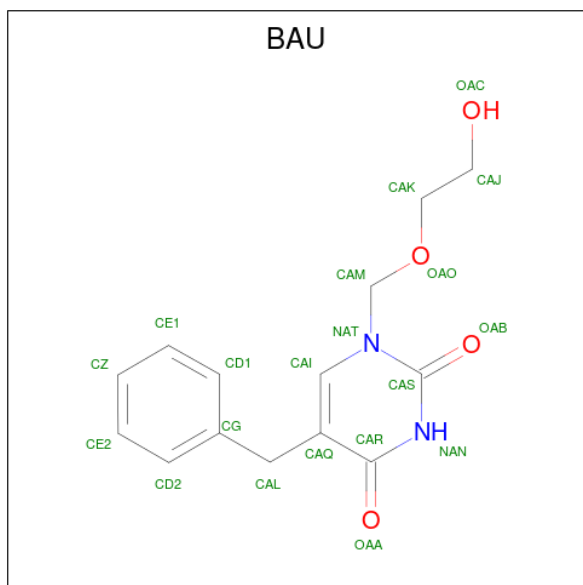


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	E	1	Total	O	P	0	0
			5	4	1		
2	F	1	Total	O	P	0	0
			5	4	1		

- Molecule 3 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total K 1 1	0	0
3	C	1	Total K 1 1	0	0
3	E	1	Total K 1 1	0	0

- Molecule 4 is 1-((2-HYDROXYETHOXY)METHYL)-5-BENZYLPIRIMIDINE-2,4(1H,3H)-DIONE (CCD ID: BAU) (formula: C₁₄H₁₆N₂O₄).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O 20 14 2 4	0	0
4	B	1	Total C N O 20 14 2 4	0	0
4	C	1	Total C N O 20 14 2 4	0	0
4	D	1	Total C N O 20 14 2 4	0	0
4	E	1	Total C N O 20 14 2 4	0	0
4	F	1	Total C N O 20 14 2 4	0	0

- Molecule 5 is water.

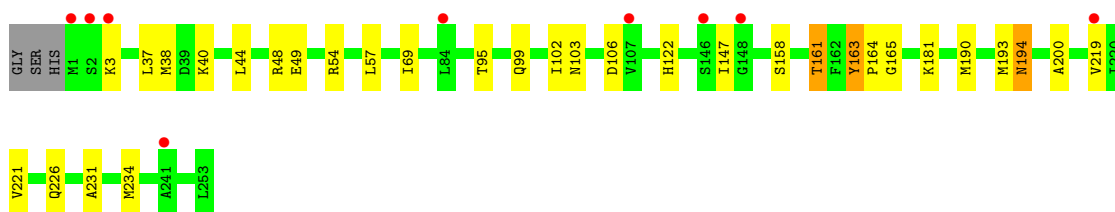
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	99	Total 99	O 99	0	0
5	B	117	Total 117	O 117	0	0
5	C	62	Total 62	O 62	0	0
5	D	70	Total 70	O 70	0	0
5	E	91	Total 91	O 91	0	0
5	F	122	Total 122	O 122	0	0

3 Residue-property plots [i](#)

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

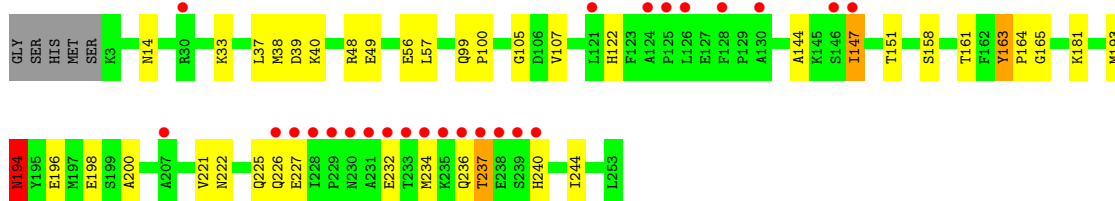
- Molecule 1: Uridine phosphorylase

Chain A: 



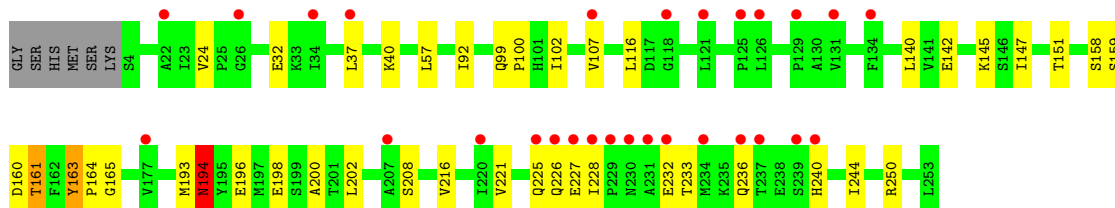
- Molecule 1: Uridine phosphorylase

Chain B: 



- Molecule 1: Uridine phosphorylase

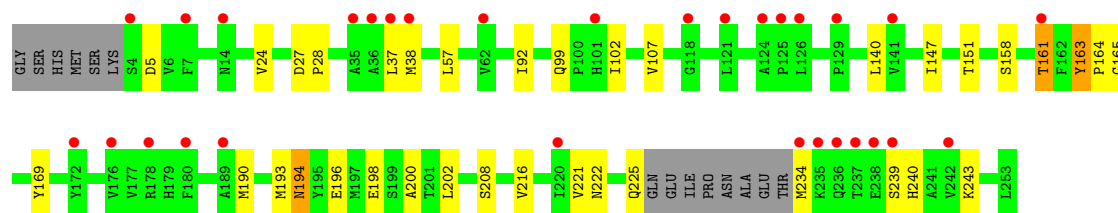
Chain C: 



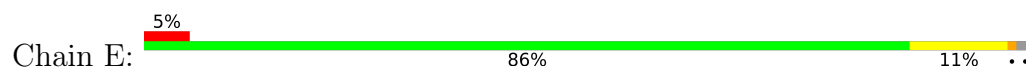
- Molecule 1: Uridine phosphorylase

Chain D: 

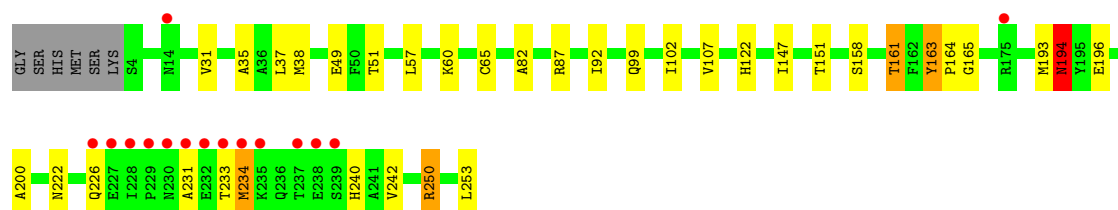
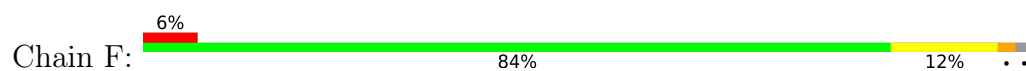




● Molecule 1: Uridine phosphorylase



● Molecule 1: Uridine phosphorylase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	91.37Å 125.97Å 141.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.07 – 2.20 38.07 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.4 (38.07-2.20) 96.3 (38.07-2.20)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.97 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.1.24, CNS	Depositor
R, R_{free}	0.215 , 0.249 0.206 , 0.239	Depositor DCC
R_{free} test set	8362 reflections (10.04%)	wwPDB-VP
Wilson B-factor (Å ²)	31.4	Xtriage
Anisotropy	0.403	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 27.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	11925	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.20% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BAU, K, PO4

