



Full wwPDB EM Validation Report ⓘ

Jul 6, 2026 – 01:02 PM JST

PDB ID : 43DY / pdb_000043dy
EMDB ID : EMD-81807
Title : In situ structure of mouse urate oxidase assembly with helical symmetry applied
Authors : Yang, J.H.; Chen, Z.; Guo, Q.
Deposited on : 2026-06-27
Resolution : 3.72 Å(reported)
Based on initial model : 4mb8

This is a Full wwPDB EM 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/EMValidationReportHelp>
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:

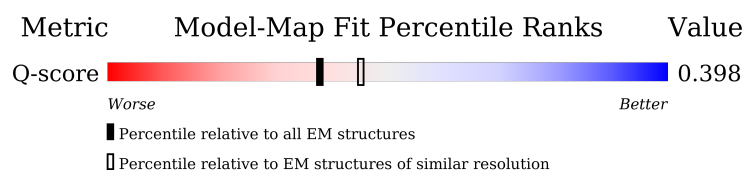
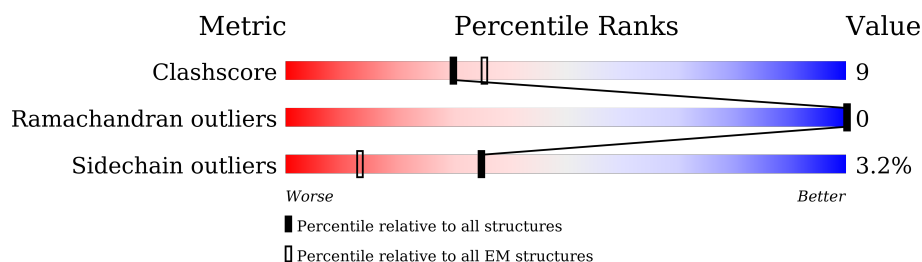
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.72 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)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10474 (3.22 - 4.22)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	287	7% 83% 17%
1	B	287	6% 80% 19% .
1	C	287	10% 77% 22% .
1	D	287	10% 73% 25% .

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Mol	Chain	Length	Quality of chain	
1	E	287		
1	F	287		
1	G	287		
1	H	287		
1	I	287		
1	J	287		
1	K	287		
1	L	287		
1	M	287		
1	N	287		
1	O	287		
1	P	287		
1	Q	287		
1	R	287		
1	S	287		
1	T	287		
1	U	287		
1	V	287		
1	W	287		
1	X	287		

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	URC	A	301	-	-	X	-
2	URC	B	301	-	-	X	-
2	URC	E	301	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	URC	F	301	-	-	X	-
2	URC	I	301	-	-	X	-
2	URC	J	301	-	-	X	-
2	URC	M	301	-	-	X	-
2	URC	N	301	-	-	X	-
2	URC	Q	301	-	-	X	-
2	URC	R	301	-	-	X	-
2	URC	U	301	-	-	X	-
2	URC	V	301	-	-	X	-

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 56352 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 Uricase.

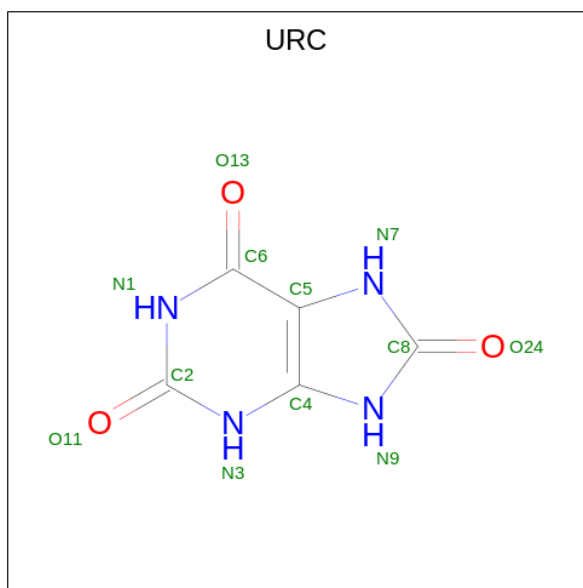
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		
1	B	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		
1	C	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		
1	D	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		
1	E	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		
1	F	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		
1	G	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		
1	H	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		
1	I	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		
1	J	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		
1	K	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		
1	L	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		
1	M	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		
1	N	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		
1	O	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		
1	P	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		
1	Q	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		
1	S	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		
1	T	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		
1	U	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		
1	V	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		
1	W	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		
1	X	287	Total	C	N	O	S	0	0
			2336	1496	405	425	10		

- Molecule 2 is URIC ACID (CCD ID: URC) (formula: $C_5H_4N_4O_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				AltConf
2	A	1	Total	C	N	O	0
			12	5	4	3	
2	B	1	Total	C	N	O	0
			12	5	4	3	
2	C	1	Total	C	N	O	0
			12	5	4	3	
2	C	1	Total	C	N	O	0
			12	5	4	3	

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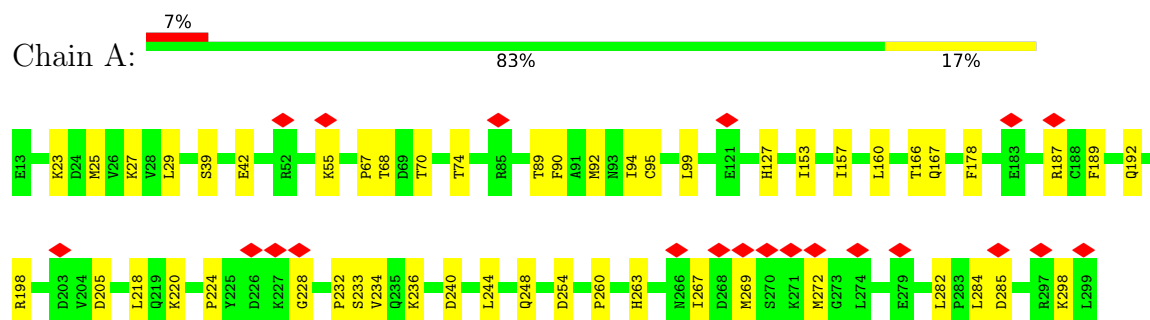
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Mol	Chain	Residues	Atoms				AltConf
2	E	1	Total 12	C 5	N 4	O 3	0
2	F	1	Total 12	C 5	N 4	O 3	0
2	G	1	Total 12	C 5	N 4	O 3	0
2	G	1	Total 12	C 5	N 4	O 3	0
2	I	1	Total 12	C 5	N 4	O 3	0
2	J	1	Total 12	C 5	N 4	O 3	0
2	K	1	Total 12	C 5	N 4	O 3	0
2	K	1	Total 12	C 5	N 4	O 3	0
2	M	1	Total 12	C 5	N 4	O 3	0
2	N	1	Total 12	C 5	N 4	O 3	0
2	O	1	Total 12	C 5	N 4	O 3	0
2	O	1	Total 12	C 5	N 4	O 3	0
2	Q	1	Total 12	C 5	N 4	O 3	0
2	R	1	Total 12	C 5	N 4	O 3	0
2	S	1	Total 12	C 5	N 4	O 3	0
2	S	1	Total 12	C 5	N 4	O 3	0
2	U	1	Total 12	C 5	N 4	O 3	0
2	V	1	Total 12	C 5	N 4	O 3	0
2	W	1	Total 12	C 5	N 4	O 3	0
2	W	1	Total 12	C 5	N 4	O 3	0

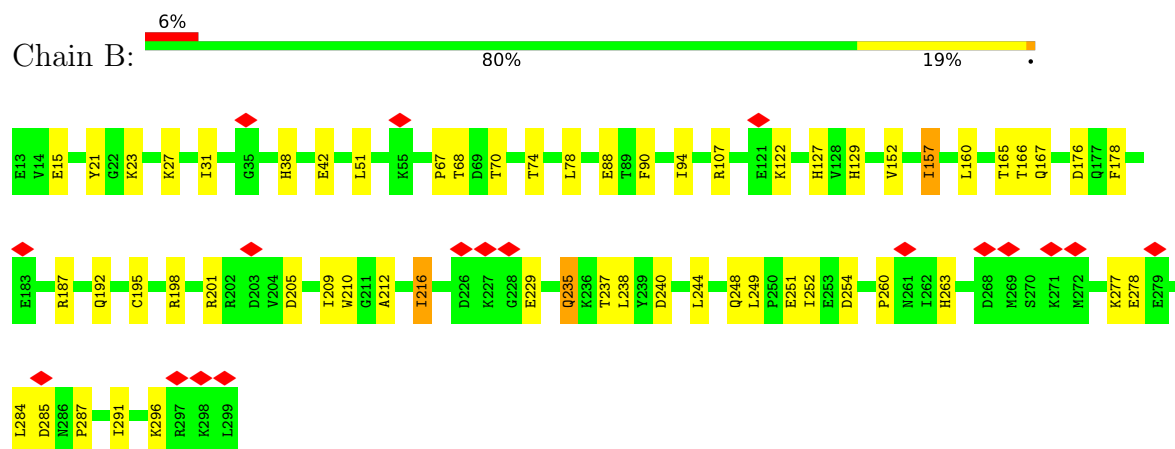
3 Residue-property plots [i](#)

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

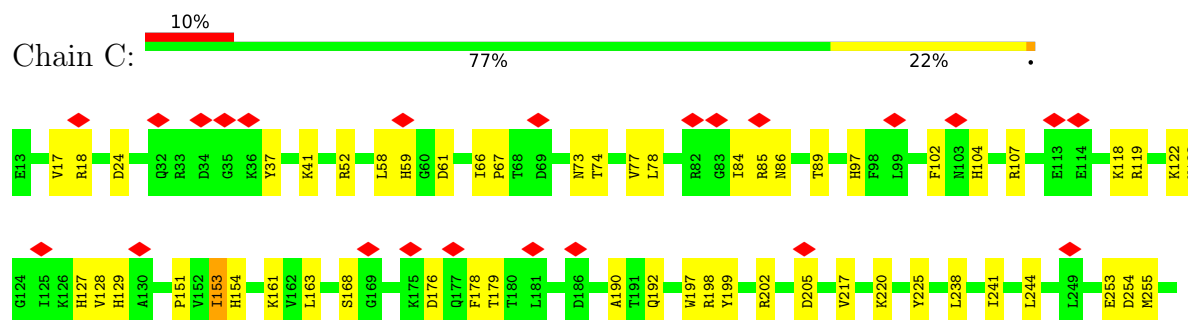
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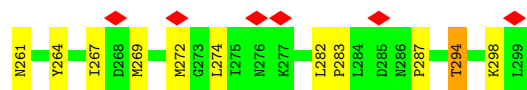


• Molecule 1: Uricase

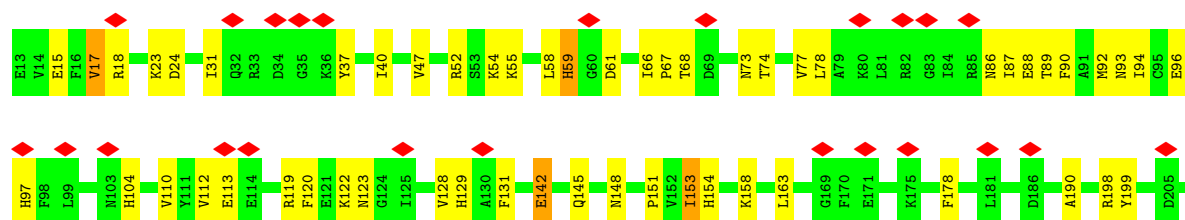
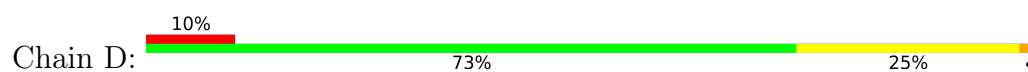


• Molecule 1: Uricase

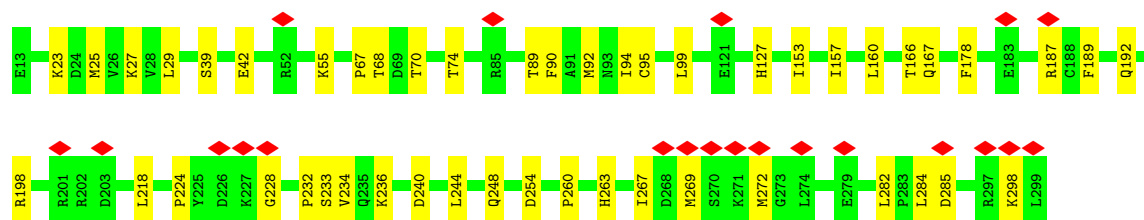
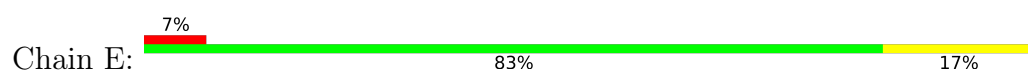




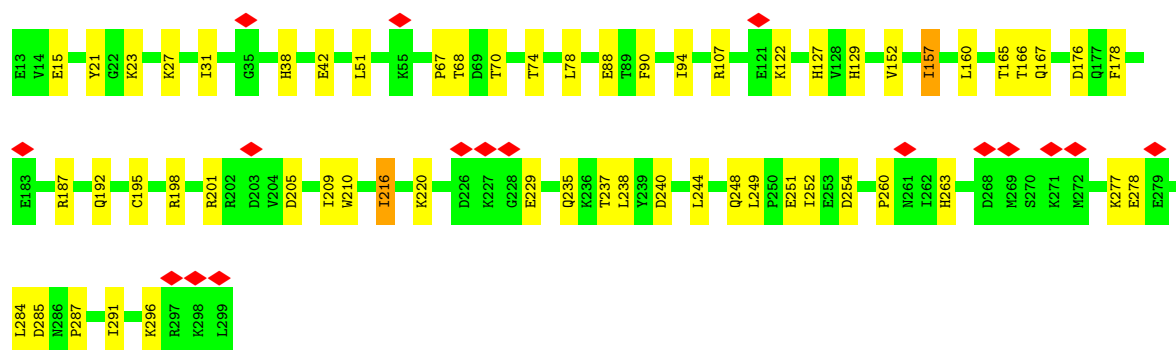
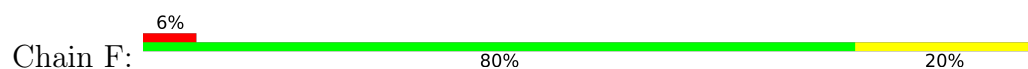
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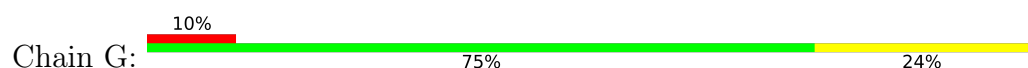
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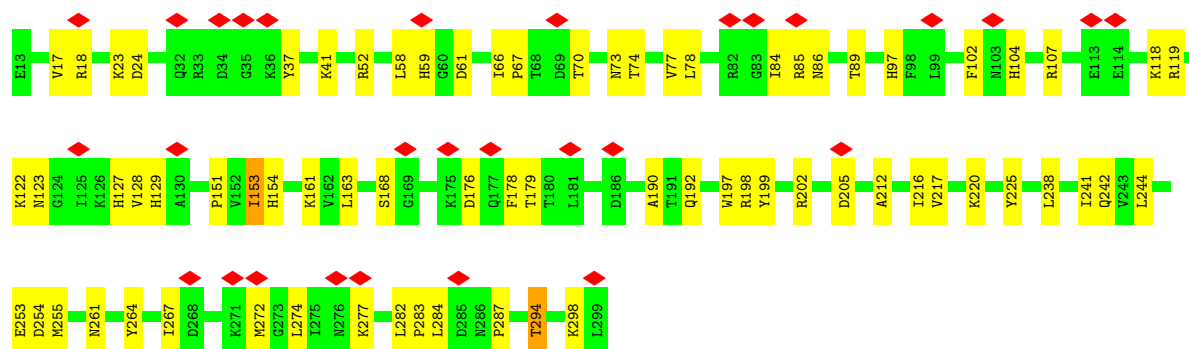


• Molecule 1: Uricase

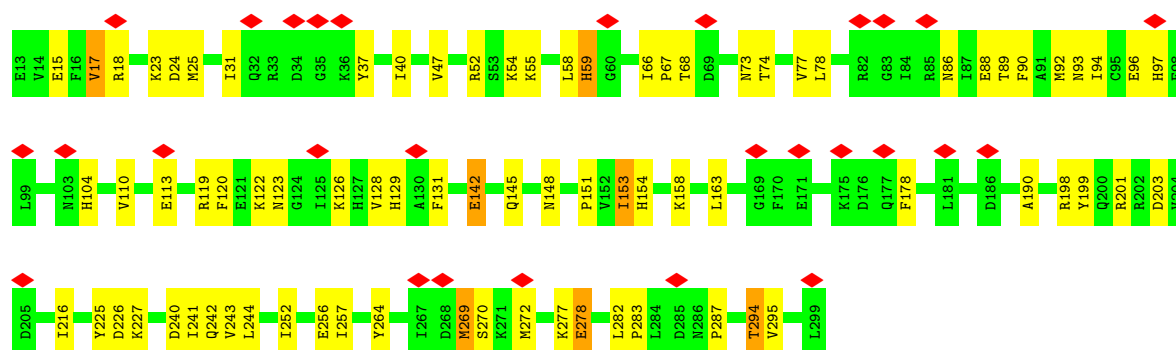


• Molecule 1: Uricase

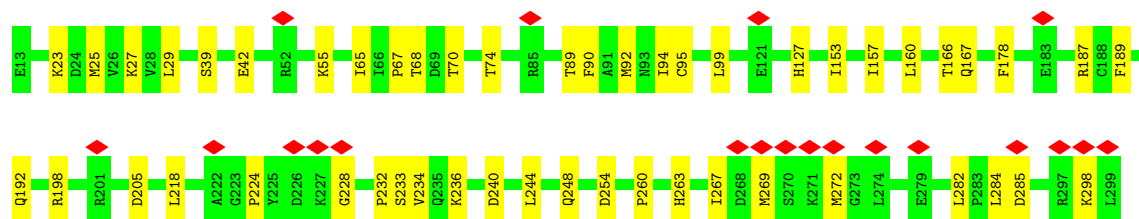
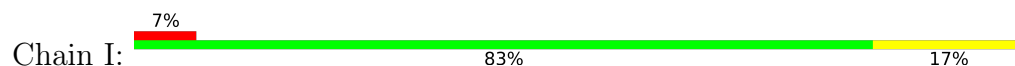




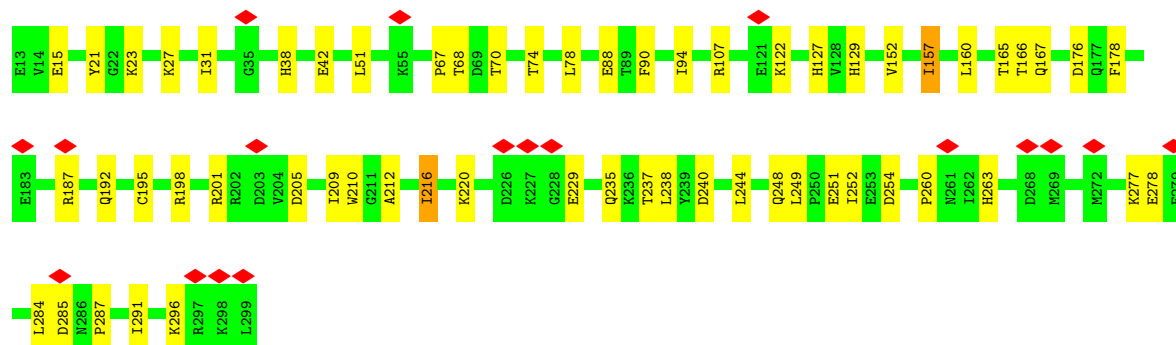
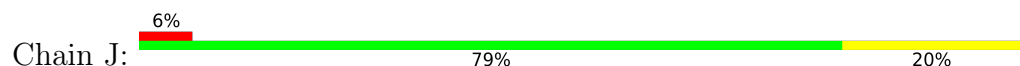
• Molecule 1: Uricase



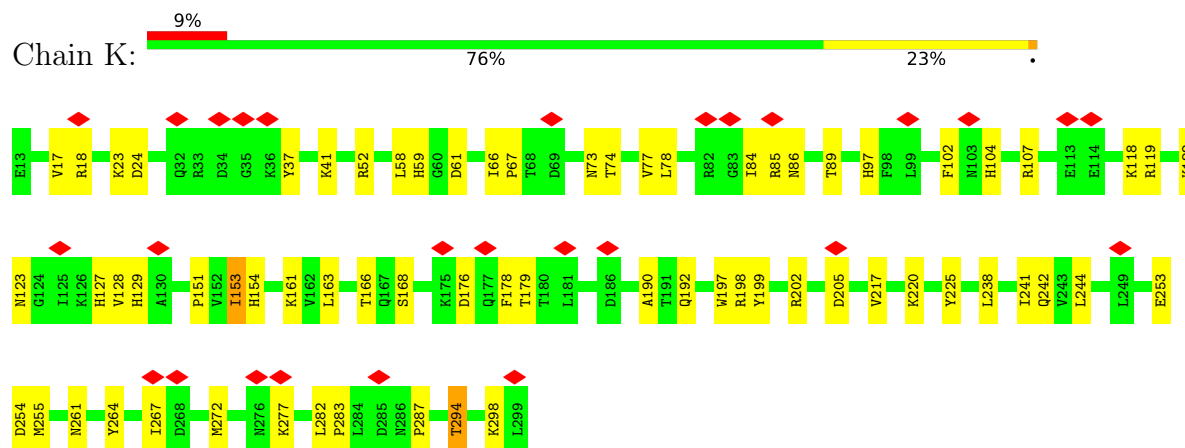
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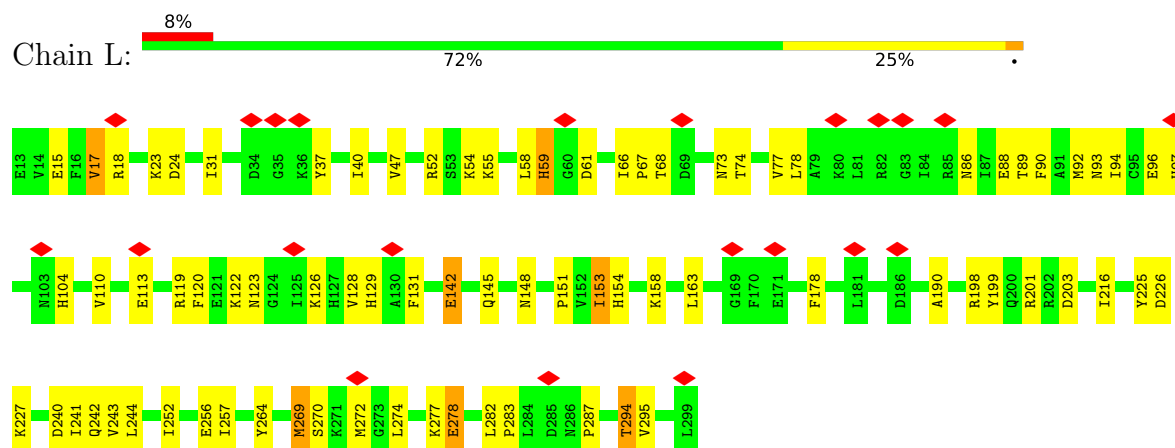
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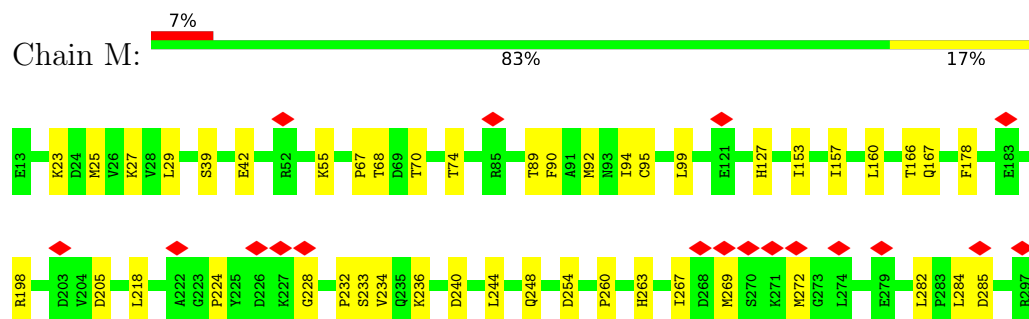
- Molecule 1: Uricase



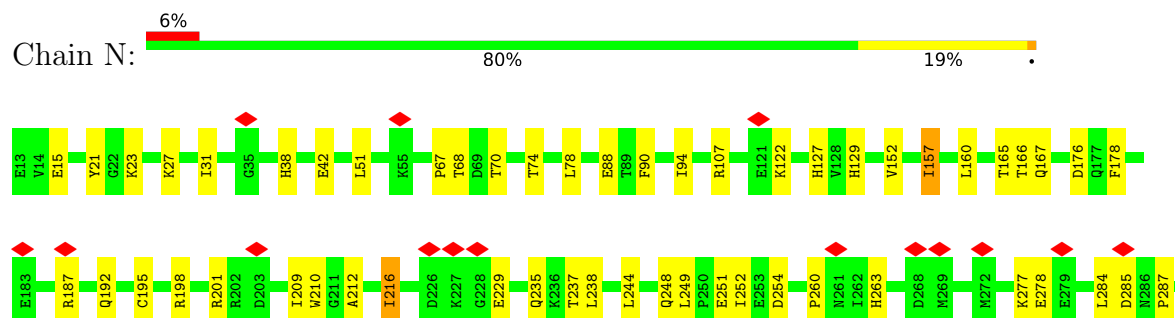
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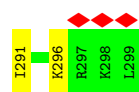


- Molecule 1: Uricase

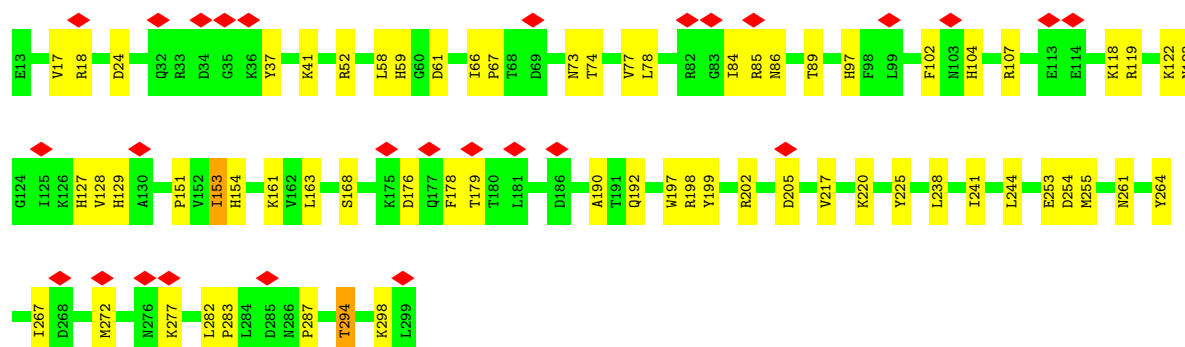
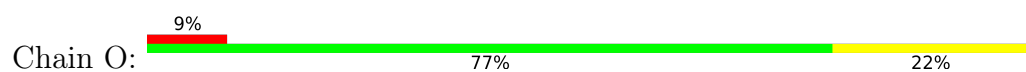


- Molecule 1: Uricase

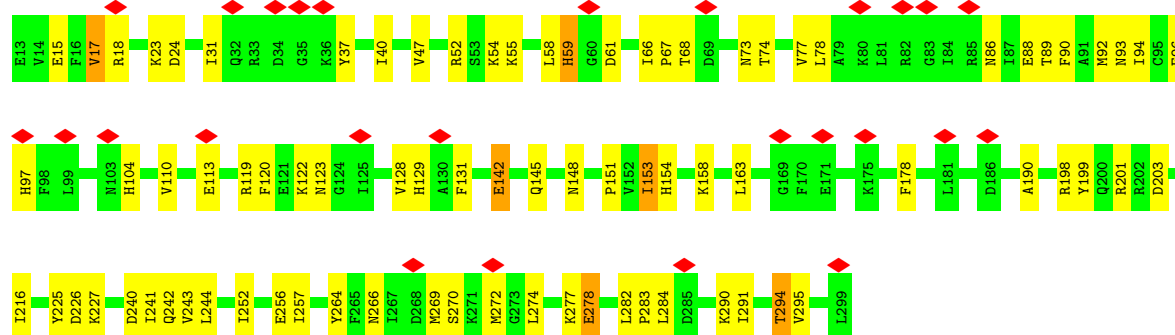
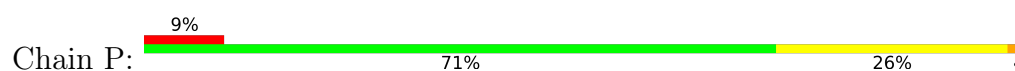




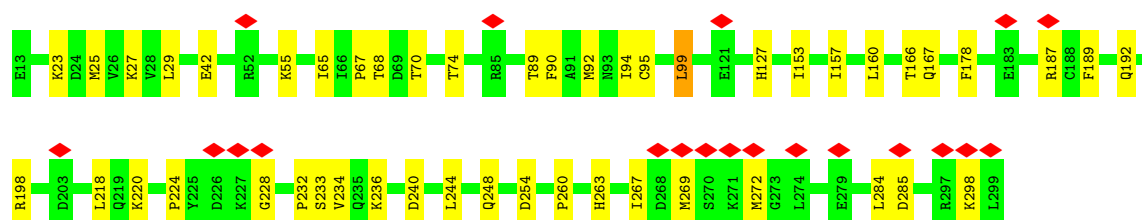
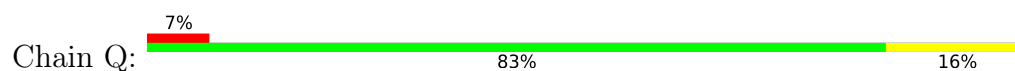
• Molecule 1: Uricase



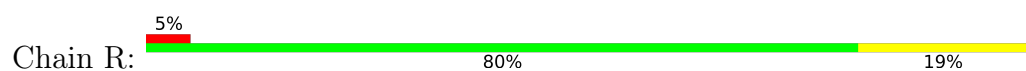
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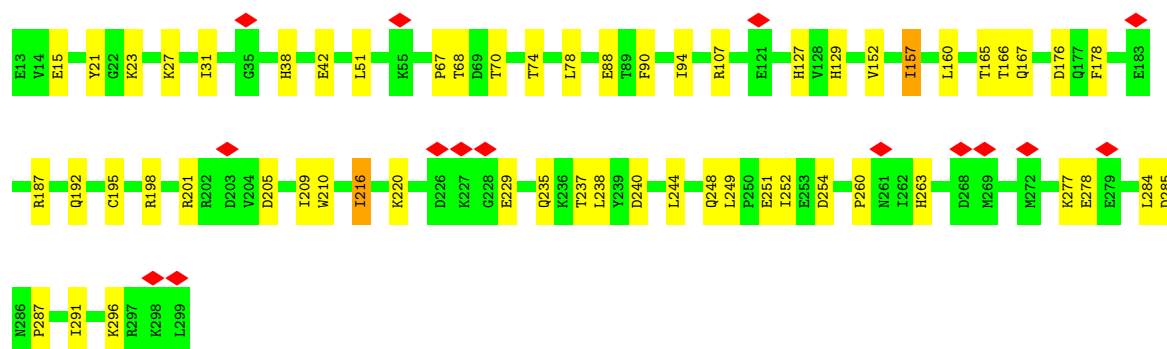


• Molecule 1: Uricase

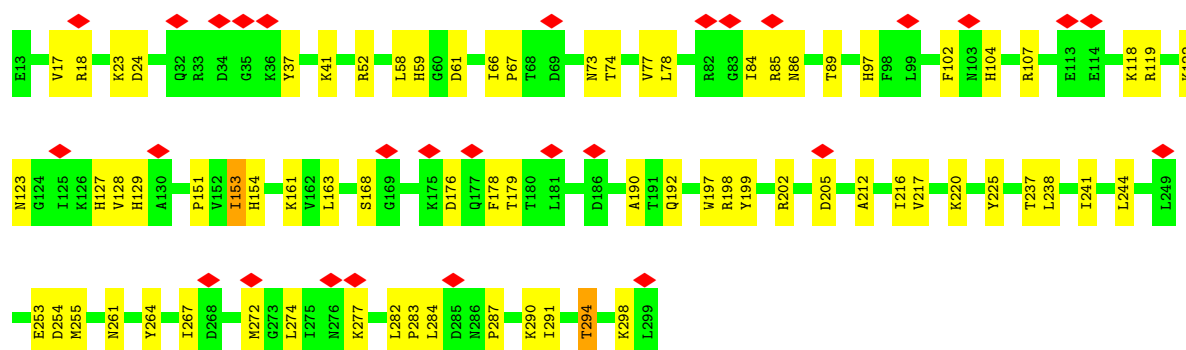


• Molecule 1: Uricase

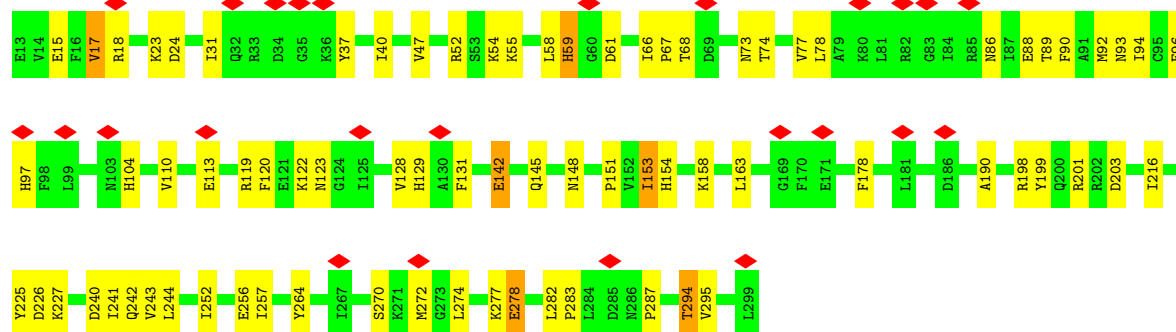




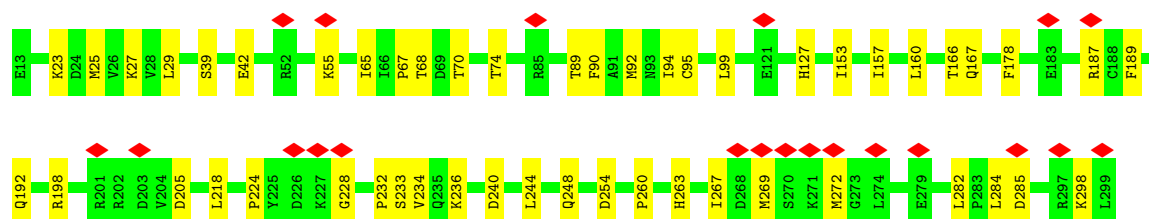
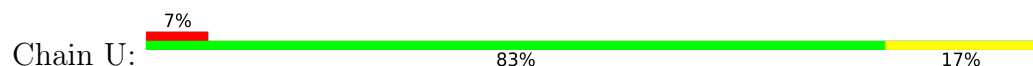
• Molecule 1: Uricase



• Molecule 1: Uricase

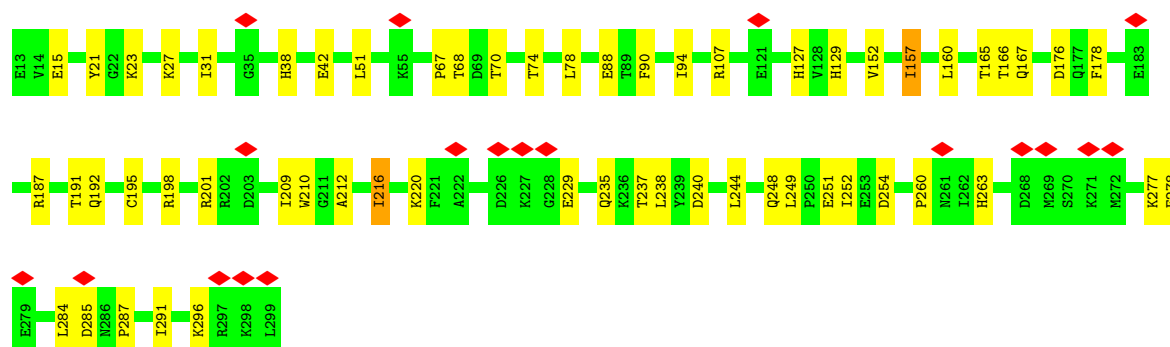


• Molecule 1: Uricase



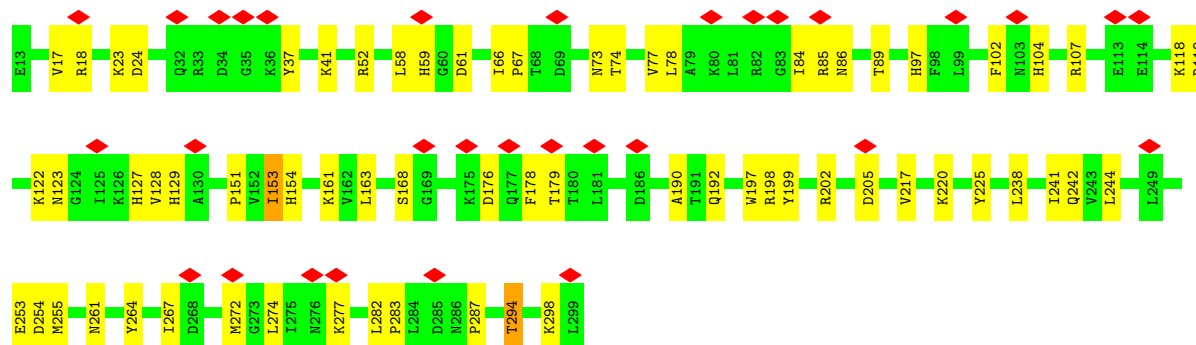
- Molecule 1: Uricase

Chain V: 



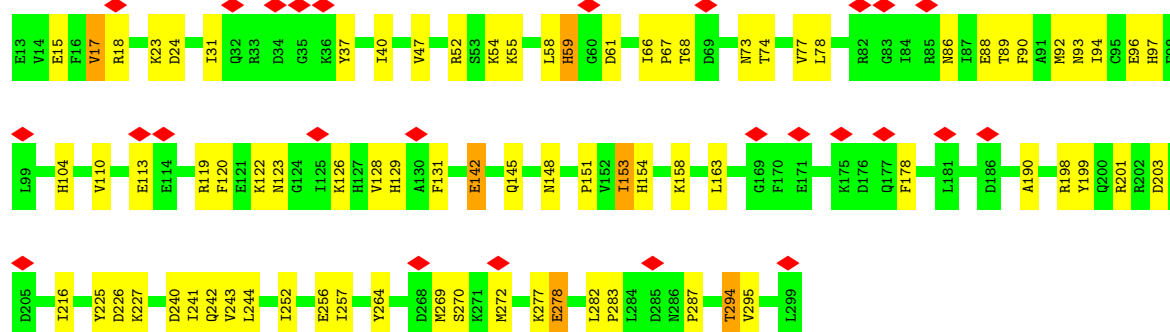
- Molecule 1: Uricase

Chain W: 



- Molecule 1: Uricase

Chain X: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	219322	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.102	Depositor
Minimum map value	-0.052	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.017	Depositor
Map size (Å)	424.08002, 424.08002, 424.08002	wwPDB
Map dimensions	456, 456, 456	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.93000007, 0.93000007, 0.93000007	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: URC

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	0.14	0/2391	0.43	0/3231
1	B	0.17	0/2391	0.46	0/3231
1	C	0.15	0/2391	0.42	0/3231
1	D	0.15	0/2391	0.44	0/3231
1	E	0.14	0/2391	0.43	0/3231
1	F	0.17	0/2391	0.46	0/3231
1	G	0.15	0/2391	0.43	0/3231
1	H	0.15	0/2391	0.45	0/3231
1	I	0.14	0/2391	0.43	0/3231
1	J	0.17	0/2391	0.46	0/3231
1	K	0.15	0/2391	0.42	0/3231
1	L	0.15	0/2391	0.45	0/3231
1	M	0.15	0/2391	0.43	0/3231
1	N	0.17	0/2391	0.46	0/3231
1	O	0.15	0/2391	0.42	0/3231
1	P	0.15	0/2391	0.45	0/3231
1	Q	0.14	0/2391	0.43	0/3231
1	R	0.17	0/2391	0.46	0/3231
1	S	0.15	0/2391	0.42	0/3231
1	T	0.15	0/2391	0.45	0/3231
1	U	0.15	0/2391	0.43	0/3231
1	V	0.17	0/2391	0.46	0/3231
1	W	0.15	0/2391	0.42	0/3231
1	X	0.15	0/2391	0.45	0/3231
All	All	0.15	0/57384	0.44	0/77544