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.42	0/1927	0.84	0/2616
1	B	0.42	0/1913	0.85	1/2598 (0.0%)
1	C	0.41	0/1904	0.85	2/2587 (0.1%)
1	D	0.40	0/1840	0.83	1/2497 (0.0%)
1	E	0.41	0/1913	0.84	0/2598
1	F	0.42	0/1904	0.84	1/2587 (0.0%)
All	All	0.41	0/11401	0.84	5/15483 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	24	VAL	N-CA-C	6.12	114.21	108.15
1	D	24	VAL	N-CA-C	5.80	113.90	108.15
1	F	194	ASN	N-CA-C	5.29	116.32	108.60
1	B	194	ASN	N-CA-C	5.21	116.20	108.60
1	C	194	ASN	N-CA-C	5.13	116.09	108.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1895	0	1892	20	0
1	B	1881	0	1875	18	0
1	C	1872	0	1862	15	0
1	D	1810	0	1805	15	0
1	E	1881	0	1875	17	0
1	F	1872	0	1862	20	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
2	E	5	0	0	0	0
2	F	5	0	0	0	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	E	1	0	0	0	0
4	A	20	0	16	0	0
4	B	20	0	16	0	0
4	C	20	0	16	0	0
4	D	20	0	16	0	0
4	E	20	0	16	0	0
4	F	20	0	16	0	0
5	A	99	0	0	0	0
5	B	117	0	0	0	0
5	C	62	0	0	0	0
5	D	70	0	0	1	0
5	E	91	0	0	0	0
5	F	122	0	0	3	0
All	All	11925	0	11267	96	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 (96) 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:F:51:THR:O	5:F:5090:HOH:O	2.06	0.73
1:B:105:GLY:HA2	1:B:237:THR:HB	1.75	0.67
1:F:161:THR:CG2	1:F:165:GLY:H	2.08	0.65
1:D:222:ASN:HB3	1:D:225:GLN:HG2	1.78	0.65
1:E:161:THR:HG21	1:E:164:PRO:HG2	1.79	0.65
1:F:65:CYS:HA	5:F:5090:HOH:O	1.97	0.64
1:A:161:THR:HG21	1:A:164:PRO:HG2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:38:MET:HG2	1:B:57:LEU:HD13	1.83	0.60
1:B:161:THR:CG2	1:B:165:GLY:H	2.15	0.60
1:F:38:MET:HG2	1:F:57:LEU:HD13	1.85	0.59
1:E:161:THR:CG2	1:E:165:GLY:H	2.16	0.59
1:C:158:SER:HB3	1:C:200:ALA:HB2	1.85	0.57
1:B:158:SER:HB3	1:B:200:ALA:HB2	1.87	0.57
1:D:161:THR:CG2	1:D:165:GLY:H	2.18	0.57
1:A:158:SER:HB3	1:A:200:ALA:HB2	1.85	0.56
1:E:158:SER:HB3	1:E:200:ALA:HB2	1.86	0.56
1:F:158:SER:HB3	1:F:200:ALA:HB2	1.87	0.55
1:E:163:TYR:HB2	1:E:164:PRO:CD	2.37	0.55
1:B:193:MET:HB2	1:B:194:ASN:HD22	1.72	0.54
1:B:163:TYR:HB2	1:B:164:PRO:HD3	1.89	0.54
1:A:161:THR:CG2	1:A:165:GLY:H	2.21	0.54
1:E:99:GLN:HB2	1:E:102:ILE:HD12	1.88	0.53
1:A:122:HIS:ND1	1:B:161:THR:HG22	2.24	0.52
1:F:161:THR:HG21	1:F:164:PRO:HG2	1.91	0.52
1:B:144:ALA:HA	1:B:244:ILE:HG12	1.92	0.51
1:B:163:TYR:HB2	1:B:164:PRO:CD	2.41	0.51
1:D:38:MET:HG2	1:D:57:LEU:HD13	1.93	0.51
1:F:82:ALA:O	1:F:87:ARG:NH2	2.43	0.51
1:A:161:THR:HG22	1:A:165:GLY:H	1.74	0.51
1:C:193:MET:HB2	1:C:194:ASN:HD22	1.75	0.51
1:C:161:THR:CG2	1:C:165:GLY:H	2.24	0.50
1:F:99:GLN:HB2	1:F:102:ILE:HD12	1.94	0.50
1:A:161:THR:HB	1:B:122:HIS:ND1	2.27	0.49
1:D:208:SER:HB2	1:E:190:MET:HG2	1.93	0.49
1:E:161:THR:HG22	1:E:165:GLY:H	1.77	0.49
1:D:193:MET:HB2	1:D:194:ASN:HD22	1.78	0.49
1:C:163:TYR:HB2	1:C:164:PRO:CD	2.43	0.48
1:A:163:TYR:HB2	1:A:164:PRO:CD	2.44	0.48
1:D:161:THR:HG21	1:D:164:PRO:HG2	1.96	0.48
1:B:107:VAL:HG13	1:B:151:THR:HG23	1.95	0.48
1:A:44:LEU:HD11	1:A:54:ARG:HB2	1.96	0.47
1:A:190:MET:HG2	1:C:208:SER:HB2	1.96	0.47
1:F:102:ILE:O	1:F:222:ASN:ND2	2.46	0.47
1:F:163:TYR:HB2	1:F:164:PRO:HD3	1.97	0.47
1:A:38:MET:HG2	1:A:57:LEU:HD13	1.97	0.47
1:D:163:TYR:HB2	1:D:164:PRO:HD3	1.97	0.47
1:F:231:ALA:HA	1:F:234:MET:HB2	1.97	0.47
1:B:222:ASN:HB3	1:B:225:GLN:HG2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:163:TYR:HB2	1:D:164:PRO:CD	2.44	0.46
1:A:231:ALA:HA	1:A:234:MET:HE3	1.97	0.46
1:D:99:GLN:HB2	1:D:102:ILE:HD12	1.97	0.46
1:F:60:LYS:HE2	1:F:253:LEU:HB3	1.97	0.46
1:A:193:MET:HB2	1:A:194:ASN:HD22	1.80	0.46
1:D:158:SER:HB3	1:D:200:ALA:HB2	1.96	0.46
1:C:163:TYR:HB2	1:C:164:PRO:HD3	1.98	0.46
1:A:49:GLU:HB3	1:B:49:GLU:HB3	1.98	0.46
1:D:169:TYR:HA	5:D:5078:HOH:O	2.15	0.46
1:D:190:MET:HG2	1:E:208:SER:HB2	1.97	0.46
1:F:163:TYR:HB2	1:F:164:PRO:CD	2.45	0.46
1:A:95:THR:HG23	1:A:219:VAL:HG12	1.98	0.45
1:E:161:THR:HG21	1:E:165:GLY:H	1.81	0.45
1:B:39:ASP:HB2	1:B:56:GLU:HB3	1.98	0.45
1:E:102:ILE:O	1:E:222:ASN:ND2	2.50	0.45
1:C:140:LEU:HD22	1:C:216:VAL:HB	1.99	0.45
1:E:161:THR:HB	1:F:122:HIS:ND1	2.32	0.44
1:F:31:VAL:HG11	5:F:5090:HOH:O	2.17	0.44
1:C:161:THR:HG21	1:C:164:PRO:HG2	1.98	0.44
1:B:147:ILE:HG12	1:B:244:ILE:HG13	2.00	0.44
1:E:163:TYR:CB	1:E:164:PRO:CD	2.95	0.43
1:E:194:ASN:N	1:E:194:ASN:HD22	2.17	0.43
1:F:35:ALA:HA	1:F:38:MET:HE3	2.01	0.43
1:E:99:GLN:HA	1:E:100:PRO:HD3	1.92	0.42
1:F:57:LEU:HG	1:F:250:ARG:HG3	2.01	0.42
1:A:99:GLN:HB2	1:A:102:ILE:HD12	2.02	0.42
1:C:107:VAL:HG21	1:C:244:ILE:HD13	2.02	0.42
1:C:57:LEU:HD21	1:C:250:ARG:HG3	2.00	0.42
1:F:193:MET:HB2	1:F:194:ASN:HD22	1.84	0.42
1:C:99:GLN:HB2	1:C:102:ILE:HD12	2.01	0.42
1:D:107:VAL:HG13	1:D:151:THR:HG23	2.01	0.42
1:E:38:MET:HG2	1:E:57:LEU:HD13	2.02	0.42
1:E:140:LEU:HD22	1:E:216:VAL:HB	2.02	0.42
1:A:69:ILE:HD11	1:B:48:ARG:HD3	2.02	0.41
1:B:163:TYR:CB	1:B:164:PRO:CD	2.97	0.41
1:A:48:ARG:HB3	1:A:49:GLU:OE2	2.19	0.41
1:A:106:ASP:O	1:A:219:VAL:HG22	2.20	0.41
1:C:107:VAL:HG13	1:C:151:THR:HG23	2.02	0.41
1:D:27:ASP:HA	1:D:28:PRO:HD2	1.91	0.41
1:A:163:TYR:CB	1:A:164:PRO:CD	2.98	0.41
1:F:107:VAL:HG13	1:F:151:THR:HG23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:140:LEU:HD22	1:D:216:VAL:HB	2.03	0.41
1:E:49:GLU:HB3	1:F:49:GLU:HB3	2.01	0.41
1:C:99:GLN:HA	1:C:100:PRO:HD3	1.93	0.40
1:C:163:TYR:CB	1:C:164:PRO:CD	2.99	0.40
1:B:99:GLN:HA	1:B:100:PRO:HD3	1.91	0.40
1:C:116:LEU:HB2	1:C:159:SER:HA	2.04	0.40
1:A:103:ASN:O	1:A:219:VAL:HG21	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	251/256 (98%)	246 (98%)	4 (2%)	1 (0%)	30	34
1	B	249/256 (97%)	247 (99%)	1 (0%)	1 (0%)	30	34
1	C	248/256 (97%)	240 (97%)	6 (2%)	2 (1%)	16	16
1	D	238/256 (93%)	233 (98%)	4 (2%)	1 (0%)	30	34
1	E	249/256 (97%)	245 (98%)	3 (1%)	1 (0%)	30	34
1	F	248/256 (97%)	245 (99%)	2 (1%)	1 (0%)	30	34
All	All	1483/1536 (96%)	1456 (98%)	20 (1%)	7 (0%)	24	27