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2336	0	2343	37	0
1	B	2336	0	2343	44	0
1	C	2336	0	2343	50	0
1	D	2336	0	2343	59	0
1	E	2336	0	2343	35	0
1	F	2336	0	2343	43	0
1	G	2336	0	2343	54	0
1	H	2336	0	2343	56	0
1	I	2336	0	2343	37	0
1	J	2336	0	2343	45	0
1	K	2336	0	2343	50	0
1	L	2336	0	2343	61	0
1	M	2336	0	2343	36	0
1	N	2336	0	2343	41	0
1	O	2336	0	2343	49	0
1	P	2336	0	2343	60	0
1	Q	2336	0	2343	37	0
1	R	2336	0	2343	43	0
1	S	2336	0	2343	54	0
1	T	2336	0	2343	58	0
1	U	2336	0	2343	37	0
1	V	2336	0	2343	43	0
1	W	2336	0	2343	52	0
1	X	2336	0	2343	59	0
2	A	12	0	4	4	0
2	B	12	0	4	4	0
2	C	24	0	8	1	0
2	E	12	0	4	4	0
2	F	12	0	4	4	0
2	G	24	0	8	1	0
2	I	12	0	4	4	0
2	J	12	0	4	4	0
2	K	24	0	8	1	0
2	M	12	0	4	4	0
2	N	12	0	4	4	0
2	O	24	0	8	1	0
2	Q	12	0	4	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	R	12	0	4	4	0
2	S	24	0	8	1	0
2	U	12	0	4	4	0
2	V	12	0	4	4	0
2	W	24	0	8	1	0
All	All	56352	0	56328	1020	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (1020) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:THR:HG23	2:B:301:URC:O13	1.57	1.04
1:Q:68:THR:HG23	2:R:301:URC:O13	1.57	1.04
1:E:68:THR:HG23	2:F:301:URC:O13	1.57	1.03
1:M:68:THR:HG23	2:N:301:URC:O13	1.57	1.03
1:I:68:THR:HG23	2:J:301:URC:O13	1.57	1.02
1:U:68:THR:HG23	2:V:301:URC:O13	1.57	1.02
1:N:187:ARG:HH12	2:N:301:URC:HN9	1.13	0.96
1:F:187:ARG:HH12	2:F:301:URC:HN9	1.13	0.95
1:R:187:ARG:HH12	2:R:301:URC:HN9	1.13	0.92
1:B:187:ARG:HH12	2:B:301:URC:HN9	1.13	0.91
1:J:187:ARG:HH12	2:J:301:URC:HN9	1.13	0.90
1:V:187:ARG:HH12	2:V:301:URC:HN9	1.13	0.90
1:B:187:ARG:NH1	2:B:301:URC:HN9	1.75	0.85
1:R:187:ARG:NH1	2:R:301:URC:HN9	1.75	0.84
1:J:187:ARG:NH1	2:J:301:URC:HN9	1.75	0.83
1:V:187:ARG:NH1	2:V:301:URC:HN9	1.75	0.83
1:F:187:ARG:NH1	2:F:301:URC:HN9	1.75	0.83
1:N:187:ARG:NH1	2:N:301:URC:HN9	1.75	0.82
1:P:55:LYS:HG2	1:P:59:HIS:HE1	1.48	0.79
1:T:55:LYS:HG2	1:T:59:HIS:HE1	1.48	0.79
1:L:55:LYS:HG2	1:L:59:HIS:HE1	1.48	0.78
1:X:55:LYS:HG2	1:X:59:HIS:HE1	1.48	0.78
1:D:55:LYS:HG2	1:D:59:HIS:HE1	1.48	0.78
1:H:55:LYS:HG2	1:H:59:HIS:HE1	1.48	0.77
1:M:68:THR:CG2	2:N:301:URC:O13	2.33	0.76
2:M:301:URC:HN7	1:N:68:THR:HG22	1.50	0.76
2:A:301:URC:HN7	1:B:68:THR:HG22	1.50	0.75
1:I:68:THR:CG2	2:J:301:URC:O13	2.33	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:68:THR:CG2	2:V:301:URC:O13	2.33	0.75
1:E:68:THR:CG2	2:F:301:URC:O13	2.33	0.74
1:A:68:THR:CG2	2:B:301:URC:O13	2.33	0.74
2:Q:301:URC:HN7	1:R:68:THR:HG22	1.50	0.74
2:I:301:URC:HN7	1:J:68:THR:HG22	1.50	0.74
2:U:301:URC:HN7	1:V:68:THR:HG22	1.50	0.74
2:E:301:URC:HN7	1:F:68:THR:HG22	1.50	0.73
1:Q:68:THR:CG2	2:R:301:URC:O13	2.33	0.73
1:H:216:ILE:HD11	1:H:244:LEU:HB3	1.73	0.70
1:D:216:ILE:HD11	1:D:244:LEU:HB3	1.73	0.70
1:O:264:TYR:HE1	1:O:283:PRO:HB3	1.57	0.69
1:P:216:ILE:HD11	1:P:244:LEU:HB3	1.73	0.69
1:W:264:TYR:HE1	1:W:283:PRO:HB3	1.57	0.69
1:K:264:TYR:HE1	1:K:283:PRO:HB3	1.58	0.69
1:L:216:ILE:HD11	1:L:244:LEU:HB3	1.73	0.69
1:X:216:ILE:HD11	1:X:244:LEU:HB3	1.73	0.69
1:G:264:TYR:HE1	1:G:283:PRO:HB3	1.57	0.68
1:S:264:TYR:HE1	1:S:283:PRO:HB3	1.57	0.68
1:T:216:ILE:HD11	1:T:244:LEU:HB3	1.73	0.68
1:O:163:LEU:HD12	1:O:190:ALA:HB2	1.76	0.68
1:C:217:VAL:HA	1:C:241:ILE:HD11	1.75	0.68
1:C:163:LEU:HD12	1:C:190:ALA:HB2	1.76	0.68
1:I:166:THR:HG23	1:I:167:GLN:HG3	1.76	0.68
1:M:187:ARG:HH12	2:M:301:URC:HN9	1.42	0.68
1:U:166:THR:HG23	1:U:167:GLN:HG3	1.76	0.67
1:A:166:THR:HG23	1:A:167:GLN:HG3	1.76	0.67
1:E:187:ARG:HH12	2:E:301:URC:HN9	1.42	0.67
1:F:70:THR:O	1:F:74:THR:HG23	1.95	0.67
1:S:163:LEU:HD12	1:S:190:ALA:HB2	1.76	0.67
1:B:70:THR:O	1:B:74:THR:HG23	1.95	0.67
1:K:161:LYS:HG3	1:K:192:GLN:HG3	1.77	0.67
1:W:161:LYS:HG3	1:W:192:GLN:HG3	1.77	0.67
1:W:217:VAL:HA	1:W:241:ILE:HD11	1.75	0.67
1:C:264:TYR:HE1	1:C:283:PRO:HB3	1.58	0.67
1:H:264:TYR:HE1	1:H:283:PRO:HB3	1.60	0.67
1:O:161:LYS:HG3	1:O:192:GLN:HG3	1.77	0.67
1:R:70:THR:O	1:R:74:THR:HG23	1.95	0.67
1:S:217:VAL:HA	1:S:241:ILE:HD11	1.75	0.67
1:X:264:TYR:HE1	1:X:283:PRO:HB3	1.60	0.67
1:K:217:VAL:HA	1:K:241:ILE:HD11	1.76	0.67
1:L:264:TYR:HE1	1:L:283:PRO:HB3	1.60	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:70:THR:O	1:N:74:THR:HG23	1.95	0.67
1:U:187:ARG:HH12	2:U:301:URC:HN9	1.42	0.67
1:A:187:ARG:HH12	2:A:301:URC:HN9	1.42	0.67
1:H:47:VAL:HG22	1:H:110:VAL:HG22	1.76	0.67
1:I:187:ARG:HH12	2:I:301:URC:HN9	1.42	0.67
1:L:47:VAL:HG22	1:L:110:VAL:HG22	1.76	0.67
1:O:41:LYS:HD2	1:O:84:ILE:HG13	1.77	0.67
1:X:47:VAL:HG22	1:X:110:VAL:HG22	1.76	0.67
1:D:47:VAL:HG22	1:D:110:VAL:HG22	1.76	0.67
1:T:47:VAL:HG22	1:T:110:VAL:HG22	1.76	0.67
1:D:264:TYR:HE1	1:D:283:PRO:HB3	1.60	0.66
1:I:244:LEU:HD11	1:I:248:GLN:HE21	1.60	0.66
1:O:217:VAL:HA	1:O:241:ILE:HD11	1.75	0.66
1:W:163:LEU:HD12	1:W:190:ALA:HB2	1.76	0.66
1:E:244:LEU:HD11	1:E:248:GLN:HE21	1.60	0.66
1:G:217:VAL:HA	1:G:241:ILE:HD11	1.75	0.66
1:Q:187:ARG:HH12	2:Q:301:URC:HN9	1.42	0.66
1:U:244:LEU:HD11	1:U:248:GLN:HE21	1.60	0.66
1:G:161:LYS:HG3	1:G:192:GLN:HG3	1.77	0.66
1:K:163:LEU:HD12	1:K:190:ALA:HB2	1.76	0.66
1:P:47:VAL:HG22	1:P:110:VAL:HG22	1.76	0.66
1:V:70:THR:O	1:V:74:THR:HG23	1.95	0.66
1:J:70:THR:O	1:J:74:THR:HG23	1.95	0.66
1:S:161:LYS:HG3	1:S:192:GLN:HG3	1.77	0.66
1:C:41:LYS:HD2	1:C:84:ILE:HG13	1.77	0.66
1:G:41:LYS:HD2	1:G:84:ILE:HG13	1.77	0.66
1:M:166:THR:HG23	1:M:167:GLN:HG3	1.76	0.66
1:T:264:TYR:HE1	1:T:283:PRO:HB3	1.60	0.66
1:E:166:THR:HG23	1:E:167:GLN:HG3	1.76	0.66
1:R:263:HIS:HB2	1:R:284:LEU:HD11	1.78	0.66
1:H:163:LEU:HD12	1:H:190:ALA:HB2	1.78	0.66
1:G:163:LEU:HD12	1:G:190:ALA:HB2	1.76	0.66
1:N:263:HIS:HB2	1:N:284:LEU:HD11	1.78	0.66
1:M:244:LEU:HD11	1:M:248:GLN:HE21	1.60	0.65
1:P:264:TYR:HE1	1:P:283:PRO:HB3	1.60	0.65
1:J:263:HIS:HB2	1:J:284:LEU:HD11	1.78	0.65
1:V:263:HIS:HB2	1:V:284:LEU:HD11	1.78	0.65
1:H:252:ILE:H	1:H:252:ILE:HD12	1.62	0.65
1:C:161:LYS:HG3	1:C:192:GLN:HG3	1.77	0.65
1:S:41:LYS:HD2	1:S:84:ILE:HG13	1.77	0.65
1:T:163:LEU:HD12	1:T:190:ALA:HB2	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:41:LYS:HD2	1:W:84:ILE:HG13	1.77	0.65
1:K:41:LYS:HD2	1:K:84:ILE:HG13	1.77	0.65
1:P:163:LEU:HD12	1:P:190:ALA:HB2	1.78	0.65
1:Q:244:LEU:HD11	1:Q:248:GLN:HE21	1.60	0.65
1:Q:166:THR:HG23	1:Q:167:GLN:HG3	1.76	0.65
1:X:163:LEU:HD12	1:X:190:ALA:HB2	1.78	0.65
1:A:244:LEU:HD11	1:A:248:GLN:HE21	1.60	0.64
1:L:163:LEU:HD12	1:L:190:ALA:HB2	1.78	0.64
1:P:252:ILE:HD12	1:P:252:ILE:H	1.62	0.64
1:B:263:HIS:HB2	1:B:284:LEU:HD11	1.78	0.64
1:L:122:LYS:HG2	1:L:123:ASN:HD22	1.63	0.64
1:X:122:LYS:HG2	1:X:123:ASN:HD22	1.63	0.64
1:D:122:LYS:HG2	1:D:123:ASN:HD22	1.63	0.64
1:D:163:LEU:HD12	1:D:190:ALA:HB2	1.78	0.64
1:F:263:HIS:HB2	1:F:284:LEU:HD11	1.78	0.64
1:T:252:ILE:HD12	1:T:252:ILE:H	1.62	0.64
1:G:17:VAL:HG22	1:G:18:ARG:HG3	1.80	0.63
1:D:252:ILE:HD12	1:D:252:ILE:H	1.62	0.63
1:P:52:ARG:HH21	1:P:104:HIS:HA	1.64	0.63
1:S:17:VAL:HG22	1:S:18:ARG:HG3	1.80	0.63
1:H:122:LYS:HG2	1:H:123:ASN:HD22	1.63	0.63
1:P:122:LYS:HG2	1:P:123:ASN:HD22	1.63	0.63
1:T:52:ARG:HH21	1:T:104:HIS:HA	1.64	0.63
1:X:252:ILE:HD12	1:X:252:ILE:H	1.62	0.63
1:L:252:ILE:HD12	1:L:252:ILE:H	1.62	0.63
1:K:17:VAL:HG22	1:K:18:ARG:HG3	1.80	0.62
1:O:17:VAL:HG22	1:O:18:ARG:HG3	1.80	0.62
1:T:122:LYS:HG2	1:T:123:ASN:HD22	1.63	0.62
1:W:17:VAL:HG22	1:W:18:ARG:HG3	1.80	0.62
1:D:52:ARG:HH21	1:D:104:HIS:HA	1.64	0.62
1:H:52:ARG:HH21	1:H:104:HIS:HA	1.64	0.62
1:X:52:ARG:HH21	1:X:104:HIS:HA	1.64	0.62
1:J:74:THR:O	1:J:78:LEU:HG	2.00	0.62
1:L:52:ARG:HH21	1:L:104:HIS:HA	1.64	0.62
1:V:74:THR:O	1:V:78:LEU:HG	2.00	0.62
1:C:17:VAL:HG22	1:C:18:ARG:HG3	1.80	0.61
1:F:74:THR:O	1:F:78:LEU:HG	2.00	0.61
1:F:160:LEU:O	1:F:192:GLN:HA	2.00	0.61
1:N:160:LEU:O	1:N:192:GLN:HA	2.00	0.61
1:N:74:THR:O	1:N:78:LEU:HG	2.00	0.61
1:R:74:THR:O	1:R:78:LEU:HG	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:160:LEU:O	1:J:192:GLN:HA	2.00	0.61
1:V:160:LEU:O	1:V:192:GLN:HA	2.00	0.61
1:B:74:THR:O	1:B:78:LEU:HG	2.00	0.61
1:M:233:SER:OG	2:M:301:URC:O11	2.19	0.60
1:K:74:THR:O	1:K:78:LEU:HD12	2.02	0.60
1:B:160:LEU:O	1:B:192:GLN:HA	2.00	0.60
1:W:74:THR:O	1:W:78:LEU:HD12	2.02	0.60
1:O:74:THR:O	1:O:78:LEU:HD12	2.02	0.60
1:R:160:LEU:O	1:R:192:GLN:HA	2.00	0.60
1:E:233:SER:OG	2:E:301:URC:O11	2.19	0.60
1:S:298:LYS:HD2	1:T:15:GLU:HB2	1.84	0.60
1:C:74:THR:O	1:C:78:LEU:HD12	2.02	0.60
1:Q:233:SER:OG	2:Q:301:URC:O11	2.19	0.60
1:O:298:LYS:HD2	1:P:15:GLU:HB2	1.84	0.59
1:B:165:THR:H	1:C:129:HIS:HD2	1.50	0.59
1:K:287:PRO:HB2	1:L:23:LYS:HD2	1.85	0.59
1:S:74:THR:O	1:S:78:LEU:HD12	2.02	0.59
1:W:287:PRO:HB2	1:X:23:LYS:HD2	1.85	0.59
1:C:287:PRO:HB2	1:D:23:LYS:HD2	1.85	0.59
1:W:298:LYS:HD2	1:X:15:GLU:HB2	1.84	0.59
1:A:233:SER:OG	2:A:301:URC:O11	2.19	0.59
1:G:298:LYS:HD2	1:H:15:GLU:HB2	1.84	0.59
1:I:233:SER:OG	2:I:301:URC:O11	2.19	0.59
1:K:298:LYS:HD2	1:L:15:GLU:HB2	1.84	0.59
1:M:160:LEU:O	1:M:192:GLN:HA	2.03	0.59
1:N:165:THR:H	1:O:129:HIS:HD2	1.50	0.59
1:R:165:THR:H	1:S:129:HIS:HD2	1.50	0.59
1:A:160:LEU:O	1:A:192:GLN:HA	2.03	0.59
1:K:73:ASN:O	1:K:77:VAL:HG13	2.03	0.59
1:S:153:ILE:HG23	1:S:199:TYR:HB2	1.85	0.59
1:T:90:PHE:O	1:T:94:ILE:HG13	2.03	0.59
1:U:233:SER:OG	2:U:301:URC:O11	2.19	0.59
1:W:73:ASN:O	1:W:77:VAL:HG13	2.03	0.59
1:D:90:PHE:O	1:D:94:ILE:HG13	2.03	0.59
1:G:74:THR:O	1:G:78:LEU:HD12	2.02	0.59
1:C:73:ASN:O	1:C:77:VAL:HG13	2.03	0.59
1:C:153:ILE:HG23	1:C:199:TYR:HB2	1.85	0.59
1:I:160:LEU:O	1:I:192:GLN:HA	2.03	0.59
1:K:153:ILE:HG23	1:K:199:TYR:HB2	1.85	0.59
1:O:153:ILE:HG23	1:O:199:TYR:HB2	1.85	0.59
1:Q:160:LEU:O	1:Q:192:GLN:HA	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:73:ASN:O	1:S:77:VAL:HG13	2.03	0.59
1:G:153:ILE:HG23	1:G:199:TYR:HB2	1.85	0.59
1:W:153:ILE:HG23	1:W:199:TYR:HB2	1.85	0.59
1:C:282:LEU:HD12	1:C:283:PRO:HD2	1.86	0.58
1:G:282:LEU:HD12	1:G:283:PRO:HD2	1.85	0.58
1:L:90:PHE:O	1:L:94:ILE:HG13	2.03	0.58
1:U:160:LEU:O	1:U:192:GLN:HA	2.03	0.58
1:X:90:PHE:O	1:X:94:ILE:HG13	2.03	0.58
1:F:165:THR:H	1:G:129:HIS:HD2	1.50	0.58
1:G:73:ASN:O	1:G:77:VAL:HG13	2.03	0.58
1:G:287:PRO:HB2	1:H:23:LYS:HD2	1.84	0.58
1:L:122:LYS:HG2	1:L:123:ASN:ND2	2.19	0.58
1:X:122:LYS:HG2	1:X:123:ASN:ND2	2.19	0.58
1:O:73:ASN:O	1:O:77:VAL:HG13	2.03	0.58
1:D:122:LYS:HG2	1:D:123:ASN:ND2	2.18	0.58
1:Q:167:GLN:HE22	1:Q:228:GLY:HA3	1.69	0.58
1:H:90:PHE:O	1:H:94:ILE:HG13	2.03	0.58
1:V:165:THR:H	1:W:129:HIS:HD2	1.50	0.58
1:E:160:LEU:O	1:E:192:GLN:HA	2.03	0.58
1:E:167:GLN:HE22	1:E:228:GLY:HA3	1.69	0.58
1:J:165:THR:H	1:K:129:HIS:HD2	1.50	0.58
1:O:287:PRO:HB2	1:P:23:LYS:HD2	1.85	0.58
1:P:90:PHE:O	1:P:94:ILE:HG13	2.03	0.58
1:T:73:ASN:O	1:T:77:VAL:HG13	2.04	0.58
1:C:298:LYS:HD2	1:D:15:GLU:HB2	1.84	0.58
1:H:122:LYS:HG2	1:H:123:ASN:ND2	2.19	0.58
1:Q:70:THR:O	1:Q:74:THR:HG23	2.04	0.58
1:M:70:THR:O	1:M:74:THR:HG23	2.04	0.58
1:H:73:ASN:O	1:H:77:VAL:HG13	2.04	0.57
1:I:167:GLN:HE22	1:I:228:GLY:HA3	1.69	0.57
1:L:73:ASN:O	1:L:77:VAL:HG13	2.04	0.57
1:P:122:LYS:HG2	1:P:123:ASN:ND2	2.18	0.57
1:T:122:LYS:HG2	1:T:123:ASN:ND2	2.18	0.57
1:U:167:GLN:HE22	1:U:228:GLY:HA3	1.69	0.57
1:X:73:ASN:O	1:X:77:VAL:HG13	2.04	0.57
1:E:70:THR:O	1:E:74:THR:HG23	2.04	0.57
1:O:282:LEU:HD12	1:O:283:PRO:HD2	1.85	0.57
1:W:282:LEU:HD12	1:W:283:PRO:HD2	1.86	0.57
1:K:282:LEU:HD12	1:K:283:PRO:HD2	1.85	0.57
1:U:187:ARG:NH1	2:U:301:URC:HN9	2.03	0.57
1:A:187:ARG:NH1	2:A:301:URC:HN9	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:187:ARG:NH1	2:I:301:URC:HN9	2.03	0.57
1:U:70:THR:O	1:U:74:THR:HG23	2.04	0.57
1:D:73:ASN:O	1:D:77:VAL:HG13	2.04	0.57
1:I:70:THR:O	1:I:74:THR:HG23	2.04	0.57
1:S:287:PRO:HB2	1:T:23:LYS:HD2	1.85	0.57
1:A:167:GLN:HE22	1:A:228:GLY:HA3	1.69	0.57
2:G:301:URC:HN7	1:H:68:THR:HG23	1.70	0.57
1:A:70:THR:O	1:A:74:THR:HG23	2.04	0.57
1:G:86:ASN:HD21	1:G:89:THR:HG23	1.70	0.57
2:S:301:URC:HN7	1:T:68:THR:HG23	1.70	0.57
1:E:187:ARG:NH1	2:E:301:URC:HN9	2.03	0.57
1:D:153:ILE:HG23	1:D:199:TYR:HB2	1.87	0.56
1:H:153:ILE:HG23	1:H:199:TYR:HB2	1.88	0.56
1:O:86:ASN:HD21	1:O:89:THR:HG23	1.70	0.56
1:O:151:PRO:HG3	1:O:202:ARG:HE	1.71	0.56
1:P:73:ASN:O	1:P:77:VAL:HG13	2.04	0.56
1:Q:263:HIS:HB2	1:Q:284:LEU:HD21	1.88	0.56
1:S:282:LEU:HD12	1:S:283:PRO:HD2	1.85	0.56
1:B:192:GLN:O	1:B:260:PRO:HD2	2.06	0.56
1:L:153:ILE:HG23	1:L:199:TYR:HB2	1.88	0.56
1:T:153:ILE:HG23	1:T:199:TYR:HB2	1.87	0.56
1:X:153:ILE:HG23	1:X:199:TYR:HB2	1.87	0.56
1:E:263:HIS:HB2	1:E:284:LEU:HD21	1.88	0.56
1:M:167:GLN:HE22	1:M:228:GLY:HA3	1.69	0.56
1:Q:187:ARG:NH1	2:Q:301:URC:HN9	2.03	0.56
2:C:301:URC:HN7	1:D:68:THR:HG23	1.70	0.56
2:K:301:URC:HN7	1:L:68:THR:HG23	1.70	0.56
2:W:301:URC:HN7	1:X:68:THR:HG23	1.70	0.56
1:I:263:HIS:HB2	1:I:284:LEU:HD21	1.88	0.56
2:O:301:URC:HN7	1:P:68:THR:HG23	1.70	0.56
1:P:153:ILE:HG23	1:P:199:TYR:HB2	1.88	0.56
1:U:263:HIS:HB2	1:U:284:LEU:HD21	1.88	0.56
1:F:192:GLN:O	1:F:260:PRO:HD2	2.06	0.56
1:T:17:VAL:HG22	1:T:18:ARG:HG3	1.88	0.56
1:J:192:GLN:O	1:J:260:PRO:HD2	2.06	0.56
1:N:192:GLN:O	1:N:260:PRO:HD2	2.06	0.56
1:V:192:GLN:O	1:V:260:PRO:HD2	2.06	0.56
1:M:263:HIS:HB2	1:M:284:LEU:HD21	1.88	0.55
1:S:86:ASN:HD21	1:S:89:THR:HG23	1.70	0.55
1:C:151:PRO:HG3	1:C:202:ARG:HE	1.71	0.55
1:D:17:VAL:HG22	1:D:18:ARG:HG3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:86:ASN:HD21	1:W:89:THR:HG23	1.70	0.55
1:E:29:LEU:HD12	1:E:42:GLU:HB2	1.89	0.55
1:K:86:ASN:HD21	1:K:89:THR:HG23	1.70	0.55
1:M:187:ARG:NH1	2:M:301:URC:HN9	2.03	0.55
1:P:17:VAL:HG22	1:P:18:ARG:HG3	1.88	0.55
1:A:263:HIS:HB2	1:A:284:LEU:HD21	1.88	0.55
1:C:86:ASN:HD21	1:C:89:THR:HG23	1.70	0.55
1:M:29:LEU:HD12	1:M:42:GLU:HB2	1.89	0.55
1:Q:29:LEU:HD12	1:Q:42:GLU:HB2	1.89	0.55
1:R:192:GLN:O	1:R:260:PRO:HD2	2.06	0.55
1:G:151:PRO:HG3	1:G:202:ARG:HE	1.71	0.55
1:I:29:LEU:HD12	1:I:42:GLU:HB2	1.89	0.55
1:A:29:LEU:HD12	1:A:42:GLU:HB2	1.89	0.55
1:H:17:VAL:HG22	1:H:18:ARG:HG3	1.88	0.55
1:H:31:ILE:HA	1:H:40:ILE:HG22	1.89	0.55
1:U:29:LEU:HD12	1:U:42:GLU:HB2	1.89	0.55
1:P:31:ILE:HA	1:P:40:ILE:HG22	1.89	0.55
1:L:17:VAL:HG22	1:L:18:ARG:HG3	1.88	0.54
1:W:151:PRO:HG3	1:W:202:ARG:HE	1.71	0.54
1:C:198:ARG:HG2	1:C:253:GLU:HB3	1.89	0.54
1:S:151:PRO:HG3	1:S:202:ARG:HE	1.71	0.54
1:T:31:ILE:HA	1:T:40:ILE:HG22	1.89	0.54
1:X:17:VAL:HG22	1:X:18:ARG:HG3	1.88	0.54
1:K:151:PRO:HG3	1:K:202:ARG:HE	1.71	0.54
1:K:198:ARG:HG2	1:K:253:GLU:HB3	1.89	0.54
1:N:166:THR:HG22	1:O:129:HIS:CD2	2.43	0.54
1:W:198:ARG:HG2	1:W:253:GLU:HB3	1.89	0.54
1:B:166:THR:HG22	1:C:129:HIS:CD2	2.43	0.54
1:G:198:ARG:HG2	1:G:253:GLU:HB3	1.89	0.54
1:O:198:ARG:HG2	1:O:253:GLU:HB3	1.89	0.54
1:O:52:ARG:HH21	1:O:104:HIS:HA	1.73	0.54
1:S:198:ARG:HG2	1:S:253:GLU:HB3	1.89	0.54
1:X:31:ILE:HA	1:X:40:ILE:HG22	1.89	0.54
1:L:31:ILE:HA	1:L:40:ILE:HG22	1.89	0.54
1:C:52:ARG:HH21	1:C:104:HIS:HA	1.73	0.54
1:R:166:THR:HG22	1:S:129:HIS:CD2	2.43	0.54
1:F:166:THR:HG22	1:G:129:HIS:CD2	2.43	0.53
1:W:52:ARG:HH21	1:W:104:HIS:HA	1.73	0.53
1:D:31:ILE:HA	1:D:40:ILE:HG22	1.89	0.53
1:K:52:ARG:HH21	1:K:104:HIS:HA	1.73	0.53
1:N:157:ILE:HG23	1:N:195:CYS:HB3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:157:ILE:HG23	1:R:195:CYS:HB3	1.91	0.53
1:J:166:THR:HG22	1:K:129:HIS:CD2	2.43	0.53
1:V:166:THR:HG22	1:W:129:HIS:CD2	2.43	0.53
1:E:192:GLN:O	1:E:260:PRO:HD2	2.09	0.53
1:G:52:ARG:HH21	1:G:104:HIS:HA	1.73	0.53
1:I:192:GLN:O	1:I:260:PRO:HD2	2.09	0.53
1:S:52:ARG:HH21	1:S:104:HIS:HA	1.73	0.53
1:U:192:GLN:O	1:U:260:PRO:HD2	2.09	0.53
1:H:74:THR:O	1:H:78:LEU:HD12	2.09	0.53
1:A:192:GLN:O	1:A:260:PRO:HD2	2.09	0.53
1:Q:192:GLN:O	1:Q:260:PRO:HD2	2.09	0.53
1:V:157:ILE:HG23	1:V:195:CYS:HB3	1.91	0.53
1:J:157:ILE:HG23	1:J:195:CYS:HB3	1.91	0.52
1:F:157:ILE:HG23	1:F:195:CYS:HB3	1.91	0.52
1:H:242:GLN:HE21	1:H:295:VAL:HG22	1.74	0.52
1:P:74:THR:O	1:P:78:LEU:HD12	2.09	0.52
1:D:74:THR:O	1:D:78:LEU:HD12	2.09	0.52
1:G:74:THR:O	1:G:77:VAL:HG22	2.10	0.52
1:Q:25:MET:HE3	1:Q:27:LYS:HD2	1.92	0.52
1:R:244:LEU:HD23	1:R:248:GLN:HG3	1.91	0.52
1:N:244:LEU:HD23	1:N:248:GLN:HG3	1.91	0.52
1:T:74:THR:O	1:T:78:LEU:HD12	2.09	0.52
1:V:244:LEU:HD23	1:V:248:GLN:HG3	1.91	0.52
1:J:244:LEU:HD23	1:J:248:GLN:HG3	1.91	0.52
1:L:74:THR:O	1:L:78:LEU:HD12	2.09	0.52
1:X:74:THR:O	1:X:78:LEU:HD12	2.09	0.52
1:M:192:GLN:O	1:M:260:PRO:HD2	2.09	0.52
1:B:127:HIS:CD2	1:C:225:TYR:HA	2.45	0.52
1:O:37:TYR:HE1	1:O:128:VAL:HG12	1.75	0.52
1:S:74:THR:O	1:S:77:VAL:HG22	2.10	0.52
1:X:282:LEU:HD12	1:X:283:PRO:HD2	1.92	0.52
1:L:274:LEU:HD13	1:S:274:LEU:HD13	1.91	0.51
1:T:242:GLN:HE21	1:T:295:VAL:HG22	1.75	0.51
1:B:244:LEU:HD23	1:B:248:GLN:HG3	1.91	0.51
1:C:74:THR:O	1:C:77:VAL:HG22	2.10	0.51
1:D:282:LEU:HD12	1:D:283:PRO:HD2	1.92	0.51
1:J:127:HIS:CD2	1:K:225:TYR:HA	2.45	0.51
1:L:282:LEU:HD12	1:L:283:PRO:HD2	1.92	0.51
1:O:74:THR:O	1:O:77:VAL:HG22	2.10	0.51
1:W:74:THR:O	1:W:77:VAL:HG22	2.10	0.51
1:B:157:ILE:HG23	1:B:195:CYS:HB3	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:25:MET:HE3	1:I:27:LYS:HD2	1.92	0.51
1:K:74:THR:O	1:K:77:VAL:HG22	2.10	0.51
1:U:25:MET:HE3	1:U:27:LYS:HD2	1.92	0.51
1:V:127:HIS:CD2	1:W:225:TYR:HA	2.46	0.51
1:A:218:LEU:HD12	1:D:120:PHE:CZ	2.46	0.51
1:E:25:MET:HE3	1:E:27:LYS:HD2	1.92	0.51
1:S:37:TYR:HE1	1:S:128:VAL:HG12	1.76	0.51
1:C:37:TYR:HE1	1:C:128:VAL:HG12	1.76	0.51
1:P:242:GLN:HE21	1:P:295:VAL:HG22	1.74	0.51
1:W:37:TYR:HE1	1:W:128:VAL:HG12	1.76	0.51
1:E:218:LEU:HD12	1:H:120:PHE:CZ	2.46	0.51
1:F:244:LEU:HD23	1:F:248:GLN:HG3	1.91	0.51
1:G:274:LEU:HD13	1:T:274:LEU:HD13	1.92	0.51
1:L:274:LEU:HD13	1:S:274:LEU:CD1	2.41	0.51
1:M:25:MET:HE3	1:M:27:LYS:HD2	1.92	0.51
1:I:218:LEU:HD12	1:L:120:PHE:CZ	2.46	0.51
1:M:218:LEU:HD12	1:P:120:PHE:CZ	2.46	0.51
1:U:218:LEU:HD12	1:X:120:PHE:CZ	2.46	0.51
1:H:282:LEU:HD12	1:H:283:PRO:HD2	1.92	0.51
1:N:127:HIS:CD2	1:O:225:TYR:HA	2.45	0.51
1:T:37:TYR:HE1	1:T:128:VAL:HG12	1.76	0.51
1:A:25:MET:HE3	1:A:27:LYS:HD2	1.92	0.51
1:K:37:TYR:HE1	1:K:128:VAL:HG12	1.76	0.51
1:Q:218:LEU:HD12	1:T:120:PHE:CZ	2.46	0.51
1:H:37:TYR:HE1	1:H:128:VAL:HG12	1.76	0.50
1:T:282:LEU:HD12	1:T:283:PRO:HD2	1.92	0.50
1:S:66:ILE:HD12	1:S:67:PRO:HD2	1.94	0.50
1:F:127:HIS:CD2	1:G:225:TYR:HA	2.45	0.50
1:G:37:TYR:HE1	1:G:128:VAL:HG12	1.76	0.50
1:G:66:ILE:HD12	1:G:67:PRO:HD2	1.94	0.50
1:R:127:HIS:CD2	1:S:225:TYR:HA	2.46	0.50
1:D:242:GLN:HE21	1:D:295:VAL:HG22	1.74	0.50
1:G:274:LEU:CD1	1:T:274:LEU:HD13	2.41	0.50
1:J:31:ILE:HD11	1:J:38:HIS:HD2	1.77	0.50
1:L:88:GLU:HG2	1:L:153:ILE:HD11	1.94	0.50
1:X:88:GLU:HG2	1:X:153:ILE:HD11	1.94	0.50
1:H:88:GLU:HG2	1:H:153:ILE:HD11	1.94	0.50
1:L:37:TYR:HE1	1:L:128:VAL:HG12	1.76	0.50
1:X:37:TYR:HE1	1:X:128:VAL:HG12	1.76	0.50
1:X:242:GLN:HE21	1:X:295:VAL:HG22	1.74	0.50
1:C:274:LEU:HD13	1:P:274:LEU:HD13	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:31:ILE:HD11	1:V:38:HIS:HD2	1.77	0.50
1:L:242:GLN:HE21	1:L:295:VAL:HG22	1.74	0.50
1:S:85:ARG:HA	1:S:85:ARG:HH11	1.77	0.50
1:R:21:TYR:HE1	1:R:51:LEU:HD13	1.77	0.50
1:D:274:LEU:HD13	1:W:274:LEU:CD1	2.42	0.49
1:P:88:GLU:HG2	1:P:153:ILE:HD11	1.94	0.49
1:S:23:LYS:HZ1	1:T:287:PRO:HG2	1.77	0.49
1:F:21:TYR:HE1	1:F:51:LEU:HD13	1.77	0.49
1:R:31:ILE:HD11	1:R:38:HIS:HD2	1.77	0.49
1:S:294:THR:HG23	1:T:17:VAL:HG13	1.94	0.49
1:C:85:ARG:HH11	1:C:85:ARG:HA	1.77	0.49
1:G:23:LYS:HZ1	1:H:287:PRO:HG2	1.77	0.49
1:G:154:HIS:CD2	1:G:198:ARG:HB2	2.48	0.49
1:O:294:THR:HG23	1:P:17:VAL:HG13	1.94	0.49
1:P:37:TYR:HE1	1:P:128:VAL:HG12	1.76	0.49
1:P:282:LEU:HD12	1:P:283:PRO:HD2	1.93	0.49
1:T:88:GLU:HG2	1:T:153:ILE:HD11	1.94	0.49
1:C:66:ILE:HD12	1:C:67:PRO:HD2	1.94	0.49
1:D:37:TYR:HE1	1:D:128:VAL:HG12	1.76	0.49
1:K:294:THR:HG23	1:L:17:VAL:HG13	1.94	0.49
1:W:294:THR:HG23	1:X:17:VAL:HG13	1.94	0.49
1:D:274:LEU:HD13	1:W:274:LEU:HD13	1.94	0.49
1:G:294:THR:HG23	1:H:17:VAL:HG13	1.95	0.49
1:K:23:LYS:HZ1	1:L:287:PRO:HG2	1.77	0.49
1:N:21:TYR:HE1	1:N:51:LEU:HD13	1.77	0.49
1:C:154:HIS:CD2	1:C:198:ARG:HB2	2.48	0.49
1:C:294:THR:HG23	1:D:17:VAL:HG13	1.94	0.49
1:S:154:HIS:CD2	1:S:198:ARG:HB2	2.48	0.49
1:V:21:TYR:HE1	1:V:51:LEU:HD13	1.77	0.49
1:F:254:ASP:HB3	1:F:296:LYS:HB2	1.95	0.49
1:J:21:TYR:HE1	1:J:51:LEU:HD13	1.77	0.49
1:O:85:ARG:HA	1:O:85:ARG:HH11	1.77	0.49
1:O:154:HIS:CD2	1:O:198:ARG:HB2	2.48	0.49
1:P:128:VAL:HG23	1:P:129:HIS:ND1	2.28	0.49
1:N:31:ILE:HD11	1:N:38:HIS:HD2	1.77	0.49
1:W:85:ARG:HH11	1:W:85:ARG:HA	1.77	0.49
1:W:154:HIS:CD2	1:W:198:ARG:HB2	2.47	0.49
1:C:274:LEU:CD1	1:P:274:LEU:HD13	2.43	0.49
1:D:128:VAL:HG23	1:D:129:HIS:ND1	2.28	0.49
1:K:85:ARG:HH11	1:K:85:ARG:HA	1.77	0.49
1:T:128:VAL:HG23	1:T:129:HIS:ND1	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:66:ILE:HD12	1:K:67:PRO:HD2	1.94	0.49
1:K:154:HIS:CD2	1:K:198:ARG:HB2	2.48	0.49
1:W:23:LYS:HZ1	1:X:287:PRO:HG2	1.78	0.49
1:C:238:LEU:O	1:C:241:ILE:HG22	2.13	0.48
1:E:127:HIS:CD2	1:H:225:TYR:HA	2.48	0.48
1:F:31:ILE:HD11	1:F:38:HIS:HD2	1.77	0.48
1:H:128:VAL:HG23	1:H:129:HIS:ND1	2.28	0.48
1:B:21:TYR:HE1	1:B:51:LEU:HD13	1.77	0.48
1:B:31:ILE:HD11	1:B:38:HIS:HD2	1.77	0.48
1:N:254:ASP:HB3	1:N:296:LYS:HB2	1.95	0.48
1:O:66:ILE:HD12	1:O:67:PRO:HD2	1.94	0.48
1:S:238:LEU:O	1:S:241:ILE:HG22	2.13	0.48
1:W:66:ILE:HD12	1:W:67:PRO:HD2	1.94	0.48
1:D:88:GLU:HG2	1:D:153:ILE:HD11	1.94	0.48
1:K:238:LEU:O	1:K:241:ILE:HG22	2.13	0.48
1:I:127:HIS:CD2	1:L:225:TYR:HA	2.49	0.48
1:M:127:HIS:CD2	1:P:225:TYR:HA	2.48	0.48
1:U:127:HIS:CD2	1:X:225:TYR:HA	2.49	0.48
1:W:238:LEU:O	1:W:241:ILE:HG22	2.13	0.48
1:F:90:PHE:CE2	1:F:94:ILE:HD11	2.49	0.48
1:J:90:PHE:CE2	1:J:94:ILE:HD11	2.49	0.48
1:L:74:THR:O	1:L:77:VAL:HG22	2.14	0.48
1:R:254:ASP:HB3	1:R:296:LYS:HB2	1.95	0.48
1:X:74:THR:O	1:X:77:VAL:HG22	2.14	0.48
1:J:254:ASP:HB3	1:J:296:LYS:HB2	1.95	0.48
1:V:90:PHE:CE2	1:V:94:ILE:HD11	2.49	0.48
1:V:254:ASP:HB3	1:V:296:LYS:HB2	1.95	0.48
1:G:85:ARG:HA	1:G:85:ARG:HH11	1.77	0.48
1:L:128:VAL:HG23	1:L:129:HIS:ND1	2.28	0.48
1:X:128:VAL:HG23	1:X:129:HIS:ND1	2.28	0.48
1:G:238:LEU:O	1:G:241:ILE:HG22	2.13	0.48
1:G:264:TYR:CE1	1:G:283:PRO:HB3	2.44	0.48
1:Q:55:LYS:HE2	1:Q:55:LYS:HB3	1.68	0.48
1:Q:127:HIS:CD2	1:T:225:TYR:HA	2.48	0.48
1:T:74:THR:O	1:T:77:VAL:HG22	2.14	0.48
1:A:127:HIS:CD2	1:D:225:TYR:HA	2.49	0.47
1:B:90:PHE:CE2	1:B:94:ILE:HD11	2.49	0.47
1:B:254:ASP:HB3	1:B:296:LYS:HB2	1.95	0.47
1:F:178:PHE:HA	1:H:272:MET:SD	2.54	0.47
1:N:178:PHE:HA	1:P:272:MET:SD	2.54	0.47
1:D:119:ARG:HA	1:D:131:PHE:CD1	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:119:ARG:HA	1:L:131:PHE:CD1	2.50	0.47
1:T:119:ARG:HA	1:T:131:PHE:CD1	2.50	0.47
1:X:119:ARG:HA	1:X:131:PHE:CD1	2.50	0.47
1:N:90:PHE:CE2	1:N:94:ILE:HD11	2.49	0.47
1:P:74:THR:O	1:P:77:VAL:HG22	2.14	0.47
1:R:90:PHE:CE2	1:R:94:ILE:HD11	2.49	0.47
1:A:269:MET:HE3	1:D:77:VAL:HG12	1.96	0.47
1:B:178:PHE:HA	1:D:272:MET:SD	2.54	0.47
1:C:198:ARG:HB3	1:C:254:ASP:OD1	2.15	0.47
1:H:277:LYS:O	1:H:278:GLU:HG3	2.15	0.47
1:J:178:PHE:HA	1:L:272:MET:SD	2.55	0.47
1:M:55:LYS:HB3	1:M:55:LYS:HE2	1.68	0.47
1:P:277:LYS:O	1:P:278:GLU:HG3	2.15	0.47
1:R:178:PHE:HA	1:T:272:MET:SD	2.54	0.47
1:S:198:ARG:HB3	1:S:254:ASP:OD1	2.15	0.47
1:S:264:TYR:CE1	1:S:283:PRO:HB3	2.44	0.47
1:D:153:ILE:HG12	1:D:199:TYR:HD2	1.80	0.47
1:J:201:ARG:HH12	1:J:251:GLU:HB3	1.80	0.47
1:O:238:LEU:O	1:O:241:ILE:HG22	2.13	0.47
1:V:178:PHE:HA	1:X:272:MET:SD	2.55	0.47
1:D:277:LYS:O	1:D:278:GLU:HG3	2.15	0.47
1:H:74:THR:O	1:H:77:VAL:HG22	2.14	0.47
1:K:198:ARG:HB3	1:K:254:ASP:OD1	2.15	0.47
1:L:277:LYS:O	1:L:278:GLU:HG3	2.15	0.47
1:N:23:LYS:HD2	1:N:68:THR:OG1	2.15	0.47
1:R:201:ARG:HH12	1:R:251:GLU:HB3	1.80	0.47
1:T:153:ILE:HG12	1:T:199:TYR:HD2	1.80	0.47
1:T:277:LYS:O	1:T:278:GLU:HG3	2.15	0.47
1:V:201:ARG:HH12	1:V:251:GLU:HB3	1.80	0.47
1:X:277:LYS:O	1:X:278:GLU:HG3	2.15	0.47
1:D:74:THR:O	1:D:77:VAL:HG22	2.14	0.47
1:D:256:GLU:HG2	1:D:294:THR:HB	1.97	0.47
1:F:201:ARG:HH12	1:F:251:GLU:HB3	1.80	0.47
1:G:198:ARG:HB3	1:G:254:ASP:OD1	2.15	0.47
1:N:167:GLN:HE22	1:N:229:GLU:N	2.13	0.47
1:W:198:ARG:HB3	1:W:254:ASP:OD1	2.15	0.47
1:A:89:THR:HA	1:A:92:MET:HE3	1.97	0.47
1:J:23:LYS:HD2	1:J:68:THR:OG1	2.15	0.47
1:P:153:ILE:HG12	1:P:199:TYR:HD2	1.80	0.47
1:V:23:LYS:HD2	1:V:68:THR:OG1	2.15	0.47
1:B:127:HIS:HE1	1:B:129:HIS:CE1	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:167:GLN:HE22	1:B:229:GLU:N	2.13	0.47
1:B:201:ARG:HH12	1:B:251:GLU:HB3	1.80	0.47
1:F:23:LYS:HD2	1:F:68:THR:OG1	2.15	0.47
1:P:119:ARG:HA	1:P:131:PHE:CD1	2.49	0.47
1:B:23:LYS:HD2	1:B:68:THR:OG1	2.15	0.46
1:V:27:LYS:HG2	1:W:283:PRO:HG3	1.97	0.46
1:G:284:LEU:HD23	1:G:284:LEU:HA	1.80	0.46
1:J:27:LYS:HG2	1:K:283:PRO:HG3	1.97	0.46
1:N:201:ARG:HH12	1:N:251:GLU:HB3	1.80	0.46
1:O:264:TYR:CE1	1:O:283:PRO:HB3	2.44	0.46
1:P:119:ARG:HA	1:P:131:PHE:HD1	1.81	0.46
1:H:142:GLU:HG2	1:H:154:HIS:HB2	1.98	0.46
1:J:127:HIS:HE1	1:J:129:HIS:CE1	2.33	0.46
1:L:142:GLU:HG2	1:L:154:HIS:HB2	1.98	0.46
1:M:89:THR:HA	1:M:92:MET:HE3	1.97	0.46
1:R:167:GLN:HE22	1:R:229:GLU:N	2.13	0.46
1:V:127:HIS:HE1	1:V:129:HIS:CE1	2.33	0.46
1:D:55:LYS:HG2	1:D:59:HIS:CE1	2.39	0.46
1:E:269:MET:HE3	1:H:77:VAL:HG12	1.96	0.46
1:F:167:GLN:HE22	1:F:229:GLU:N	2.13	0.46
1:H:119:ARG:HA	1:H:131:PHE:CD1	2.49	0.46
1:X:142:GLU:HG2	1:X:154:HIS:HB2	1.98	0.46
1:F:27:LYS:HG2	1:G:283:PRO:HG3	1.97	0.46
1:H:119:ARG:HA	1:H:131:PHE:HD1	1.81	0.46
1:H:153:ILE:HG12	1:H:199:TYR:HD2	1.80	0.46
1:J:167:GLN:HE22	1:J:229:GLU:N	2.13	0.46
1:P:142:GLU:HG2	1:P:154:HIS:HB2	1.98	0.46
1:D:142:GLU:HG2	1:D:154:HIS:HB2	1.98	0.46
1:G:197:TRP:HB3	1:G:255:MET:SD	2.56	0.46
1:T:142:GLU:HG2	1:T:154:HIS:HB2	1.98	0.46
1:F:127:HIS:HE1	1:F:129:HIS:CE1	2.33	0.46
1:R:23:LYS:HD2	1:R:68:THR:OG1	2.15	0.46
1:V:167:GLN:HE22	1:V:229:GLU:N	2.13	0.46
1:E:89:THR:HA	1:E:92:MET:HE3	1.97	0.46
1:H:256:GLU:HG2	1:H:294:THR:HB	1.97	0.46
1:I:89:THR:HA	1:I:92:MET:HE3	1.97	0.46
1:K:176:ASP:O	1:K:179:THR:HG22	2.16	0.46
1:N:127:HIS:HE1	1:N:129:HIS:CE1	2.33	0.46
1:O:197:TRP:HB3	1:O:255:MET:SD	2.56	0.46
1:Q:269:MET:HE3	1:T:77:VAL:HG12	1.96	0.46
1:R:127:HIS:HE1	1:R:129:HIS:CE1	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:154:HIS:CD2	1:L:198:ARG:HB2	2.51	0.46
1:N:67:PRO:HG2	1:N:70:THR:OG1	2.16	0.46
1:O:198:ARG:HB3	1:O:254:ASP:OD1	2.15	0.46
1:P:55:LYS:HG2	1:P:59:HIS:CE1	2.39	0.46
1:U:269:MET:HE3	1:X:77:VAL:HG12	1.96	0.46
1:W:176:ASP:O	1:W:179:THR:HG22	2.16	0.46
1:X:240:ASP:HA	1:X:243:VAL:HG12	1.98	0.46
1:B:27:LYS:HG2	1:C:283:PRO:HG3	1.97	0.46
1:F:67:PRO:HG2	1:F:70:THR:OG1	2.16	0.46
1:I:269:MET:HE3	1:L:77:VAL:HG12	1.96	0.46
1:K:197:TRP:HB3	1:K:255:MET:SD	2.56	0.46
1:U:89:THR:HA	1:U:92:MET:HE3	1.97	0.46
1:X:154:HIS:CD2	1:X:198:ARG:HB2	2.51	0.46
1:L:240:ASP:HA	1:L:243:VAL:HG12	1.98	0.45
1:N:27:LYS:HG2	1:O:283:PRO:HG3	1.97	0.45
1:N:238:LEU:HD13	1:N:291:ILE:HG22	1.98	0.45
1:S:197:TRP:HB3	1:S:255:MET:SD	2.56	0.45
1:A:224:PRO:HD2	1:A:228:GLY:HA2	1.98	0.45
1:C:176:ASP:O	1:C:179:THR:HG22	2.16	0.45
1:C:197:TRP:HB3	1:C:255:MET:SD	2.56	0.45
1:E:224:PRO:HD2	1:E:228:GLY:HA2	1.98	0.45
1:G:176:ASP:O	1:G:179:THR:HG22	2.16	0.45
1:H:154:HIS:CD2	1:H:198:ARG:HB2	2.51	0.45
1:I:224:PRO:HD2	1:I:228:GLY:HA2	1.98	0.45
1:L:256:GLU:HG2	1:L:294:THR:HB	1.97	0.45
1:M:269:MET:HE3	1:P:77:VAL:HG12	1.97	0.45
1:P:256:GLU:HG2	1:P:294:THR:HB	1.97	0.45
1:R:27:LYS:HG2	1:S:283:PRO:HG3	1.97	0.45
1:R:67:PRO:HG2	1:R:70:THR:OG1	2.16	0.45
1:S:176:ASP:O	1:S:179:THR:HG22	2.16	0.45
1:U:224:PRO:HD2	1:U:228:GLY:HA2	1.98	0.45
1:W:197:TRP:HB3	1:W:255:MET:SD	2.56	0.45
1:B:238:LEU:HD13	1:B:291:ILE:HG22	1.98	0.45
1:C:102:PHE:HB3	1:C:104:HIS:CE1	2.51	0.45
1:G:102:PHE:HB3	1:G:104:HIS:CE1	2.52	0.45
1:K:102:PHE:HB3	1:K:104:HIS:CE1	2.51	0.45
1:W:102:PHE:HB3	1:W:104:HIS:CE1	2.51	0.45
1:X:256:GLU:HG2	1:X:294:THR:HB	1.97	0.45
1:D:154:HIS:CD2	1:D:198:ARG:HB2	2.52	0.45
1:J:157:ILE:HB	1:J:210:TRP:HE1	1.81	0.45
1:T:66:ILE:HD12	1:T:67:PRO:HD2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:264:TYR:CE1	1:W:283:PRO:HB3	2.44	0.45
1:X:153:ILE:HG12	1:X:199:TYR:HD2	1.80	0.45
1:A:178:PHE:HA	1:C:272:MET:SD	2.57	0.45
1:B:157:ILE:HB	1:B:210:TRP:HE1	1.82	0.45
1:D:240:ASP:HA	1:D:243:VAL:HG12	1.98	0.45
1:E:178:PHE:HA	1:G:272:MET:SD	2.57	0.45
1:G:128:VAL:HG23	1:G:129:HIS:ND1	2.32	0.45
1:G:277:LYS:HE2	1:G:277:LYS:HB2	1.73	0.45
1:K:264:TYR:CE1	1:K:283:PRO:HB3	2.44	0.45
1:L:153:ILE:HG12	1:L:199:TYR:HD2	1.80	0.45
1:M:224:PRO:HD2	1:M:228:GLY:HA2	1.98	0.45
1:T:256:GLU:HG2	1:T:294:THR:HB	1.97	0.45
1:V:157:ILE:HB	1:V:210:TRP:HE1	1.81	0.45
1:X:226:ASP:OD1	1:X:227:LYS:HG2	2.17	0.45
1:D:119:ARG:HA	1:D:131:PHE:HD1	1.81	0.45
1:D:226:ASP:OD1	1:D:227:LYS:HG2	2.17	0.45
1:F:152:VAL:HG13	1:F:198:ARG:HH21	1.82	0.45
1:H:66:ILE:HD12	1:H:67:PRO:HD2	1.99	0.45
1:I:178:PHE:HA	1:K:272:MET:SD	2.57	0.45
1:J:122:LYS:HB3	1:J:122:LYS:HE2	1.77	0.45
1:L:226:ASP:OD1	1:L:227:LYS:HG2	2.17	0.45
1:O:128:VAL:HG23	1:O:129:HIS:ND1	2.32	0.45
1:O:176:ASP:O	1:O:179:THR:HG22	2.16	0.45
1:Q:224:PRO:HD2	1:Q:228:GLY:HA2	1.98	0.45
1:S:102:PHE:HB3	1:S:104:HIS:CE1	2.51	0.45
1:B:67:PRO:HG2	1:B:70:THR:OG1	2.16	0.45
1:C:97:HIS:C	1:C:97:HIS:CD2	2.95	0.45
1:J:67:PRO:HG2	1:J:70:THR:OG1	2.16	0.45
1:O:277:LYS:HE2	1:O:277:LYS:HB2	1.73	0.45
1:U:178:PHE:HA	1:W:272:MET:SD	2.57	0.45
1:K:128:VAL:HG23	1:K:129:HIS:ND1	2.32	0.45
1:N:152:VAL:HG13	1:N:198:ARG:HH21	1.82	0.45
1:T:240:ASP:HA	1:T:243:VAL:HG12	1.98	0.45
1:V:67:PRO:HG2	1:V:70:THR:OG1	2.16	0.45
1:W:128:VAL:HG23	1:W:129:HIS:ND1	2.32	0.45
1:E:90:PHE:CZ	1:E:94:ILE:HD11	2.52	0.45
1:I:298:LYS:HG2	1:J:15:GLU:OE2	2.17	0.45
1:J:90:PHE:CZ	1:J:94:ILE:HD11	2.52	0.45
1:O:102:PHE:HB3	1:O:104:HIS:CE1	2.51	0.45
1:Q:89:THR:HA	1:Q:92:MET:HE3	1.97	0.45
1:Q:160:LEU:HD21	1:Q:218:LEU:HD21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:90:PHE:CZ	1:R:94:ILE:HD11	2.52	0.45
1:R:152:VAL:HG13	1:R:198:ARG:HH21	1.82	0.45
1:T:226:ASP:OD1	1:T:227:LYS:HG2	2.17	0.45
1:V:90:PHE:CZ	1:V:94:ILE:HD11	2.52	0.45
1:P:154:HIS:CD2	1:P:198:ARG:HB2	2.52	0.45
1:P:226:ASP:OD1	1:P:227:LYS:HG2	2.17	0.45
1:U:298:LYS:HG2	1:V:15:GLU:OE2	2.17	0.45
1:X:119:ARG:HA	1:X:131:PHE:HD1	1.81	0.45
1:B:90:PHE:CZ	1:B:94:ILE:HD11	2.52	0.44
1:F:238:LEU:HD13	1:F:291:ILE:HG22	1.98	0.44
1:G:97:HIS:C	1:G:97:HIS:CD2	2.95	0.44
1:I:160:LEU:HD21	1:I:218:LEU:HD21	1.99	0.44
1:L:119:ARG:HA	1:L:131:PHE:HD1	1.81	0.44
1:Q:178:PHE:HA	1:S:272:MET:SD	2.57	0.44
1:R:157:ILE:HB	1:R:210:TRP:HE1	1.81	0.44
1:S:128:VAL:HG23	1:S:129:HIS:ND1	2.32	0.44
1:S:277:LYS:HB2	1:S:277:LYS:HE2	1.73	0.44
1:U:160:LEU:HD21	1:U:218:LEU:HD21	1.99	0.44
1:A:90:PHE:CZ	1:A:94:ILE:HD11	2.52	0.44
1:H:240:ASP:HA	1:H:243:VAL:HG12	1.98	0.44
1:M:298:LYS:HG2	1:N:15:GLU:OE2	2.17	0.44
1:N:90:PHE:CZ	1:N:94:ILE:HD11	2.52	0.44
1:O:267:ILE:HD11	1:O:282:LEU:HB2	2.00	0.44
1:P:240:ASP:HA	1:P:243:VAL:HG12	1.98	0.44
1:T:154:HIS:CD2	1:T:198:ARG:HB2	2.51	0.44
1:V:152:VAL:HG13	1:V:198:ARG:HH21	1.82	0.44
1:W:97:HIS:C	1:W:97:HIS:CD2	2.95	0.44
1:F:166:THR:HG22	1:G:129:HIS:NE2	2.32	0.44
1:F:220:LYS:HD3	1:F:220:LYS:HA	1.82	0.44
1:J:152:VAL:HG13	1:J:198:ARG:HH21	1.82	0.44
1:M:178:PHE:HA	1:O:272:MET:SD	2.57	0.44
1:N:166:THR:HG22	1:O:129:HIS:NE2	2.32	0.44
1:Q:298:LYS:HG2	1:R:15:GLU:OE2	2.17	0.44
1:V:238:LEU:HD13	1:V:291:ILE:HG22	1.98	0.44
1:C:128:VAL:HG23	1:C:129:HIS:ND1	2.32	0.44
1:C:267:ILE:HD11	1:C:282:LEU:HB2	2.00	0.44
1:J:238:LEU:HD13	1:J:291:ILE:HG22	1.98	0.44
1:J:277:LYS:O	1:J:278:GLU:HG3	2.18	0.44
1:K:97:HIS:C	1:K:97:HIS:CD2	2.95	0.44
1:I:90:PHE:CZ	1:I:94:ILE:HD11	2.52	0.44
1:M:160:LEU:HD21	1:M:218:LEU:HD21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:157:ILE:HB	1:N:210:TRP:HE1	1.82	0.44
1:N:277:LYS:O	1:N:278:GLU:HG3	2.18	0.44
1:Q:90:PHE:CZ	1:Q:94:ILE:HD11	2.52	0.44
1:S:267:ILE:HD11	1:S:282:LEU:HB2	2.00	0.44
1:X:66:ILE:HD12	1:X:67:PRO:HD2	1.99	0.44
1:X:126:LYS:HE2	1:X:126:LYS:HB2	1.79	0.44
1:F:90:PHE:CZ	1:F:94:ILE:HD11	2.52	0.44
1:F:157:ILE:HB	1:F:210:TRP:HE1	1.81	0.44
1:H:86:ASN:HD21	1:H:89:THR:HG23	1.83	0.44
1:H:226:ASP:OD1	1:H:227:LYS:HG2	2.17	0.44
1:L:145:GLN:OE1	1:L:151:PRO:HB3	2.18	0.44
1:M:198:ARG:HD2	1:M:254:ASP:OD2	2.18	0.44
1:R:238:LEU:HD13	1:R:291:ILE:HG22	1.98	0.44
1:U:90:PHE:CZ	1:U:94:ILE:HD11	2.52	0.44
1:V:277:LYS:O	1:V:278:GLU:HG3	2.18	0.44
1:B:152:VAL:HG13	1:B:198:ARG:HH21	1.82	0.44
1:D:242:GLN:HE22	1:D:295:VAL:HG13	1.83	0.44
1:L:66:ILE:HD12	1:L:67:PRO:HD2	1.99	0.44
1:P:66:ILE:HD12	1:P:67:PRO:HD2	1.99	0.44
1:P:86:ASN:HD21	1:P:89:THR:HG23	1.83	0.44
1:T:119:ARG:HA	1:T:131:PHE:HD1	1.81	0.44
1:U:282:LEU:HD23	1:U:282:LEU:HA	1.85	0.44
1:X:145:GLN:OE1	1:X:151:PRO:HB3	2.18	0.44
1:B:277:LYS:O	1:B:278:GLU:HG3	2.18	0.44
1:F:277:LYS:O	1:F:278:GLU:HG3	2.18	0.44
1:L:242:GLN:HE22	1:L:295:VAL:HG13	1.83	0.44
1:X:242:GLN:HE22	1:X:295:VAL:HG13	1.83	0.44
1:C:264:TYR:CE1	1:C:283:PRO:HB3	2.44	0.44
1:E:67:PRO:HG2	1:E:70:THR:OG1	2.18	0.44
1:I:198:ARG:HD2	1:I:254:ASP:OD2	2.18	0.44
1:I:282:LEU:HD23	1:I:282:LEU:HA	1.85	0.44
1:M:90:PHE:CZ	1:M:94:ILE:HD11	2.52	0.44
1:Q:65:ILE:HD13	1:Q:65:ILE:HA	1.84	0.44
1:T:55:LYS:HG2	1:T:59:HIS:CE1	2.39	0.44
1:U:198:ARG:HD2	1:U:254:ASP:OD2	2.18	0.44
1:F:122:LYS:HB3	1:F:122:LYS:HE2	1.77	0.43
1:H:145:GLN:OE1	1:H:151:PRO:HB3	2.18	0.43
1:P:242:GLN:HE22	1:P:295:VAL:HG13	1.83	0.43
1:Q:67:PRO:HG2	1:Q:70:THR:OG1	2.18	0.43
1:V:166:THR:HG22	1:W:129:HIS:NE2	2.32	0.43
1:A:198:ARG:HD2	1:A:254:ASP:OD2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:166:THR:HG22	1:C:129:HIS:NE2	2.32	0.43
1:E:198:ARG:HD2	1:E:254:ASP:OD2	2.18	0.43
1:E:298:LYS:HG2	1:F:15:GLU:OE2	2.17	0.43
1:I:55:LYS:HE2	1:I:55:LYS:HB3	1.68	0.43
1:J:166:THR:HG22	1:K:129:HIS:NE2	2.32	0.43
1:L:126:LYS:HE2	1:L:126:LYS:HB2	1.79	0.43
1:Q:198:ARG:HD2	1:Q:254:ASP:OD2	2.18	0.43
1:Q:284:LEU:HD23	1:Q:284:LEU:H	1.83	0.43
1:R:166:THR:HG22	1:S:129:HIS:NE2	2.33	0.43
1:F:216:ILE:HD11	1:F:244:LEU:HB3	2.01	0.43
1:M:284:LEU:H	1:M:284:LEU:HD23	1.83	0.43
1:W:267:ILE:HD11	1:W:282:LEU:HB2	2.00	0.43
1:A:160:LEU:HD21	1:A:218:LEU:HD21	1.99	0.43
1:A:284:LEU:H	1:A:284:LEU:HD23	1.83	0.43
1:A:298:LYS:HG2	1:B:15:GLU:OE2	2.17	0.43
1:E:160:LEU:HD21	1:E:218:LEU:HD21	1.99	0.43
1:K:267:ILE:HD11	1:K:282:LEU:HB2	1.99	0.43
1:R:277:LYS:O	1:R:278:GLU:HG3	2.18	0.43
1:S:97:HIS:C	1:S:97:HIS:CD2	2.95	0.43
1:T:86:ASN:HD21	1:T:89:THR:HG23	1.83	0.43
1:V:201:ARG:HG2	1:V:201:ARG:HH11	1.84	0.43
1:A:272:MET:HA	1:A:272:MET:HE2	2.01	0.43
1:J:201:ARG:HG2	1:J:201:ARG:HH11	1.84	0.43
1:R:216:ILE:HD11	1:R:244:LEU:HB3	2.00	0.43
1:B:201:ARG:HH11	1:B:201:ARG:HG2	1.84	0.43
1:D:66:ILE:HD12	1:D:67:PRO:HD2	1.99	0.43
1:H:242:GLN:HE22	1:H:295:VAL:HG13	1.83	0.43
1:M:272:MET:HA	1:M:272:MET:HE2	2.01	0.43
1:O:97:HIS:CD2	1:O:97:HIS:C	2.95	0.43
1:P:145:GLN:OE1	1:P:151:PRO:HB3	2.18	0.43
1:S:59:HIS:HB2	1:S:61:ASP:OD1	2.19	0.43
1:T:145:GLN:OE1	1:T:151:PRO:HB3	2.18	0.43
1:U:284:LEU:HD23	1:U:284:LEU:H	1.83	0.43
1:W:24:ASP:OD1	1:W:24:ASP:C	2.62	0.43
1:W:59:HIS:HB2	1:W:61:ASP:OD1	2.19	0.43
1:G:24:ASP:OD1	1:G:24:ASP:C	2.62	0.43
1:I:272:MET:HE2	1:I:272:MET:HA	2.01	0.43
1:I:284:LEU:HD23	1:I:284:LEU:H	1.83	0.43
1:K:24:ASP:OD1	1:K:24:ASP:C	2.62	0.43
1:K:59:HIS:HB2	1:K:61:ASP:OD1	2.19	0.43
1:S:122:LYS:HG2	1:S:123:ASN:ND2	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:55:LYS:HE2	1:U:55:LYS:HB3	1.68	0.43
1:A:67:PRO:HG2	1:A:70:THR:OG1	2.18	0.43
1:D:86:ASN:HD21	1:D:89:THR:HG23	1.83	0.43
1:D:145:GLN:OE1	1:D:151:PRO:HB3	2.18	0.43
1:G:267:ILE:HD11	1:G:282:LEU:HB2	1.99	0.43
1:M:282:LEU:HD23	1:M:282:LEU:HA	1.85	0.43
1:N:216:ILE:HD11	1:N:244:LEU:HB3	2.01	0.43
1:T:242:GLN:HE22	1:T:295:VAL:HG13	1.83	0.43
1:E:282:LEU:HD23	1:E:282:LEU:HA	1.85	0.43
1:G:59:HIS:HB2	1:G:61:ASP:OD1	2.19	0.43
1:I:67:PRO:HG2	1:I:70:THR:OG1	2.18	0.43
1:J:220:LYS:HD3	1:J:220:LYS:HA	1.82	0.43
1:T:97:HIS:CD2	1:T:97:HIS:C	2.97	0.43
1:U:67:PRO:HG2	1:U:70:THR:OG1	2.18	0.43
1:K:122:LYS:HG2	1:K:123:ASN:ND2	2.34	0.43
1:L:113:GLU:OE1	1:L:158:LYS:HE3	2.19	0.43
1:M:67:PRO:HG2	1:M:70:THR:OG1	2.18	0.43
1:U:272:MET:HA	1:U:272:MET:HE2	2.01	0.43
1:W:37:TYR:CE1	1:W:128:VAL:HG12	2.54	0.43
1:W:122:LYS:HG2	1:W:123:ASN:ND2	2.34	0.43
1:B:122:LYS:HB3	1:B:122:LYS:HE2	1.77	0.42
1:C:59:HIS:HB2	1:C:61:ASP:OD1	2.19	0.42
1:L:94:ILE:HG13	1:L:94:ILE:H	1.69	0.42
1:O:122:LYS:HG2	1:O:123:ASN:ND2	2.34	0.42
1:X:113:GLU:OE1	1:X:158:LYS:HE3	2.19	0.42
1:C:77:VAL:HG11	1:D:178:PHE:CE1	2.54	0.42
1:D:113:GLU:OE1	1:D:158:LYS:HE3	2.19	0.42
1:G:77:VAL:HG11	1:H:178:PHE:CE1	2.54	0.42
1:H:126:LYS:HE2	1:H:126:LYS:HB2	1.79	0.42
1:K:37:TYR:CE1	1:K:128:VAL:HG12	2.55	0.42
1:X:94:ILE:HG13	1:X:94:ILE:H	1.69	0.42
1:D:55:LYS:HB2	1:D:55:LYS:HE3	1.85	0.42
1:E:232:PRO:HD2	1:E:236:LYS:HG2	2.02	0.42
1:E:272:MET:HE2	1:E:272:MET:HA	2.01	0.42
1:E:284:LEU:HD23	1:E:284:LEU:H	1.83	0.42
1:O:24:ASP:OD1	1:O:24:ASP:C	2.62	0.42
1:O:59:HIS:HB2	1:O:61:ASP:OD1	2.19	0.42
1:R:201:ARG:HG2	1:R:201:ARG:HH11	1.84	0.42
1:C:37:TYR:CE1	1:C:128:VAL:HG12	2.54	0.42
1:E:90:PHE:CE2	1:E:94:ILE:HD11	2.55	0.42
1:G:122:LYS:HG2	1:G:123:ASN:ND2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:97:HIS:CD2	1:H:97:HIS:C	2.97	0.42
1:X:86:ASN:HD21	1:X:89:THR:HG23	1.83	0.42
1:C:122:LYS:HG2	1:C:123:ASN:ND2	2.34	0.42
1:Q:272:MET:HE2	1:Q:272:MET:HA	2.01	0.42
1:V:220:LYS:HD3	1:V:220:LYS:HA	1.82	0.42
1:X:97:HIS:CD2	1:X:97:HIS:C	2.97	0.42
1:C:24:ASP:OD1	1:C:24:ASP:C	2.62	0.42
1:D:52:ARG:NH2	1:D:104:HIS:HA	2.34	0.42
1:P:113:GLU:OE1	1:P:158:LYS:HE3	2.19	0.42
1:Q:90:PHE:CE2	1:Q:94:ILE:HD11	2.55	0.42
1:R:220:LYS:HD3	1:R:220:LYS:HA	1.82	0.42
1:A:90:PHE:CE2	1:A:94:ILE:HD11	2.55	0.42
1:B:216:ILE:HD11	1:B:244:LEU:HB3	2.01	0.42
1:G:52:ARG:NH2	1:G:104:HIS:HA	2.34	0.42
1:G:178:PHE:CE1	1:H:77:VAL:HG11	2.55	0.42
1:L:52:ARG:NH2	1:L:104:HIS:HA	2.34	0.42
1:L:86:ASN:HD21	1:L:89:THR:HG23	1.83	0.42
1:M:166:THR:HG22	1:P:129:HIS:CD2	2.55	0.42
1:O:77:VAL:HG11	1:P:178:PHE:CE1	2.54	0.42
1:P:284:LEU:HD12	1:P:284:LEU:HA	1.89	0.42
1:Q:232:PRO:HD2	1:Q:236:LYS:HG2	2.02	0.42
1:L:24:ASP:OD1	1:L:24:ASP:C	2.63	0.42
1:L:97:HIS:CD2	1:L:97:HIS:C	2.97	0.42
1:M:232:PRO:HD2	1:M:236:LYS:HG2	2.02	0.42
1:N:201:ARG:HH11	1:N:201:ARG:HG2	1.84	0.42
1:U:166:THR:HG22	1:X:129:HIS:CD2	2.55	0.42
1:A:23:LYS:HD2	1:B:287:PRO:HB2	2.02	0.42
1:H:88:GLU:O	1:H:92:MET:SD	2.78	0.42
1:I:23:LYS:HD2	1:J:287:PRO:HB2	2.02	0.42
1:I:166:THR:HG22	1:L:129:HIS:CD2	2.55	0.42
1:K:77:VAL:HG11	1:L:178:PHE:CE1	2.54	0.42
1:L:88:GLU:O	1:L:92:MET:SD	2.78	0.42
1:O:178:PHE:CE1	1:P:77:VAL:HG11	2.55	0.42
1:P:88:GLU:O	1:P:92:MET:SD	2.78	0.42
1:S:24:ASP:OD1	1:S:24:ASP:C	2.62	0.42
1:U:23:LYS:HD2	1:V:287:PRO:HB2	2.02	0.42
1:X:24:ASP:OD1	1:X:24:ASP:C	2.63	0.42
1:X:54:LYS:O	1:X:58:LEU:HD23	2.20	0.42
1:X:88:GLU:O	1:X:92:MET:SD	2.78	0.42
1:X:269:MET:HE3	1:X:269:MET:HB2	1.88	0.42
1:H:113:GLU:OE1	1:H:158:LYS:HE3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:90:PHE:CE2	1:I:94:ILE:HD11	2.55	0.42
1:L:54:LYS:O	1:L:58:LEU:HD23	2.20	0.42
1:P:54:LYS:O	1:P:58:LEU:HD23	2.20	0.42
1:R:209:ILE:HD11	1:R:251:GLU:HG3	2.02	0.42
1:S:52:ARG:NH2	1:S:104:HIS:HA	2.34	0.42
1:S:127:HIS:HE1	1:S:129:HIS:CE1	2.38	0.42
1:U:90:PHE:CE2	1:U:94:ILE:HD11	2.55	0.42
1:W:77:VAL:HG11	1:X:178:PHE:CE1	2.54	0.42
1:X:52:ARG:NH2	1:X:104:HIS:HA	2.34	0.42
1:A:240:ASP:OD1	1:A:240:ASP:C	2.63	0.41
1:C:127:HIS:HE1	1:C:129:HIS:CE1	2.38	0.41
1:D:54:LYS:O	1:D:58:LEU:HD23	2.20	0.41
1:D:97:HIS:CD2	1:D:97:HIS:C	2.97	0.41
1:G:127:HIS:HE1	1:G:129:HIS:CE1	2.38	0.41
1:J:209:ILE:HD11	1:J:251:GLU:HG3	2.02	0.41
1:J:216:ILE:HD11	1:J:244:LEU:HB3	2.01	0.41
1:K:178:PHE:CE1	1:L:77:VAL:HG11	2.55	0.41
1:M:90:PHE:CE2	1:M:94:ILE:HD11	2.55	0.41
1:N:122:LYS:HB3	1:N:122:LYS:HE2	1.77	0.41
1:O:52:ARG:NH2	1:O:104:HIS:HA	2.34	0.41
1:P:94:ILE:HG13	1:P:94:ILE:H	1.69	0.41
1:Q:166:THR:HG22	1:T:129:HIS:CD2	2.55	0.41
1:S:77:VAL:HG11	1:T:178:PHE:CE1	2.54	0.41
1:T:113:GLU:OE1	1:T:158:LYS:HE3	2.19	0.41
1:V:216:ILE:HD11	1:V:244:LEU:HB3	2.00	0.41
1:W:178:PHE:CE1	1:X:77:VAL:HG11	2.55	0.41
1:F:201:ARG:HG2	1:F:201:ARG:HH11	1.84	0.41
1:F:209:ILE:HD11	1:F:251:GLU:HG3	2.02	0.41
1:G:37:TYR:CE1	1:G:128:VAL:HG12	2.54	0.41
1:G:220:LYS:HD2	1:G:220:LYS:O	2.21	0.41
1:I:232:PRO:HD2	1:I:236:LYS:HG2	2.02	0.41
1:J:176:ASP:OD1	1:J:176:ASP:C	2.63	0.41
1:M:240:ASP:OD1	1:M:240:ASP:C	2.63	0.41
1:N:176:ASP:OD1	1:N:176:ASP:C	2.63	0.41
1:O:127:HIS:HE1	1:O:129:HIS:CE1	2.38	0.41
1:P:55:LYS:HB3	1:P:61:ASP:OD1	2.21	0.41
1:P:97:HIS:CD2	1:P:97:HIS:C	2.97	0.41
1:U:232:PRO:HD2	1:U:236:LYS:HG2	2.02	0.41
1:V:209:ILE:HD11	1:V:251:GLU:HG3	2.02	0.41
1:A:166:THR:HG22	1:D:129:HIS:CD2	2.55	0.41
1:A:220:LYS:HA	1:A:220:LYS:HD3	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:232:PRO:HD2	1:A:236:LYS:HG2	2.02	0.41
1:C:52:ARG:NH2	1:C:104:HIS:HA	2.34	0.41
1:E:55:LYS:HB3	1:E:55:LYS:HE2	1.68	0.41
1:L:269:MET:HE3	1:L:269:MET:HB2	1.89	0.41
1:N:88:GLU:OE2	1:N:88:GLU:HA	2.21	0.41
1:Q:240:ASP:OD1	1:Q:240:ASP:C	2.63	0.41
1:S:178:PHE:CE1	1:T:77:VAL:HG11	2.55	0.41
1:B:209:ILE:HD11	1:B:251:GLU:HG3	2.02	0.41
1:H:54:LYS:O	1:H:58:LEU:HD23	2.20	0.41
1:I:240:ASP:OD1	1:I:240:ASP:C	2.63	0.41
1:K:220:LYS:HD2	1:K:220:LYS:O	2.20	0.41
1:N:209:ILE:HD11	1:N:251:GLU:HG3	2.02	0.41
1:P:24:ASP:OD1	1:P:24:ASP:C	2.63	0.41
1:T:24:ASP:OD1	1:T:24:ASP:C	2.63	0.41
1:T:88:GLU:O	1:T:92:MET:SD	2.78	0.41
1:V:176:ASP:OD1	1:V:176:ASP:C	2.63	0.41
1:W:52:ARG:NH2	1:W:104:HIS:HA	2.34	0.41
1:C:220:LYS:HD2	1:C:220:LYS:O	2.20	0.41
1:J:88:GLU:HA	1:J:88:GLU:OE2	2.21	0.41
1:K:52:ARG:NH2	1:K:104:HIS:HA	2.34	0.41
1:K:118:LYS:HD2	1:K:119:ARG:O	2.21	0.41
1:Q:189:PHE:HZ	1:Q:234:VAL:HG12	1.86	0.41
1:R:166:THR:HG23	1:R:167:GLN:HG2	2.03	0.41
1:S:220:LYS:HD2	1:S:220:LYS:O	2.20	0.41
1:T:55:LYS:HB3	1:T:61:ASP:OD1	2.21	0.41
1:U:240:ASP:OD1	1:U:240:ASP:C	2.63	0.41
1:V:88:GLU:HA	1:V:88:GLU:OE2	2.21	0.41
1:W:118:LYS:HD2	1:W:119:ARG:O	2.21	0.41
1:D:55:LYS:HB3	1:D:61:ASP:OD1	2.21	0.41
1:F:88:GLU:HA	1:F:88:GLU:OE2	2.21	0.41
1:G:118:LYS:HD2	1:G:119:ARG:O	2.21	0.41
1:M:23:LYS:HD2	1:N:287:PRO:HB2	2.02	0.41
1:T:54:LYS:O	1:T:58:LEU:HD23	2.20	0.41
1:W:220:LYS:HD2	1:W:220:LYS:O	2.20	0.41
1:W:277:LYS:HB2	1:W:277:LYS:HE2	1.73	0.41
1:X:55:LYS:HB2	1:X:55:LYS:HE3	1.85	0.41
1:C:178:PHE:CE1	1:D:77:VAL:HG11	2.55	0.41
1:E:166:THR:HG22	1:H:129:HIS:CD2	2.55	0.41
1:H:201:ARG:HG3	1:H:203:ASP:H	1.86	0.41
1:I:189:PHE:HZ	1:I:234:VAL:HG12	1.86	0.41
1:O:220:LYS:HD2	1:O:220:LYS:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:23:LYS:HD2	1:R:287:PRO:HB2	2.02	0.41
1:R:88:GLU:OE2	1:R:88:GLU:HA	2.21	0.41
1:R:249:LEU:HD22	1:R:252:ILE:HD11	2.02	0.41
1:D:24:ASP:OD1	1:D:24:ASP:C	2.63	0.41
1:E:23:LYS:HD2	1:F:287:PRO:HB2	2.02	0.41
1:H:24:ASP:OD1	1:H:24:ASP:C	2.63	0.41
1:L:93:ASN:HA	1:L:96:GLU:HG2	2.03	0.41
1:T:52:ARG:NH2	1:T:104:HIS:HA	2.34	0.41
1:T:201:ARG:HG3	1:T:203:ASP:H	1.86	0.41
1:U:189:PHE:HZ	1:U:234:VAL:HG12	1.86	0.41
1:V:166:THR:HG23	1:V:167:GLN:HG2	2.03	0.41
1:X:93:ASN:HA	1:X:96:GLU:HG2	2.03	0.41
1:A:282:LEU:HD23	1:A:282:LEU:HA	1.85	0.41
1:B:88:GLU:HA	1:B:88:GLU:OE2	2.21	0.41
1:B:205:ASP:OD1	1:B:205:ASP:C	2.64	0.41
1:C:118:LYS:HD2	1:C:119:ARG:O	2.21	0.41
1:D:88:GLU:O	1:D:92:MET:SD	2.78	0.41
1:E:189:PHE:HZ	1:E:234:VAL:HG12	1.86	0.41
1:E:240:ASP:OD1	1:E:240:ASP:C	2.63	0.41
1:F:176:ASP:OD1	1:F:176:ASP:C	2.63	0.41
1:F:249:LEU:HD22	1:F:252:ILE:HD11	2.02	0.41
1:J:166:THR:HG23	1:J:167:GLN:HG2	2.03	0.41
1:L:55:LYS:HB2	1:L:55:LYS:HE3	1.85	0.41
1:M:205:ASP:C	1:M:205:ASP:OD1	2.64	0.41
1:O:37:TYR:CE1	1:O:128:VAL:HG12	2.54	0.41
1:O:118:LYS:HD2	1:O:119:ARG:O	2.21	0.41
1:Q:99:LEU:HD22	1:Q:99:LEU:HA	1.94	0.41
1:Q:220:LYS:HD3	1:Q:220:LYS:HA	1.85	0.41
1:T:93:ASN:HA	1:T:96:GLU:HG2	2.03	0.41
1:U:65:ILE:HD13	1:U:65:ILE:HA	1.83	0.41
1:W:127:HIS:HE1	1:W:129:HIS:CE1	2.38	0.41
1:A:55:LYS:HB3	1:A:55:LYS:HE2	1.68	0.41
1:B:209:ILE:HG12	1:B:249:LEU:HD23	2.03	0.41
1:D:93:ASN:HA	1:D:96:GLU:HG2	2.03	0.41
1:D:269:MET:HE3	1:D:269:MET:HB2	1.88	0.41
1:I:65:ILE:HD13	1:I:65:ILE:HA	1.84	0.41
1:K:127:HIS:HE1	1:K:129:HIS:CE1	2.38	0.41
1:R:176:ASP:OD1	1:R:176:ASP:C	2.63	0.41
1:S:118:LYS:HD2	1:S:119:ARG:O	2.21	0.41
1:V:240:ASP:OD1	1:V:240:ASP:C	2.64	0.41
1:B:176:ASP:OD1	1:B:176:ASP:C	2.63	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:240:ASP:OD1	1:B:240:ASP:C	2.64	0.40
1:G:242:GLN:HE21	1:G:255:MET:HG2	1.86	0.40
1:J:240:ASP:OD1	1:J:240:ASP:C	2.64	0.40
1:J:249:LEU:HD22	1:J:252:ILE:HD11	2.02	0.40
1:N:166:THR:HG23	1:N:167:GLN:HG2	2.03	0.40
1:P:93:ASN:HA	1:P:96:GLU:HG2	2.03	0.40
1:R:205:ASP:OD1	1:R:205:ASP:C	2.64	0.40
1:V:249:LEU:HD22	1:V:252:ILE:HD11	2.02	0.40
1:F:240:ASP:OD1	1:F:240:ASP:C	2.64	0.40
1:H:93:ASN:HA	1:H:96:GLU:HG2	2.03	0.40
1:I:205:ASP:OD1	1:I:205:ASP:C	2.64	0.40
1:J:209:ILE:HG12	1:J:249:LEU:HD23	2.04	0.40
1:J:212:ALA:O	1:J:216:ILE:HG22	2.22	0.40
1:K:277:LYS:HB2	1:K:277:LYS:HE2	1.73	0.40
1:U:205:ASP:C	1:U:205:ASP:OD1	2.64	0.40
1:V:212:ALA:O	1:V:216:ILE:HG22	2.22	0.40
1:F:205:ASP:OD1	1:F:205:ASP:C	2.64	0.40
1:H:269:MET:HE3	1:H:269:MET:HB2	1.88	0.40
1:K:242:GLN:HE21	1:K:255:MET:HG2	1.86	0.40
1:N:212:ALA:O	1:N:216:ILE:HG22	2.22	0.40
1:V:209:ILE:HG12	1:V:249:LEU:HD23	2.04	0.40
1:X:201:ARG:HG3	1:X:203:ASP:H	1.86	0.40
1:A:189:PHE:HZ	1:A:234:VAL:HG12	1.86	0.40
1:B:249:LEU:HD22	1:B:252:ILE:HD11	2.02	0.40
1:D:87:ILE:HG21	1:D:112:VAL:HG21	2.04	0.40
1:F:209:ILE:HG12	1:F:249:LEU:HD23	2.03	0.40
1:H:25:MET:HE2	1:H:25:MET:HB2	1.98	0.40
1:M:189:PHE:HZ	1:M:234:VAL:HG12	1.86	0.40
1:N:249:LEU:HD22	1:N:252:ILE:HD11	2.02	0.40
1:O:78:LEU:HD11	1:O:97:HIS:HD1	1.85	0.40
1:R:209:ILE:HG12	1:R:249:LEU:HD23	2.03	0.40
1:S:212:ALA:O	1:S:216:ILE:HG22	2.22	0.40
1:S:290:LYS:C	1:S:291:ILE:HD12	2.47	0.40
1:W:242:GLN:HE21	1:W:255:MET:HG2	1.86	0.40
1:A:205:ASP:OD1	1:A:205:ASP:C	2.64	0.40
1:B:212:ALA:O	1:B:216:ILE:HG22	2.22	0.40
1:B:235:GLN:H	1:B:235:GLN:HG2	1.59	0.40
1:C:269:MET:HE2	1:C:269:MET:HB3	1.89	0.40
1:G:212:ALA:O	1:G:216:ILE:HG22	2.22	0.40
1:J:205:ASP:OD1	1:J:205:ASP:C	2.64	0.40
1:L:55:LYS:HB3	1:L:61:ASP:OD1	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:201:ARG:HG3	1:L:203:ASP:H	1.86	0.40
1:P:201:ARG:HG3	1:P:203:ASP:H	1.86	0.40
1:P:266:ASN:OD1	1:P:278:GLU:HA	2.22	0.40
1:P:290:LYS:C	1:P:291:ILE:HD12	2.47	0.40
1:R:240:ASP:OD1	1:R:240:ASP:C	2.64	0.40
1:S:220:LYS:HE3	1:S:237:THR:HG23	2.04	0.40
1:S:284:LEU:HD23	1:S:284:LEU:HA	1.80	0.40
1:X:55:LYS:HB3	1:X:61:ASP:OD1	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 PDB entries followed by that with respect to all EM entries.