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	163	TYR
1	A	163	TYR
1	B	163	TYR
1	C	163	TYR
1	D	163	TYR

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Mol	Chain	Res	Type
1	F	163	TYR
1	C	228	ILE

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	202/206 (98%)	193 (96%)	9 (4%)	24	33
1	B	200/206 (97%)	183 (92%)	17 (8%)	10	11
1	C	199/206 (97%)	178 (89%)	21 (11%)	6	6
1	D	192/206 (93%)	178 (93%)	14 (7%)	13	15
1	E	200/206 (97%)	185 (92%)	15 (8%)	12	14
1	F	199/206 (97%)	187 (94%)	12 (6%)	17	21
All	All	1192/1236 (96%)	1104 (93%)	88 (7%)	13	14

All (88) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LYS
1	A	37	LEU
1	A	40	LYS
1	A	147	ILE
1	A	161	THR
1	A	181	LYS
1	A	194	ASN
1	A	221	VAL
1	A	226	GLN
1	B	14	ASN
1	B	33	LYS
1	B	37	LEU
1	B	40	LYS
1	B	147	ILE
1	B	181	LYS
1	B	194	ASN

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Mol	Chain	Res	Type
1	B	196	GLU
1	B	198	GLU
1	B	221	VAL
1	B	226	GLN
1	B	227	GLU
1	B	232	GLU
1	B	234	MET
1	B	236	GLN
1	B	237	THR
1	B	240	HIS
1	C	32	GLU
1	C	37	LEU
1	C	40	LYS
1	C	92	ILE
1	C	142	GLU
1	C	145	LYS
1	C	147	ILE
1	C	160	ASP
1	C	161	THR
1	C	194	ASN
1	C	196	GLU
1	C	198	GLU
1	C	202	LEU
1	C	221	VAL
1	C	225	GLN
1	C	226	GLN
1	C	227	GLU
1	C	232	GLU
1	C	233	THR
1	C	236	GLN
1	C	240	HIS
1	D	5	ASP
1	D	37	LEU
1	D	92	ILE
1	D	147	ILE
1	D	161	THR
1	D	194	ASN
1	D	196	GLU
1	D	198	GLU
1	D	202	LEU
1	D	221	VAL
1	D	234	MET

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Mol	Chain	Res	Type
1	D	239	SER
1	D	240	HIS
1	D	243	LYS
1	E	3	LYS
1	E	13	LYS
1	E	92	ILE
1	E	142	GLU
1	E	147	ILE
1	E	161	THR
1	E	181	LYS
1	E	194	ASN
1	E	196	GLU
1	E	221	VAL
1	E	232	GLU
1	E	234	MET
1	E	238	GLU
1	E	239	SER
1	E	240	HIS
1	F	37	LEU
1	F	92	ILE
1	F	147	ILE
1	F	161	THR
1	F	194	ASN
1	F	196	GLU
1	F	226	GLN
1	F	233	THR
1	F	234	MET
1	F	240	HIS
1	F	242	VAL
1	F	250	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	GLN
1	A	47	HIS
1	A	194	ASN
1	B	17	GLN
1	B	47	HIS
1	B	194	ASN
1	B	225	GLN
1	B	230	ASN

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Mol	Chain	Res	Type
1	C	101	HIS
1	C	103	ASN
1	C	152	HIS
1	C	194	ASN
1	C	209	GLN
1	D	101	HIS
1	D	152	HIS
1	D	179	HIS
1	D	194	ASN
1	E	47	HIS
1	E	152	HIS
1	E	194	ASN
1	E	236	GLN
1	E	240	HIS
1	F	17	GLN
1	F	194	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 3 are monoatomic - leaving 12 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	BAU	A	5400	-	21,21,21	3.16	14 (66%)	25,27,27	2.64	8 (32%)
2	PO4	F	3052	-	4,4,4	0.93	0	6,6,6	0.43	0
4	BAU	B	5011	-	21,21,21	3.16	14 (66%)	25,27,27	2.67	8 (32%)
4	BAU	F	5051	-	21,21,21	3.14	13 (61%)	25,27,27	2.64	9 (36%)
2	PO4	C	3022	-	4,4,4	0.98	0	6,6,6	0.44	0
2	PO4	A	3030	-	4,4,4	0.96	0	6,6,6	0.48	0
4	BAU	D	5031	-	21,21,21	3.15	14 (66%)	25,27,27	2.62	9 (36%)
2	PO4	B	3012	-	4,4,4	0.99	0	6,6,6	0.46	0
4	BAU	E	5041	-	21,21,21	3.16	14 (66%)	25,27,27	2.63	8 (32%)
2	PO4	E	3042	-	4,4,4	1.01	0	6,6,6	0.45	0
2	PO4	D	3032	-	4,4,4	1.00	0	6,6,6	0.46	0
4	BAU	C	5021	-	21,21,21	3.18	14 (66%)	25,27,27	2.63	9 (36%)

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
4	BAU	A	5400	-	-	3/9/9/9	0/2/2/2
4	BAU	F	5051	-	-	3/9/9/9	0/2/2/2
4	BAU	B	5011	-	-	2/9/9/9	0/2/2/2
4	BAU	D	5031	-	-	2/9/9/9	0/2/2/2
4	BAU	C	5021	-	-	4/9/9/9	0/2/2/2
4	BAU	E	5041	-	-	3/9/9/9	0/2/2/2