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	285/287 (99%)	275 (96%)	10 (4%)	0	100	100
1	B	285/287 (99%)	275 (96%)	10 (4%)	0	100	100
1	C	285/287 (99%)	276 (97%)	9 (3%)	0	100	100
1	D	285/287 (99%)	274 (96%)	11 (4%)	0	100	100
1	E	285/287 (99%)	274 (96%)	11 (4%)	0	100	100
1	F	285/287 (99%)	275 (96%)	10 (4%)	0	100	100
1	G	285/287 (99%)	276 (97%)	9 (3%)	0	100	100
1	H	285/287 (99%)	274 (96%)	11 (4%)	0	100	100
1	I	285/287 (99%)	275 (96%)	10 (4%)	0	100	100
1	J	285/287 (99%)	275 (96%)	10 (4%)	0	100	100
1	K	285/287 (99%)	276 (97%)	9 (3%)	0	100	100
1	L	285/287 (99%)	274 (96%)	11 (4%)	0	100	100
1	M	285/287 (99%)	275 (96%)	10 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	N	285/287 (99%)	275 (96%)	10 (4%)	0	100	100
1	O	285/287 (99%)	276 (97%)	9 (3%)	0	100	100
1	P	285/287 (99%)	274 (96%)	11 (4%)	0	100	100
1	Q	285/287 (99%)	274 (96%)	11 (4%)	0	100	100
1	R	285/287 (99%)	275 (96%)	10 (4%)	0	100	100
1	S	285/287 (99%)	276 (97%)	9 (3%)	0	100	100
1	T	285/287 (99%)	274 (96%)	11 (4%)	0	100	100
1	U	285/287 (99%)	275 (96%)	10 (4%)	0	100	100
1	V	285/287 (99%)	275 (96%)	10 (4%)	0	100	100
1	W	285/287 (99%)	276 (97%)	9 (3%)	0	100	100
1	X	285/287 (99%)	274 (96%)	11 (4%)	0	100	100
All	All	6840/6888 (99%)	6598 (96%)	242 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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	261/261 (100%)	254 (97%)	7 (3%)	39	59
1	B	261/261 (100%)	254 (97%)	7 (3%)	39	59
1	C	261/261 (100%)	253 (97%)	8 (3%)	35	56
1	D	261/261 (100%)	250 (96%)	11 (4%)	26	51
1	E	261/261 (100%)	254 (97%)	7 (3%)	39	59
1	F	261/261 (100%)	254 (97%)	7 (3%)	39	59
1	G	261/261 (100%)	252 (97%)	9 (3%)	32	55
1	H	261/261 (100%)	250 (96%)	11 (4%)	26	51
1	I	261/261 (100%)	254 (97%)	7 (3%)	39	59
1	J	261/261 (100%)	254 (97%)	7 (3%)	39	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	261/261 (100%)	252 (97%)	9 (3%)	32	55
1	L	261/261 (100%)	250 (96%)	11 (4%)	26	51
1	M	261/261 (100%)	254 (97%)	7 (3%)	39	59
1	N	261/261 (100%)	254 (97%)	7 (3%)	39	59
1	O	261/261 (100%)	253 (97%)	8 (3%)	35	56
1	P	261/261 (100%)	250 (96%)	11 (4%)	26	51
1	Q	261/261 (100%)	255 (98%)	6 (2%)	44	62
1	R	261/261 (100%)	254 (97%)	7 (3%)	39	59
1	S	261/261 (100%)	253 (97%)	8 (3%)	35	56
1	T	261/261 (100%)	251 (96%)	10 (4%)	29	53
1	U	261/261 (100%)	254 (97%)	7 (3%)	39	59
1	V	261/261 (100%)	253 (97%)	8 (3%)	35	56
1	W	261/261 (100%)	253 (97%)	8 (3%)	35	56
1	X	261/261 (100%)	251 (96%)	10 (4%)	29	53
All	All	6264/6264 (100%)	6066 (97%)	198 (3%)	35	55

All (198) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	SER
1	A	95	CYS
1	A	99	LEU
1	A	153	ILE
1	A	157	ILE
1	A	267	ILE
1	A	285	ASP
1	B	42	GLU
1	B	107	ARG
1	B	157	ILE
1	B	216	ILE
1	B	235	GLN
1	B	237	THR
1	B	285	ASP
1	C	58	LEU
1	C	107	ARG
1	C	153	ILE
1	C	168	SER

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Mol	Chain	Res	Type
1	C	205	ASP
1	C	244	LEU
1	C	261	ASN
1	C	294	THR
1	D	17	VAL
1	D	59	HIS
1	D	142	GLU
1	D	148	ASN
1	D	153	ILE
1	D	241	ILE
1	D	257	ILE
1	D	269	MET
1	D	270	SER
1	D	278	GLU
1	D	294	THR
1	E	39	SER
1	E	95	CYS
1	E	99	LEU
1	E	153	ILE
1	E	157	ILE
1	E	267	ILE
1	E	285	ASP
1	F	42	GLU
1	F	107	ARG
1	F	157	ILE
1	F	216	ILE
1	F	235	GLN
1	F	237	THR
1	F	285	ASP
1	G	58	LEU
1	G	70	THR
1	G	107	ARG
1	G	153	ILE
1	G	168	SER
1	G	205	ASP
1	G	244	LEU
1	G	261	ASN
1	G	294	THR
1	H	17	VAL
1	H	59	HIS
1	H	142	GLU
1	H	148	ASN