All (83) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	5041	BAU	CAM-NAT	-7.62	1.36	1.47
4	A	5400	BAU	CAM-NAT	-7.62	1.36	1.47
4	C	5021	BAU	CAM-NAT	-7.55	1.36	1.47
4	B	5011	BAU	CAM-NAT	-7.52	1.36	1.47
4	F	5051	BAU	CAM-NAT	-7.49	1.36	1.47
4	D	5031	BAU	CAM-NAT	-7.45	1.36	1.47
4	E	5041	BAU	CAS-NAT	6.03	1.46	1.37
4	D	5031	BAU	CAS-NAT	6.03	1.46	1.37
4	C	5021	BAU	CAS-NAT	6.02	1.46	1.37
4	B	5011	BAU	CAS-NAT	6.00	1.46	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	5051	BAU	CAS-NAT	5.93	1.45	1.37
4	A	5400	BAU	CAS-NAT	5.93	1.45	1.37
4	C	5021	BAU	CAL-CAQ	4.00	1.58	1.51
4	A	5400	BAU	CAI-NAT	4.00	1.44	1.37
4	A	5400	BAU	CAL-CAQ	3.98	1.58	1.51
4	E	5041	BAU	CAI-NAT	3.91	1.44	1.37
4	D	5031	BAU	CAI-NAT	3.89	1.44	1.37
4	E	5041	BAU	CAL-CAQ	3.89	1.58	1.51
4	B	5011	BAU	CAI-NAT	3.88	1.44	1.37
4	D	5031	BAU	CAL-CAQ	3.87	1.58	1.51
4	C	5021	BAU	CAI-NAT	3.85	1.44	1.37
4	B	5011	BAU	CAL-CAQ	3.84	1.58	1.51
4	F	5051	BAU	CAL-CAQ	3.84	1.58	1.51
4	F	5051	BAU	CAI-NAT	3.81	1.44	1.37
4	C	5021	BAU	CE2-CD2	3.64	1.45	1.38
4	D	5031	BAU	CE2-CD2	3.57	1.45	1.38
4	B	5011	BAU	CE2-CD2	3.56	1.45	1.38
4	F	5051	BAU	CE2-CD2	3.56	1.45	1.38
4	A	5400	BAU	CE2-CD2	3.54	1.45	1.38
4	E	5041	BAU	CE2-CD2	3.54	1.45	1.38
4	B	5011	BAU	CD2-CG	3.50	1.45	1.38
4	D	5031	BAU	CD2-CG	3.46	1.45	1.38
4	F	5051	BAU	CD2-CG	3.46	1.45	1.38
4	A	5400	BAU	CD2-CG	3.43	1.45	1.38
4	C	5021	BAU	CD2-CG	3.42	1.45	1.38
4	E	5041	BAU	CD2-CG	3.40	1.45	1.38
4	C	5021	BAU	CD1-CG	3.02	1.44	1.38
4	B	5011	BAU	CZ-CE2	3.01	1.44	1.38
4	F	5051	BAU	CZ-CE2	3.00	1.44	1.38
4	C	5021	BAU	CZ-CE2	3.00	1.44	1.38
4	E	5041	BAU	CZ-CE2	2.99	1.44	1.38
4	A	5400	BAU	CD1-CG	2.97	1.44	1.38
4	C	5021	BAU	CE1-CZ	2.96	1.44	1.38
4	F	5051	BAU	CD1-CG	2.96	1.44	1.38
4	D	5031	BAU	CZ-CE2	2.96	1.44	1.38
4	D	5031	BAU	CE1-CZ	2.95	1.44	1.38
4	A	5400	BAU	CZ-CE2	2.95	1.44	1.38
4	E	5041	BAU	CD1-CG	2.94	1.44	1.38
4	D	5031	BAU	CD1-CG	2.94	1.44	1.38
4	B	5011	BAU	CD1-CG	2.92	1.44	1.38
4	B	5011	BAU	CE1-CZ	2.92	1.44	1.38
4	F	5051	BAU	CE1-CZ	2.89	1.44	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	5041	BAU	CE1-CZ	2.87	1.44	1.38
4	A	5400	BAU	CE1-CZ	2.83	1.44	1.38
4	C	5021	BAU	CAS-NAN	2.79	1.42	1.38
4	F	5051	BAU	CAS-NAN	2.78	1.42	1.38
4	B	5011	BAU	CE1-CD1	2.70	1.43	1.38
4	B	5011	BAU	CAS-NAN	2.69	1.42	1.38
4	D	5031	BAU	CAS-NAN	2.69	1.42	1.38
4	A	5400	BAU	CAS-NAN	2.67	1.42	1.38
4	E	5041	BAU	CAS-NAN	2.62	1.42	1.38
4	F	5051	BAU	CE1-CD1	2.60	1.43	1.38
4	C	5021	BAU	CE1-CD1	2.58	1.43	1.38
4	E	5041	BAU	CE1-CD1	2.58	1.43	1.38
4	D	5031	BAU	CE1-CD1	2.57	1.43	1.38
4	A	5400	BAU	CE1-CD1	2.47	1.43	1.38
4	A	5400	BAU	OAO-CAM	-2.42	1.34	1.40
4	E	5041	BAU	OAO-CAM	-2.39	1.34	1.40
4	F	5051	BAU	OAO-CAM	-2.36	1.34	1.40
4	D	5031	BAU	OAO-CAM	-2.35	1.34	1.40
4	C	5021	BAU	OAO-CAM	-2.34	1.34	1.40
4	B	5011	BAU	OAO-CAM	-2.33	1.34	1.40
4	C	5021	BAU	CAR-NAN	2.23	1.43	1.38
4	F	5051	BAU	CAI-CAQ	2.21	1.41	1.35
4	D	5031	BAU	CAI-CAQ	2.20	1.41	1.35
4	E	5041	BAU	CAI-CAQ	2.20	1.41	1.35
4	C	5021	BAU	CAI-CAQ	2.18	1.41	1.35
4	B	5011	BAU	CAI-CAQ	2.17	1.41	1.35
4	A	5400	BAU	CAI-CAQ	2.15	1.41	1.35
4	D	5031	BAU	CAR-NAN	2.11	1.42	1.38
4	B	5011	BAU	CAR-NAN	2.08	1.42	1.38
4	E	5041	BAU	CAR-NAN	2.07	1.42	1.38
4	A	5400	BAU	CAR-NAN	2.03	1.42	1.38

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	5400	BAU	OAO-CAM-NAT	8.19	127.98	111.58
4	B	5011	BAU	OAO-CAM-NAT	8.18	127.97	111.58
4	F	5051	BAU	OAO-CAM-NAT	8.18	127.97	111.58
4	D	5031	BAU	OAO-CAM-NAT	8.11	127.83	111.58
4	C	5021	BAU	OAO-CAM-NAT	8.06	127.73	111.58
4	E	5041	BAU	OAO-CAM-NAT	8.06	127.72	111.58
4	B	5011	BAU	CAM-NAT-CAS	5.47	123.48	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	5021	BAU	CAM-NAT-CAS	5.46	123.46	117.20
4	E	5041	BAU	CAM-NAT-CAS	5.40	123.40	117.20
4	F	5051	BAU	CAM-NAT-CAS	5.30	123.28	117.20
4	D	5031	BAU	CAM-NAT-CAS	5.19	123.16	117.20
4	A	5400	BAU	CAM-NAT-CAS	5.10	123.05	117.20
4	B	5011	BAU	CAK-OAO-CAM	-4.32	104.62	113.55
4	A	5400	BAU	CAK-OAO-CAM	-4.27	104.73	113.55
4	C	5021	BAU	CAK-OAO-CAM	-4.13	105.02	113.55
4	E	5041	BAU	CAK-OAO-CAM	-4.08	105.12	113.55
4	F	5051	BAU	CAK-OAO-CAM	-4.04	105.20	113.55
4	D	5031	BAU	CAK-OAO-CAM	-3.99	105.31	113.55
4	A	5400	BAU	CAQ-CAR-NAN	3.86	121.10	115.21
4	D	5031	BAU	CAQ-CAR-NAN	3.85	121.09	115.21
4	B	5011	BAU	CAQ-CAR-NAN	3.84	121.07	115.21
4	D	5031	BAU	CAR-NAN-CAS	-3.83	122.32	127.34
4	C	5021	BAU	CAQ-CAR-NAN	3.82	121.05	115.21
4	E	5041	BAU	CAQ-CAR-NAN	3.80	121.00	115.21
4	F	5051	BAU	CAR-NAN-CAS	-3.78	122.38	127.34
4	E	5041	BAU	CAR-NAN-CAS	-3.72	122.46	127.34
4	F	5051	BAU	CAQ-CAR-NAN	3.72	120.88	115.21
4	B	5011	BAU	CAR-NAN-CAS	-3.71	122.47	127.34
4	A	5400	BAU	CAR-NAN-CAS	-3.70	122.48	127.34
4	C	5021	BAU	CAR-NAN-CAS	-3.70	122.49	127.34
4	A	5400	BAU	OAO-CAK-CAJ	2.89	122.86	110.11
4	C	5021	BAU	OAO-CAK-CAJ	2.88	122.81	110.11
4	B	5011	BAU	OAO-CAK-CAJ	2.87	122.78	110.11
4	E	5041	BAU	OAO-CAK-CAJ	2.87	122.75	110.11
4	D	5031	BAU	OAO-CAK-CAJ	2.86	122.71	110.11
4	F	5051	BAU	OAO-CAK-CAJ	2.74	122.19	110.11
4	F	5051	BAU	NAN-CAS-NAT	2.44	116.96	114.86
4	E	5041	BAU	NAN-CAS-NAT	2.32	116.86	114.86
4	D	5031	BAU	NAN-CAS-NAT	2.30	116.83	114.86
4	D	5031	BAU	OAA-CAR-CAQ	-2.20	121.00	124.71
4	A	5400	BAU	NAN-CAS-NAT	2.15	116.71	114.86
4	C	5021	BAU	OAA-CAR-CAQ	-2.11	121.16	124.71
4	B	5011	BAU	NAN-CAS-NAT	2.09	116.65	114.86
4	B	5011	BAU	OAA-CAR-CAQ	-2.08	121.21	124.71
4	D	5031	BAU	OAC-CAJ-CAK	2.07	123.98	111.82
4	C	5021	BAU	NAN-CAS-NAT	2.06	116.63	114.86
4	C	5021	BAU	OAC-CAJ-CAK	2.04	123.81	111.82
4	E	5041	BAU	OAC-CAJ-CAK	2.03	123.78	111.82
4	F	5051	BAU	OAA-CAR-CAQ	-2.02	121.32	124.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	5400	BAU	OAC-CAJ-CAK	2.01	123.66	111.82
4	F	5051	BAU	OAC-CAJ-CAK	2.00	123.62	111.82