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Mol	Chain	Res	Type
1	H	153	ILE
1	H	241	ILE
1	H	257	ILE
1	H	269	MET
1	H	270	SER
1	H	278	GLU
1	H	294	THR
1	I	39	SER
1	I	95	CYS
1	I	99	LEU
1	I	153	ILE
1	I	157	ILE
1	I	267	ILE
1	I	285	ASP
1	J	42	GLU
1	J	107	ARG
1	J	157	ILE
1	J	216	ILE
1	J	235	GLN
1	J	237	THR
1	J	285	ASP
1	K	58	LEU
1	K	107	ARG
1	K	153	ILE
1	K	166	THR
1	K	168	SER
1	K	205	ASP
1	K	244	LEU
1	K	261	ASN
1	K	294	THR
1	L	17	VAL
1	L	59	HIS
1	L	142	GLU
1	L	148	ASN
1	L	153	ILE
1	L	241	ILE
1	L	257	ILE
1	L	269	MET
1	L	270	SER
1	L	278	GLU
1	L	294	THR
1	M	39	SER

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Mol	Chain	Res	Type
1	M	95	CYS
1	M	99	LEU
1	M	153	ILE
1	M	157	ILE
1	M	267	ILE
1	M	285	ASP
1	N	42	GLU
1	N	107	ARG
1	N	157	ILE
1	N	216	ILE
1	N	235	GLN
1	N	237	THR
1	N	285	ASP
1	O	58	LEU
1	O	107	ARG
1	O	153	ILE
1	O	168	SER
1	O	205	ASP
1	O	244	LEU
1	O	261	ASN
1	O	294	THR
1	P	17	VAL
1	P	59	HIS
1	P	142	GLU
1	P	148	ASN
1	P	153	ILE
1	P	241	ILE
1	P	257	ILE
1	P	269	MET
1	P	270	SER
1	P	278	GLU
1	P	294	THR
1	Q	95	CYS
1	Q	99	LEU
1	Q	153	ILE
1	Q	157	ILE
1	Q	267	ILE
1	Q	285	ASP
1	R	42	GLU
1	R	107	ARG
1	R	157	ILE
1	R	216	ILE

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Mol	Chain	Res	Type
1	R	235	GLN
1	R	237	THR
1	R	285	ASP
1	S	58	LEU
1	S	107	ARG
1	S	153	ILE
1	S	168	SER
1	S	205	ASP
1	S	244	LEU
1	S	261	ASN
1	S	294	THR
1	T	17	VAL
1	T	59	HIS
1	T	142	GLU
1	T	148	ASN
1	T	153	ILE
1	T	241	ILE
1	T	257	ILE
1	T	270	SER
1	T	278	GLU
1	T	294	THR
1	U	39	SER
1	U	95	CYS
1	U	99	LEU
1	U	153	ILE
1	U	157	ILE
1	U	267	ILE
1	U	285	ASP
1	V	42	GLU
1	V	107	ARG
1	V	157	ILE
1	V	191	THR
1	V	216	ILE
1	V	235	GLN
1	V	237	THR
1	V	285	ASP
1	W	58	LEU
1	W	107	ARG
1	W	153	ILE
1	W	168	SER
1	W	205	ASP
1	W	244	LEU

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Mol	Chain	Res	Type
1	W	261	ASN
1	W	294	THR
1	X	17	VAL
1	X	59	HIS
1	X	142	GLU
1	X	148	ASN
1	X	153	ILE
1	X	241	ILE
1	X	257	ILE
1	X	270	SER
1	X	278	GLU
1	X	294	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (154) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	129	HIS
1	A	154	HIS
1	A	248	GLN
1	A	266	ASN
1	B	127	HIS
1	B	276	ASN
1	C	76	HIS
1	C	97	HIS
1	C	104	HIS
1	C	123	ASN
1	C	154	HIS
1	C	167	GLN
1	C	242	GLN
1	C	248	GLN
1	C	261	ASN
1	C	263	HIS
1	D	59	HIS
1	D	76	HIS
1	D	97	HIS
1	D	123	ASN
1	D	133	HIS
1	D	154	HIS
1	D	219	GLN
1	D	242	GLN
1	D	261	ASN
1	D	263	HIS

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Mol	Chain	Res	Type
1	D	276	ASN
1	E	129	HIS
1	E	154	HIS
1	E	248	GLN
1	E	266	ASN
1	F	76	HIS
1	F	97	HIS
1	F	129	HIS
1	F	276	ASN
1	G	76	HIS
1	G	97	HIS
1	G	123	ASN
1	G	154	HIS
1	G	167	GLN
1	G	242	GLN
1	G	248	GLN
1	G	261	ASN
1	G	263	HIS
1	H	59	HIS
1	H	76	HIS
1	H	97	HIS
1	H	123	ASN
1	H	133	HIS
1	H	154	HIS
1	H	242	GLN
1	H	261	ASN
1	H	263	HIS
1	H	276	ASN
1	I	154	HIS
1	I	248	GLN
1	I	266	ASN
1	J	76	HIS
1	J	129	HIS
1	J	276	ASN
1	K	97	HIS
1	K	123	ASN
1	K	154	HIS
1	K	167	GLN
1	K	248	GLN
1	K	261	ASN
1	K	263	HIS
1	L	59	HIS

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Mol	Chain	Res	Type
1	L	76	HIS
1	L	97	HIS
1	L	123	ASN
1	L	133	HIS
1	L	154	HIS
1	L	242	GLN
1	L	261	ASN
1	L	263	HIS
1	L	276	ASN
1	M	129	HIS
1	M	154	HIS
1	M	248	GLN
1	M	266	ASN
1	N	76	HIS
1	N	129	HIS
1	N	276	ASN
1	O	76	HIS
1	O	97	HIS
1	O	123	ASN
1	O	154	HIS
1	O	167	GLN
1	O	242	GLN
1	O	248	GLN
1	O	261	ASN
1	O	263	HIS
1	P	59	HIS
1	P	76	HIS
1	P	97	HIS
1	P	123	ASN
1	P	133	HIS
1	P	154	HIS
1	P	242	GLN
1	P	261	ASN
1	P	263	HIS
1	P	276	ASN
1	Q	129	HIS
1	Q	154	HIS
1	Q	248	GLN
1	Q	266	ASN
1	R	76	HIS
1	R	129	HIS
1	R	276	ASN

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Mol	Chain	Res	Type
1	S	76	HIS
1	S	97	HIS
1	S	104	HIS
1	S	123	ASN
1	S	154	HIS
1	S	167	GLN
1	S	242	GLN
1	S	248	GLN
1	S	261	ASN
1	S	263	HIS
1	T	59	HIS
1	T	76	HIS
1	T	97	HIS
1	T	123	ASN
1	T	133	HIS
1	T	154	HIS
1	T	242	GLN
1	T	261	ASN
1	T	263	HIS
1	T	276	ASN
1	U	129	HIS
1	U	154	HIS
1	U	248	GLN
1	U	266	ASN
1	V	76	HIS
1	V	129	HIS
1	V	276	ASN
1	W	97	HIS
1	W	123	ASN
1	W	154	HIS
1	W	167	GLN
1	W	248	GLN
1	W	261	ASN
1	W	263	HIS
1	X	59	HIS
1	X	76	HIS
1	X	97	HIS
1	X	123	ASN
1	X	133	HIS
1	X	154	HIS
1	X	242	GLN
1	X	261	ASN

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Mol	Chain	Res	Type
1	X	263	HIS
1	X	276	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

24 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	URC	S	301	-	11,13,13	2.39	7 (63%)	12,19,19	2.11	5 (41%)
2	URC	C	301	-	11,13,13	2.39	7 (63%)	12,19,19	2.10	5 (41%)
2	URC	K	302	-	11,13,13	2.39	7 (63%)	12,19,19	2.11	5 (41%)
2	URC	G	301	-	11,13,13	2.39	7 (63%)	12,19,19	2.10	5 (41%)
2	URC	R	301	-	11,13,13	0.56	0	12,19,19	0.96	1 (8%)
2	URC	C	302	-	11,13,13	2.39	7 (63%)	12,19,19	2.11	5 (41%)
2	URC	F	301	-	11,13,13	0.57	0	12,19,19	0.96	1 (8%)
2	URC	Q	301	-	11,13,13	0.58	0	12,19,19	0.99	1 (8%)
2	URC	M	301	-	11,13,13	0.59	0	12,19,19	0.99	1 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	URC	W	302	-	11,13,13	2.39	7 (63%)	12,19,19	2.10	5 (41%)
2	URC	I	301	-	11,13,13	0.58	0	12,19,19	0.99	1 (8%)
2	URC	O	301	-	11,13,13	2.40	7 (63%)	12,19,19	2.11	5 (41%)
2	URC	A	301	-	11,13,13	0.58	0	12,19,19	0.99	1 (8%)
2	URC	S	302	-	11,13,13	2.40	7 (63%)	12,19,19	2.11	5 (41%)
2	URC	N	301	-	11,13,13	0.57	0	12,19,19	0.97	1 (8%)
2	URC	E	301	-	11,13,13	0.59	0	12,19,19	0.98	1 (8%)
2	URC	B	301	-	11,13,13	0.57	0	12,19,19	0.96	1 (8%)
2	URC	K	301	-	11,13,13	2.40	7 (63%)	12,19,19	2.10	5 (41%)
2	URC	O	302	-	11,13,13	2.39	7 (63%)	12,19,19	2.11	5 (41%)
2	URC	G	302	-	11,13,13	2.40	7 (63%)	12,19,19	2.11	5 (41%)
2	URC	J	301	-	11,13,13	0.57	0	12,19,19	0.95	1 (8%)
2	URC	V	301	-	11,13,13	0.58	0	12,19,19	0.96	1 (8%)
2	URC	U	301	-	11,13,13	0.58	0	12,19,19	0.99	1 (8%)
2	URC	W	301	-	11,13,13	2.40	7 (63%)	12,19,19	2.10	5 (41%)

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	URC	S	301	-	-	-	0/2/2/2
2	URC	C	301	-	-	-	0/2/2/2
2	URC	K	302	-	-	-	0/2/2/2
2	URC	G	301	-	-	-	0/2/2/2
2	URC	R	301	-	-	-	0/2/2/2
2	URC	C	302	-	-	-	0/2/2/2
2	URC	F	301	-	-	-	0/2/2/2
2	URC	Q	301	-	-	-	0/2/2/2
2	URC	M	301	-	-	-	0/2/2/2
2	URC	W	302	-	-	-	0/2/2/2
2	URC	I	301	-	-	-	0/2/2/2
2	URC	O	301	-	-	-	0/2/2/2
2	URC	A	301	-	-	-	0/2/2/2
2	URC	S	302	-	-	-	0/2/2/2
2	URC	N	301	-	-	-	0/2/2/2
2	URC	E	301	-	-	-	0/2/2/2
2	URC	B	301	-	-	-	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	URC	K	301	-	-	-	0/2/2/2
2	URC	O	302	-	-	-	0/2/2/2
2	URC	G	302	-	-	-	0/2/2/2
2	URC	J	301	-	-	-	0/2/2/2
2	URC	V	301	-	-	-	0/2/2/2
2	URC	U	301	-	-	-	0/2/2/2
2	URC	W	301	-	-	-	0/2/2/2