There are no chirality outliers.

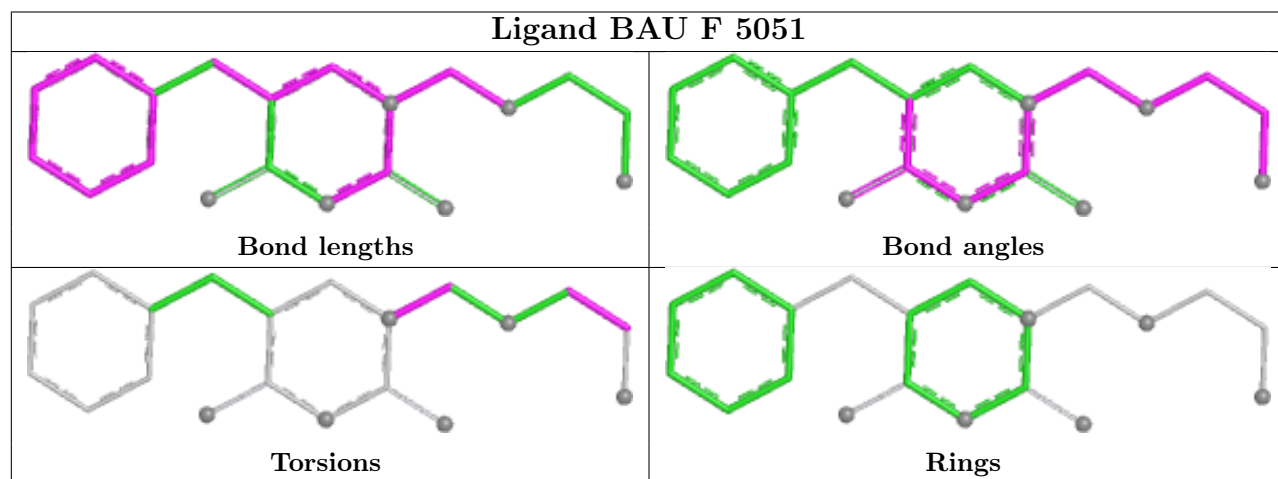
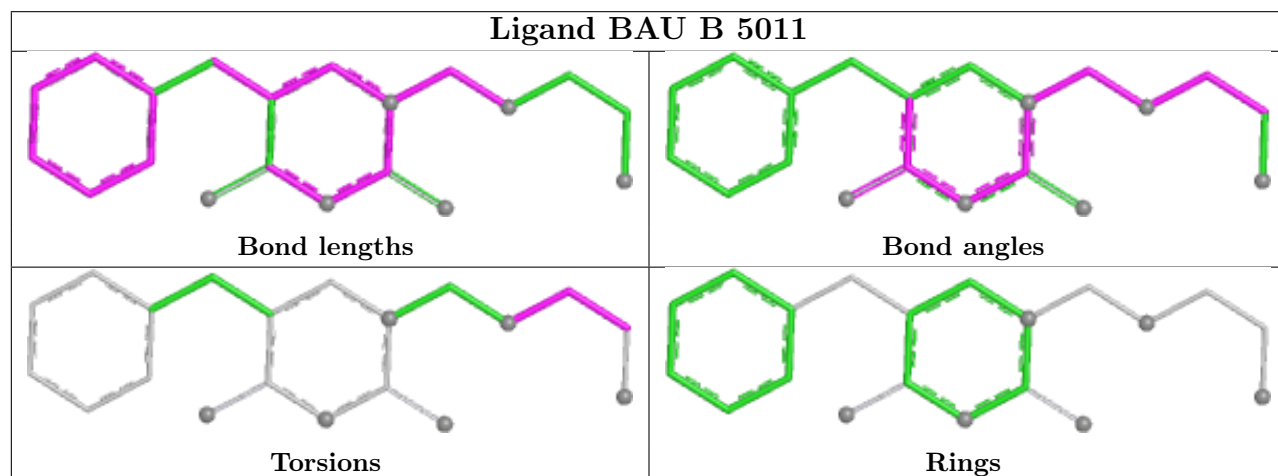
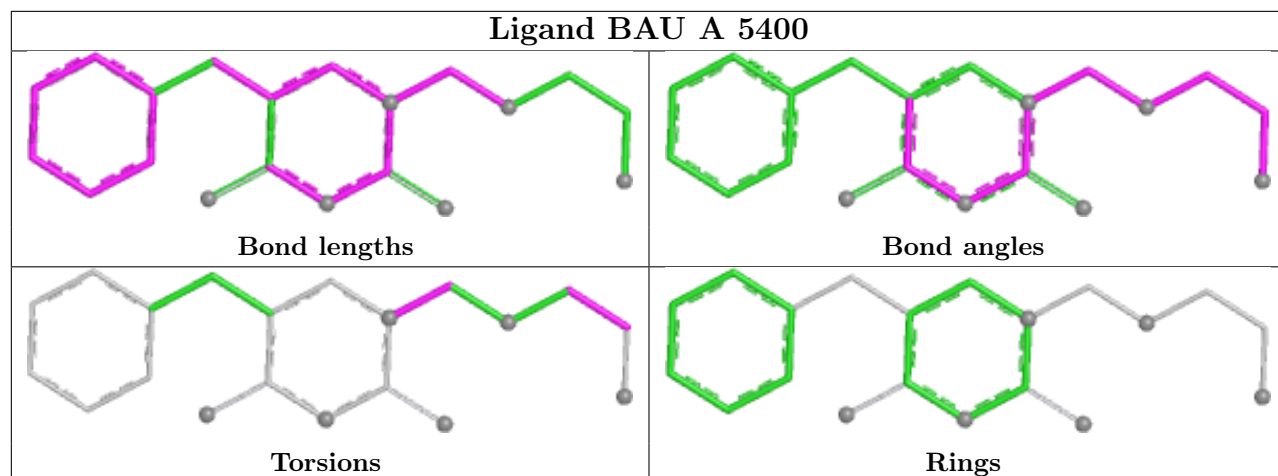
All (17) torsion outliers are listed below:

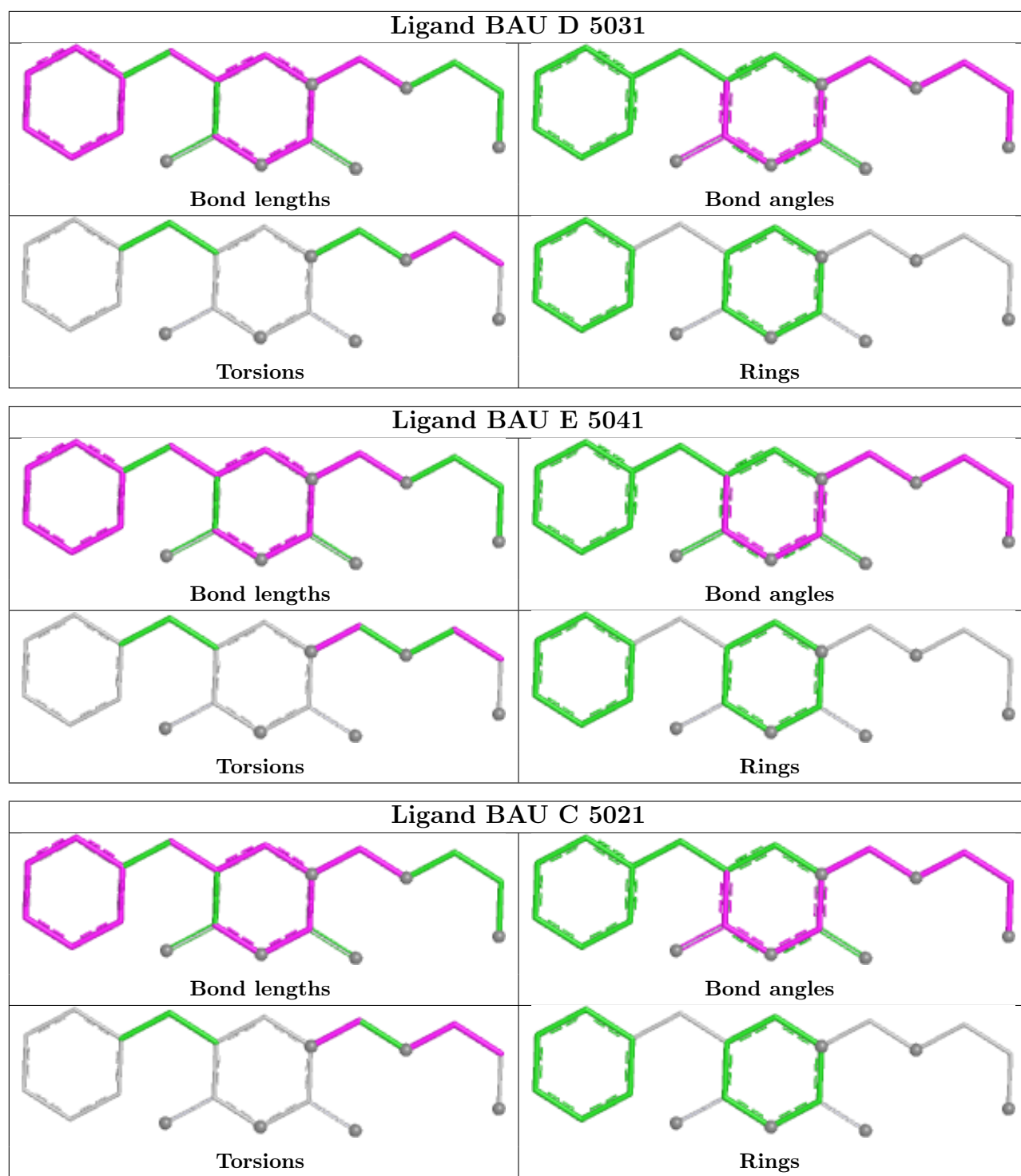
Mol	Chain	Res	Type	Atoms
4	A	5400	BAU	OAO-CAM-NAT-CAS
4	B	5011	BAU	CAJ-CAK-OAO-CAM
4	C	5021	BAU	OAC-CAJ-CAK-OAO
4	D	5031	BAU	OAC-CAJ-CAK-OAO
4	B	5011	BAU	OAC-CAJ-CAK-OAO
4	D	5031	BAU	CAJ-CAK-OAO-CAM
4	A	5400	BAU	OAC-CAJ-CAK-OAO
4	E	5041	BAU	OAC-CAJ-CAK-OAO
4	F	5051	BAU	OAC-CAJ-CAK-OAO
4	E	5041	BAU	OAO-CAM-NAT-CAS
4	F	5051	BAU	OAO-CAM-NAT-CAS
4	A	5400	BAU	OAO-CAM-NAT-CAI
4	C	5021	BAU	OAO-CAM-NAT-CAI
4	E	5041	BAU	OAO-CAM-NAT-CAI
4	F	5051	BAU	OAO-CAM-NAT-CAI
4	C	5021	BAU	CAJ-CAK-OAO-CAM
4	C	5021	BAU	OAO-CAM-NAT-CAS

There are no ring outliers.

No monomer is involved in short contacts.

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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	253/256 (98%)	0.56	9 (3%) 46 43	23, 32, 43, 46	0
1	B	251/256 (98%)	0.73	25 (9%) 12 10	17, 19, 25, 31	0
1	C	250/256 (97%)	1.00	28 (11%) 10 8	17, 20, 22, 23	0
1	D	242/256 (94%)	0.91	30 (12%) 8 6	17, 19, 22, 27	0
1	E	251/256 (98%)	0.40	12 (4%) 35 32	17, 19, 24, 27	0
1	F	250/256 (97%)	0.38	15 (6%) 27 24	17, 19, 26, 30	0
All	All	1497/1536 (97%)	0.66	119 (7%) 18 16	17, 20, 36, 46	0

All (119) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	SER	7.2
1	D	237	THR	6.7
1	E	229	PRO	6.7
1	F	230	ASN	6.6
1	B	230	ASN	6.3
1	B	231	ALA	6.0
1	B	238	GLU	5.9
1	B	227	GLU	5.7
1	E	227	GLU	5.6
1	C	225	GLN	5.6
1	D	234	MET	5.5
1	E	228	ILE	5.5
1	E	234	MET	5.4
1	F	228	ILE	5.4
1	B	234	MET	5.4
1	C	226	GLN	5.4
1	B	229	PRO	5.4
1	B	228	ILE	5.3
1	B	233	THR	5.3

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Mol	Chain	Res	Type	RSRZ
1	F	237	THR	5.1
1	B	237	THR	5.0
1	C	227	GLU	4.9
1	B	232	GLU	4.9
1	F	229	PRO	4.9
1	F	227	GLU	4.9
1	B	226	GLN	4.8
1	F	226	GLN	4.7
1	C	228	ILE	4.7
1	D	239	SER	4.6
1	D	238	GLU	4.5
1	A	1	MET	4.4
1	F	233	THR	4.4
1	D	235	LYS	3.9
1	E	231	ALA	3.9
1	D	126	LEU	3.7
1	C	234	MET	3.7
1	C	229	PRO	3.6
1	C	236	GLN	3.6
1	B	125	PRO	3.5
1	F	238	GLU	3.5
1	F	234	MET	3.5
1	C	126	LEU	3.2
1	B	207	ALA	3.1
1	B	236	GLN	3.1
1	B	235	LYS	3.1
1	C	237	THR	3.0
1	C	121	LEU	3.0
1	F	232	GLU	2.9
1	E	226	GLN	2.9
1	D	38	MET	2.9
1	C	232	GLU	2.8
1	B	121	LEU	2.8
1	A	146	SER	2.7
1	D	121	LEU	2.7
1	C	125	PRO	2.7
1	F	235	LYS	2.7
1	D	220	ILE	2.7
1	D	176	VAL	2.6
1	C	239	SER	2.6
1	D	35	ALA	2.6
1	C	230	ASN	2.6

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Mol	Chain	Res	Type	RSRZ
1	E	147	ILE	2.6
1	E	238	GLU	2.5
1	E	233	THR	2.5
1	C	220	ILE	2.5
1	B	146	SER	2.5
1	D	180	PHE	2.5
1	B	147	ILE	2.5
1	C	207	ALA	2.5
1	E	237	THR	2.4
1	C	34	ILE	2.4
1	C	131	VAL	2.4
1	C	37	LEU	2.4
1	D	125	PRO	2.4
1	F	231	ALA	2.4
1	A	3	LYS	2.4
1	B	128	PHE	2.4
1	C	240	HIS	2.3
1	B	126	LEU	2.3
1	F	239	SER	2.3
1	D	62	VAL	2.3
1	D	14	ASN	2.3
1	C	129	PRO	2.3
1	B	124	ALA	2.3
1	C	231	ALA	2.3
1	D	124	ALA	2.3
1	E	240	HIS	2.3
1	A	84	LEU	2.2
1	A	241	ALA	2.2
1	D	242	VAL	2.2
1	D	129	PRO	2.2
1	B	130	ALA	2.2
1	C	134	PHE	2.2
1	C	26	GLY	2.2
1	C	118	GLY	2.2
1	B	239	SER	2.2
1	D	172	TYR	2.2
1	C	107	VAL	2.2
1	D	7	PHE	2.2
1	B	240	HIS	2.2
1	D	101	HIS	2.2
1	D	36	ALA	2.2
1	D	178	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	118	GLY	2.1
1	E	172	TYR	2.1
1	F	14	ASN	2.1
1	A	219	VAL	2.1
1	A	148	GLY	2.1
1	D	4	SER	2.1
1	D	161	THR	2.1
1	D	236	GLN	2.1
1	A	107	VAL	2.1
1	C	177	VAL	2.1
1	D	141	VAL	2.1
1	B	30	ARG	2.1
1	F	175	ARG	2.1
1	D	37	LEU	2.0
1	C	22	ALA	2.0
1	D	189	ALA	2.0

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($\text{\AA}^2$)	Q<0.9
3	K	C	1003	1/1	0.68	0.30	71,71,71,71	0
3	K	A	1001	1/1	0.82	0.30	54,54,54,54	0
3	K	E	1002	1/1	0.86	0.31	59,59,59,59	0
4	BAU	C	5021	20/20	0.86	0.12	41,41,42,42	0
4	BAU	A	5400	20/20	0.90	0.10	31,32,34,34	0
4	BAU	D	5031	20/20	0.90	0.10	36,37,39,40	0
4	BAU	F	5051	20/20	0.92	0.10	31,31,32,32	0

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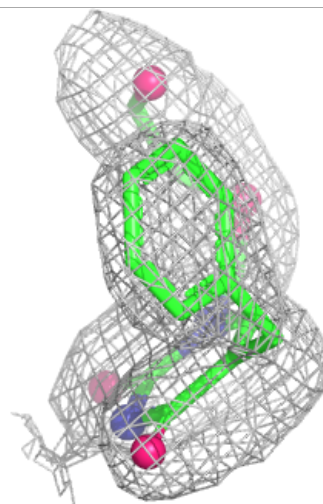
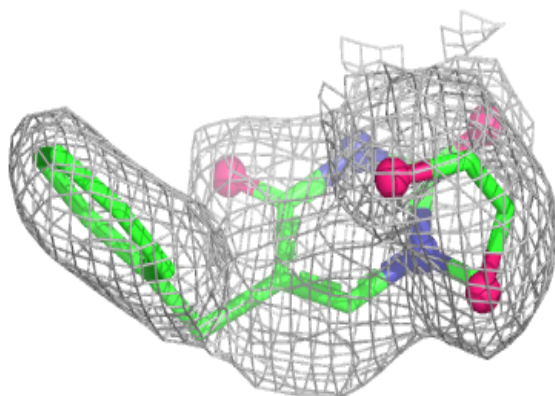
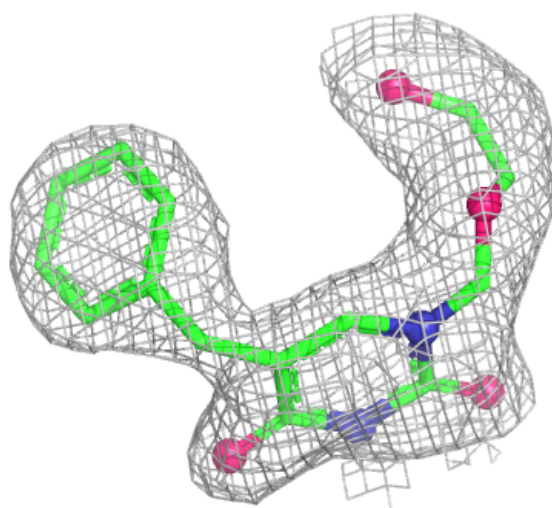
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	BAU	E	5041	20/20	0.93	0.09	33,33,34,34	0
4	BAU	B	5011	20/20	0.93	0.09	32,33,34,35	0
2	PO4	C	3022	5/5	0.94	0.10	41,41,41,41	0
2	PO4	E	3042	5/5	0.96	0.08	37,37,38,38	0
2	PO4	A	3030	5/5	0.96	0.06	29,29,30,30	0
2	PO4	D	3032	5/5	0.97	0.06	38,38,38,38	0
2	PO4	F	3052	5/5	0.98	0.05	31,31,31,31	0
2	PO4	B	3012	5/5	0.98	0.06	30,30,31,31	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.

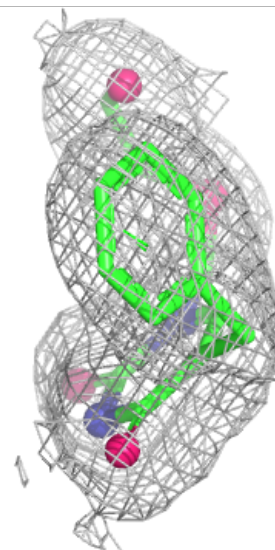
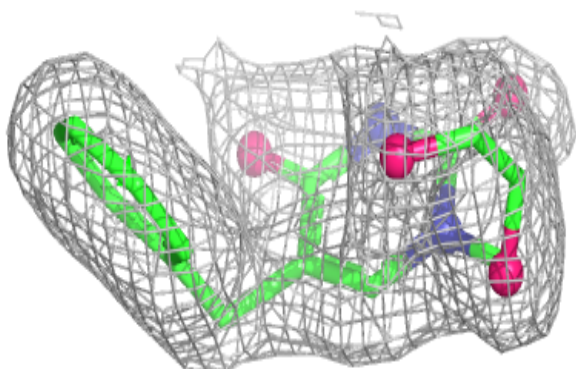
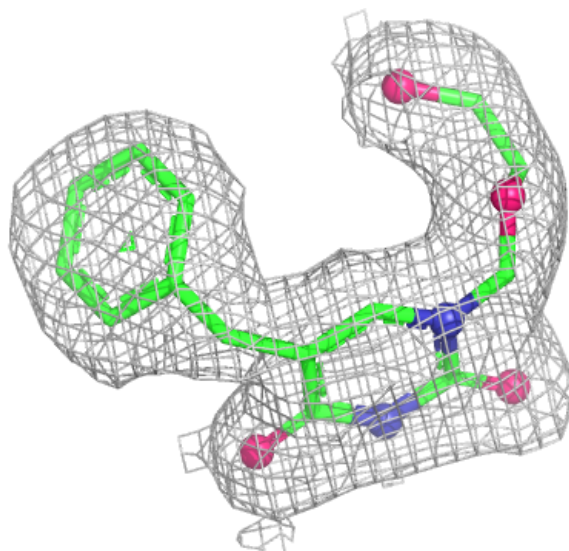
Electron density around BAU C 5021:

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



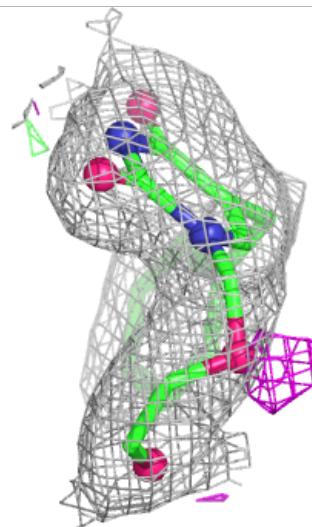
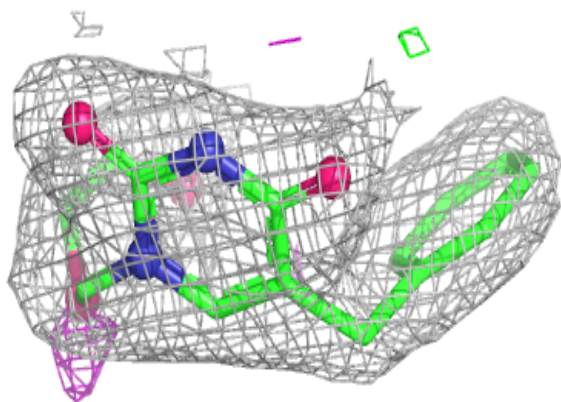
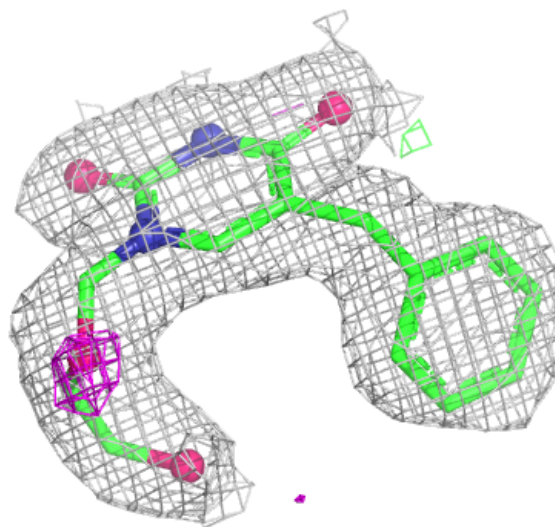
Electron density around BAU A 5400:

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



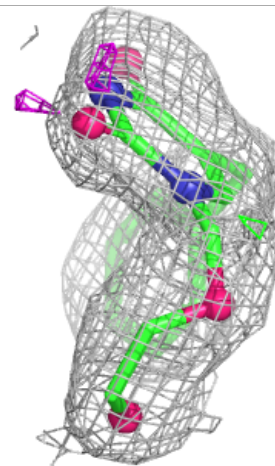
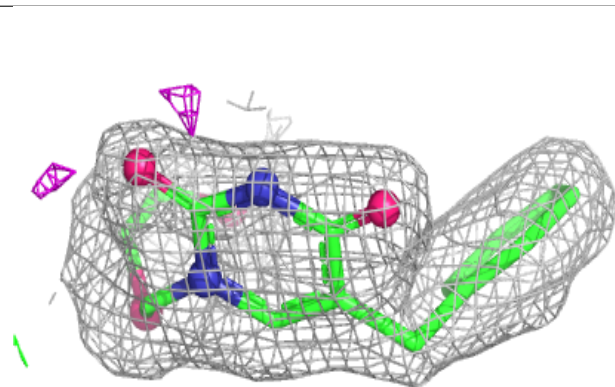
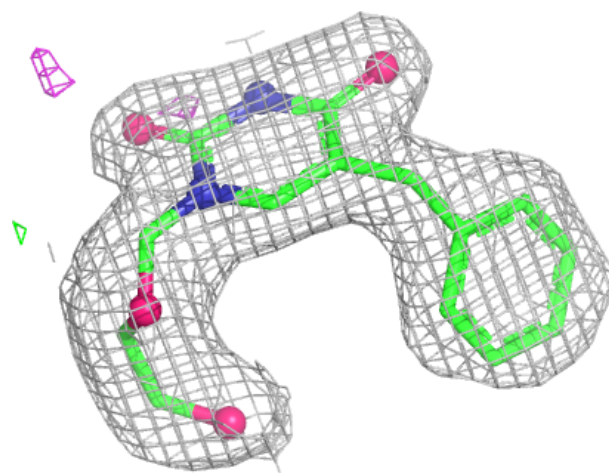
Electron density around BAU D 5031:

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



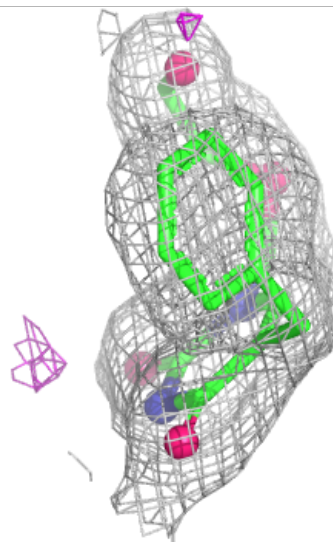
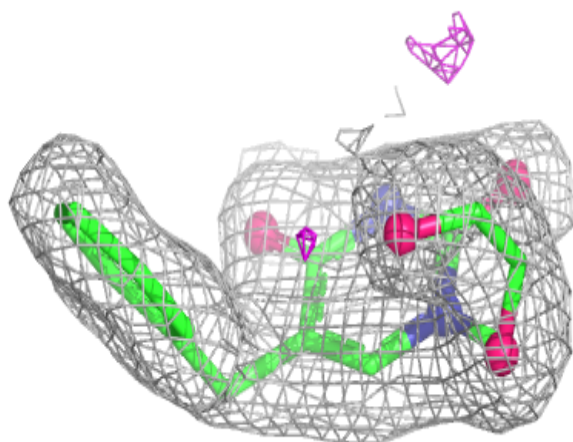
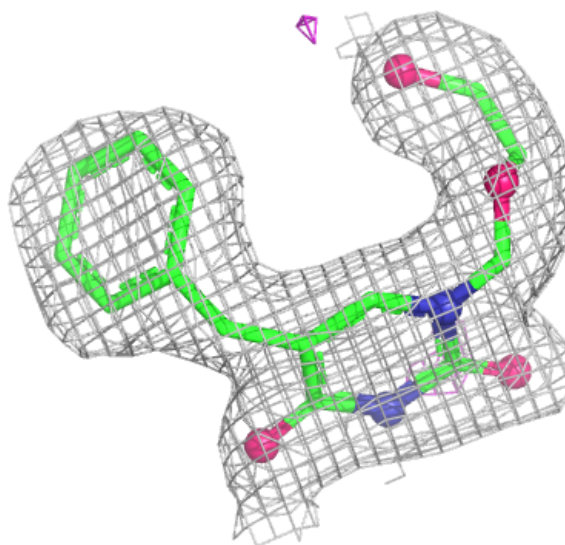
Electron density around BAU F 5051:

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



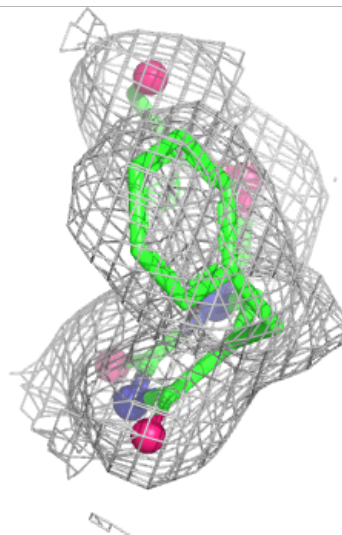
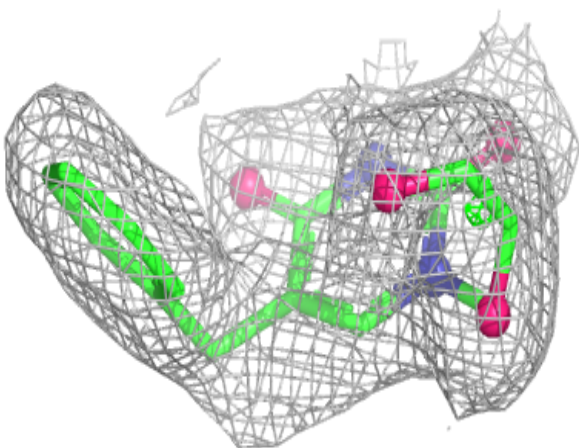
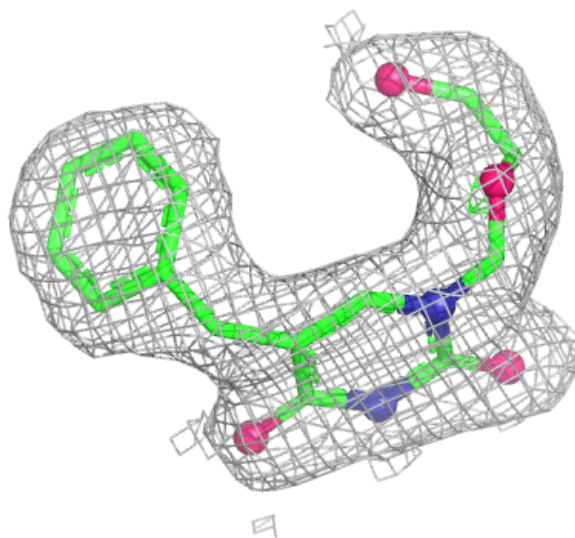
Electron density around BAU E 5041:

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



Electron density around BAU B 5011:

$2mF_o-DF_c$ (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.