All (84) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	S	302	URC	C6-N1	-3.61	1.32	1.38
2	G	302	URC	C6-N1	-3.61	1.32	1.38
2	O	302	URC	C6-N1	-3.60	1.32	1.38
2	K	301	URC	C6-N1	-3.60	1.32	1.38
2	K	302	URC	C6-N1	-3.59	1.32	1.38
2	C	302	URC	C6-N1	-3.59	1.32	1.38
2	O	301	URC	C6-N1	-3.58	1.32	1.38
2	C	301	URC	C6-N1	-3.56	1.32	1.38
2	W	302	URC	C6-N1	-3.56	1.32	1.38
2	W	301	URC	C6-N1	-3.53	1.32	1.38
2	G	301	URC	C6-N1	-3.53	1.32	1.38
2	S	301	URC	C6-N1	-3.53	1.32	1.38
2	G	301	URC	C8-N9	-3.01	1.33	1.39
2	S	302	URC	C8-N9	-3.00	1.33	1.39
2	C	301	URC	C8-N9	-2.99	1.33	1.39
2	W	301	URC	C8-N9	-2.98	1.33	1.39
2	K	301	URC	C8-N9	-2.97	1.33	1.39
2	S	301	URC	C8-N9	-2.97	1.33	1.39
2	O	302	URC	C8-N9	-2.97	1.33	1.39
2	C	302	URC	C8-N9	-2.95	1.33	1.39
2	O	301	URC	C8-N9	-2.95	1.33	1.39
2	K	302	URC	C8-N9	-2.95	1.33	1.39
2	W	302	URC	C8-N9	-2.94	1.33	1.39
2	G	302	URC	C8-N9	-2.94	1.33	1.39
2	O	301	URC	C8-N7	-2.93	1.33	1.39
2	G	302	URC	C8-N7	-2.91	1.33	1.39
2	S	301	URC	C8-N7	-2.91	1.33	1.39
2	G	301	URC	C8-N7	-2.89	1.33	1.39
2	K	302	URC	C8-N7	-2.88	1.33	1.39
2	C	302	URC	C8-N7	-2.88	1.33	1.39
2	C	301	URC	C8-N7	-2.87	1.33	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	S	302	URC	C8-N7	-2.86	1.33	1.39
2	O	302	URC	C8-N7	-2.86	1.33	1.39
2	W	301	URC	C8-N7	-2.86	1.33	1.39
2	W	302	URC	C8-N7	-2.85	1.33	1.39
2	K	301	URC	C8-N7	-2.85	1.33	1.39
2	W	302	URC	O13-C6	-2.77	1.18	1.23
2	W	301	URC	O13-C6	-2.77	1.18	1.23
2	G	302	URC	O13-C6	-2.76	1.18	1.23
2	C	302	URC	O13-C6	-2.74	1.18	1.23
2	G	301	URC	O13-C6	-2.74	1.18	1.23
2	S	302	URC	O13-C6	-2.74	1.18	1.23
2	K	302	URC	O13-C6	-2.73	1.18	1.23
2	S	301	URC	O13-C6	-2.72	1.18	1.23
2	C	301	URC	O13-C6	-2.72	1.18	1.23
2	O	302	URC	O13-C6	-2.72	1.18	1.23
2	K	301	URC	O13-C6	-2.72	1.18	1.23
2	O	301	URC	O13-C6	-2.71	1.18	1.23
2	O	301	URC	C5-N7	-2.38	1.33	1.37
2	K	301	URC	C5-N7	-2.38	1.33	1.37
2	W	301	URC	C5-N7	-2.37	1.33	1.37
2	C	301	URC	C5-N7	-2.36	1.33	1.37
2	W	302	URC	O24-C8	-2.35	1.18	1.23
2	W	301	URC	O11-C2	-2.35	1.18	1.23
2	K	301	URC	O11-C2	-2.34	1.18	1.23
2	O	302	URC	C5-N7	-2.34	1.34	1.37
2	G	301	URC	C5-N7	-2.34	1.34	1.37
2	S	302	URC	C5-N7	-2.33	1.34	1.37
2	W	302	URC	C5-N7	-2.33	1.34	1.37
2	C	301	URC	O11-C2	-2.33	1.18	1.23
2	C	302	URC	C5-N7	-2.32	1.34	1.37
2	G	302	URC	C5-N7	-2.32	1.34	1.37
2	S	301	URC	C5-N7	-2.32	1.34	1.37
2	C	302	URC	O24-C8	-2.31	1.18	1.23
2	G	302	URC	O11-C2	-2.31	1.18	1.23
2	K	302	URC	O11-C2	-2.31	1.18	1.23
2	K	302	URC	O24-C8	-2.31	1.18	1.23
2	O	301	URC	O11-C2	-2.31	1.18	1.23
2	K	301	URC	O24-C8	-2.31	1.18	1.23
2	O	302	URC	O11-C2	-2.31	1.18	1.23
2	O	301	URC	O24-C8	-2.31	1.18	1.23
2	K	302	URC	C5-N7	-2.30	1.34	1.37
2	S	301	URC	O11-C2	-2.30	1.18	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	302	URC	O24-C8	-2.30	1.18	1.23
2	S	301	URC	O24-C8	-2.30	1.18	1.23
2	W	302	URC	O11-C2	-2.30	1.18	1.23
2	G	301	URC	O11-C2	-2.30	1.18	1.23
2	S	302	URC	O11-C2	-2.30	1.18	1.23
2	S	302	URC	O24-C8	-2.30	1.18	1.23
2	G	301	URC	O24-C8	-2.29	1.18	1.23
2	C	301	URC	O24-C8	-2.29	1.18	1.23
2	C	302	URC	O11-C2	-2.29	1.18	1.23
2	O	302	URC	O24-C8	-2.29	1.18	1.23
2	W	301	URC	O24-C8	-2.29	1.18	1.23

All (72) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	S	301	URC	C6-N1-C2	-4.57	119.75	126.34
2	O	301	URC	C6-N1-C2	-4.56	119.77	126.34
2	G	301	URC	C6-N1-C2	-4.56	119.77	126.34
2	C	301	URC	C6-N1-C2	-4.55	119.78	126.34
2	W	301	URC	C6-N1-C2	-4.55	119.79	126.34
2	K	302	URC	C6-N1-C2	-4.54	119.80	126.34
2	C	302	URC	C6-N1-C2	-4.52	119.83	126.34
2	G	302	URC	C6-N1-C2	-4.52	119.83	126.34
2	K	301	URC	C6-N1-C2	-4.52	119.83	126.34
2	S	302	URC	C6-N1-C2	-4.52	119.83	126.34
2	W	302	URC	C6-N1-C2	-4.51	119.84	126.34
2	O	302	URC	C6-N1-C2	-4.51	119.84	126.34
2	G	302	URC	O13-C6-C5	-3.19	119.92	127.24
2	S	302	URC	O13-C6-C5	-3.18	119.95	127.24
2	O	302	URC	O13-C6-C5	-3.18	119.95	127.24
2	O	301	URC	O13-C6-C5	-3.18	119.96	127.24
2	C	302	URC	O13-C6-C5	-3.17	119.98	127.24
2	K	301	URC	O13-C6-C5	-3.17	119.98	127.24
2	C	301	URC	O13-C6-C5	-3.16	120.00	127.24
2	K	302	URC	O13-C6-C5	-3.16	120.00	127.24
2	S	301	URC	O13-C6-C5	-3.16	120.01	127.24
2	W	302	URC	O13-C6-C5	-3.15	120.01	127.24
2	W	301	URC	O13-C6-C5	-3.14	120.05	127.24
2	G	301	URC	O13-C6-C5	-3.13	120.06	127.24
2	O	302	URC	N3-C2-N1	2.85	120.39	115.80
2	W	302	URC	N3-C2-N1	2.85	120.38	115.80
2	C	302	URC	N3-C2-N1	2.85	120.38	115.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	S	302	URC	N3-C2-N1	2.85	120.38	115.80
2	K	302	URC	N3-C2-N1	2.84	120.36	115.80
2	S	301	URC	N3-C2-N1	2.83	120.36	115.80
2	G	302	URC	N3-C2-N1	2.83	120.35	115.80
2	G	301	URC	N3-C2-N1	2.81	120.32	115.80
2	O	301	URC	N3-C2-N1	2.81	120.32	115.80
2	C	301	URC	N3-C2-N1	2.80	120.30	115.80
2	W	301	URC	N3-C2-N1	2.78	120.28	115.80
2	K	301	URC	N3-C2-N1	2.78	120.27	115.80
2	O	301	URC	C5-C6-N1	2.62	120.13	112.31
2	K	302	URC	C5-C6-N1	2.62	120.12	112.31
2	G	302	URC	C5-C6-N1	2.62	120.10	112.31
2	O	302	URC	C5-C6-N1	2.61	120.10	112.31
2	C	301	URC	C5-C6-N1	2.61	120.09	112.31
2	S	302	URC	C5-C6-N1	2.61	120.08	112.31
2	C	302	URC	C5-C6-N1	2.61	120.08	112.31
2	K	301	URC	C5-C6-N1	2.61	120.08	112.31
2	S	301	URC	C5-C6-N1	2.60	120.06	112.31
2	W	301	URC	C5-C6-N1	2.60	120.06	112.31
2	G	301	URC	C5-C6-N1	2.60	120.06	112.31
2	W	302	URC	C5-C6-N1	2.59	120.02	112.31
2	W	302	URC	N9-C4-N3	2.26	132.04	122.78
2	S	302	URC	N9-C4-N3	2.26	132.02	122.78
2	K	302	URC	N9-C4-N3	2.26	132.01	122.78
2	C	302	URC	N9-C4-N3	2.25	132.00	122.78
2	W	301	URC	N9-C4-N3	2.25	132.00	122.78
2	K	301	URC	N9-C4-N3	2.25	131.98	122.78
2	O	302	URC	N9-C4-N3	2.25	131.98	122.78
2	C	301	URC	N9-C4-N3	2.25	131.97	122.78
2	G	302	URC	N9-C4-N3	2.24	131.96	122.78
2	O	301	URC	N9-C4-N3	2.24	131.96	122.78
2	G	301	URC	N9-C4-N3	2.24	131.94	122.78
2	V	301	URC	N9-C4-N3	2.24	131.93	122.78
2	N	301	URC	N9-C4-N3	2.23	131.92	122.78
2	S	301	URC	N9-C4-N3	2.23	131.91	122.78
2	F	301	URC	N9-C4-N3	2.23	131.89	122.78
2	B	301	URC	N9-C4-N3	2.23	131.89	122.78
2	J	301	URC	N9-C4-N3	2.22	131.86	122.78
2	R	301	URC	N9-C4-N3	2.21	131.84	122.78
2	M	301	URC	N9-C4-N3	2.21	131.84	122.78
2	E	301	URC	N9-C4-N3	2.21	131.83	122.78
2	A	301	URC	N9-C4-N3	2.21	131.81	122.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	301	URC	N9-C4-N3	2.21	131.80	122.78
2	Q	301	URC	N9-C4-N3	2.21	131.80	122.78
2	U	301	URC	N9-C4-N3	2.20	131.78	122.78

There are no chirality outliers.

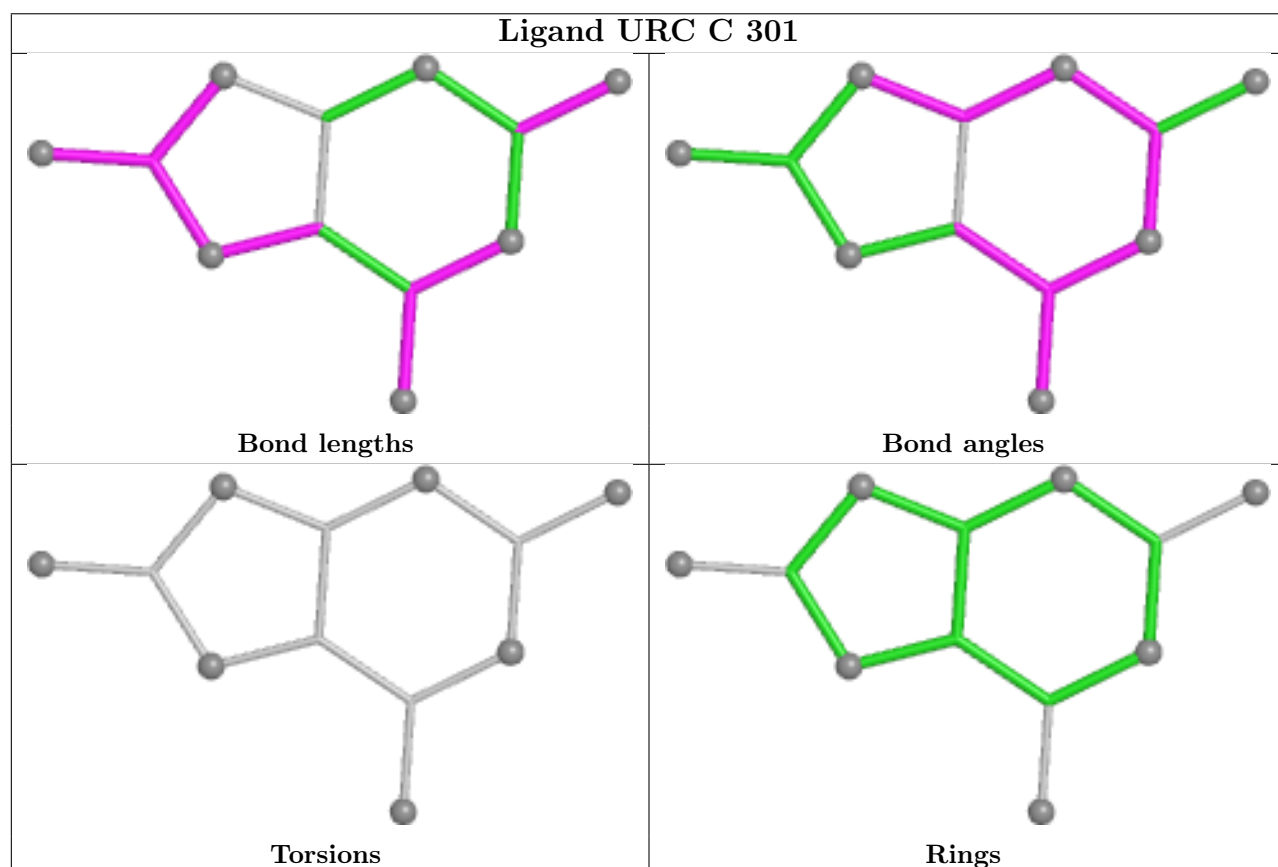
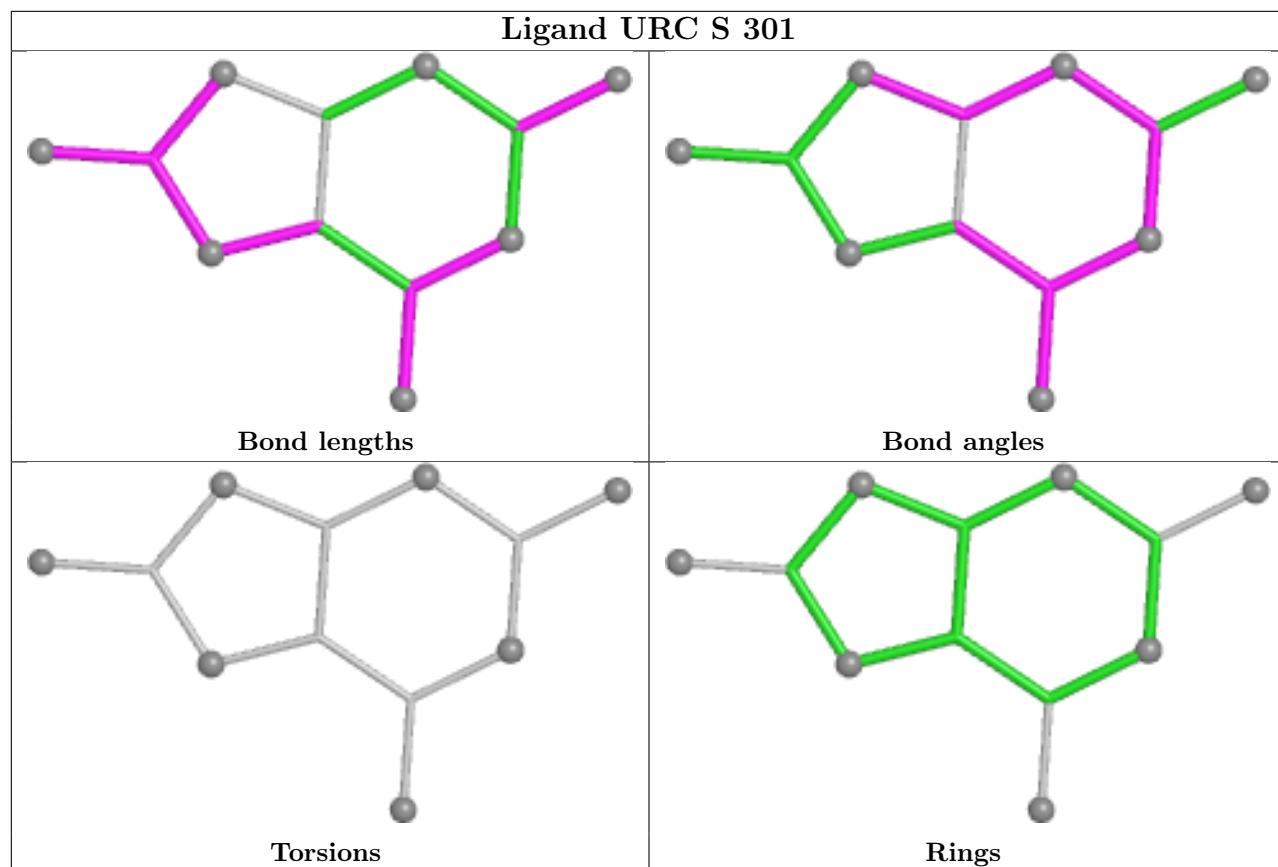
There are no torsion outliers.

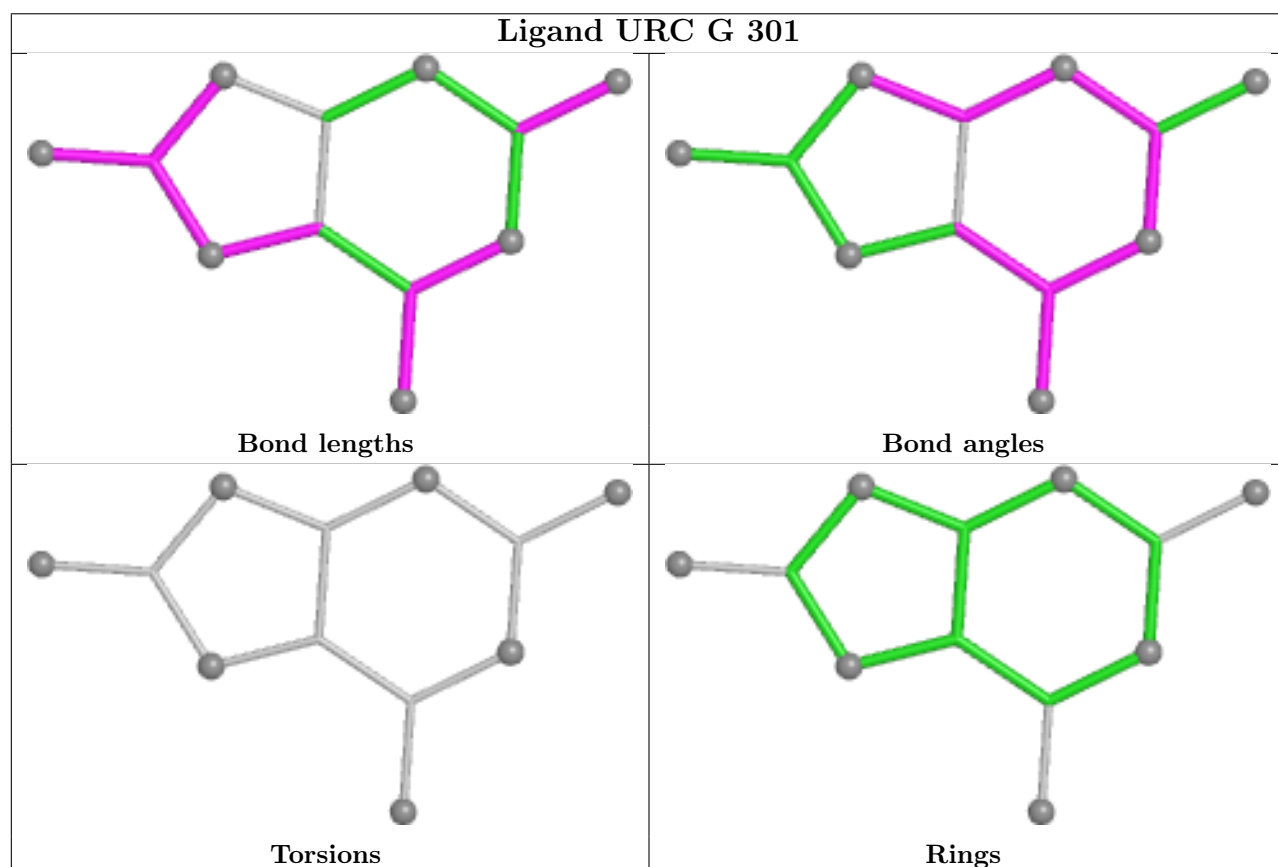
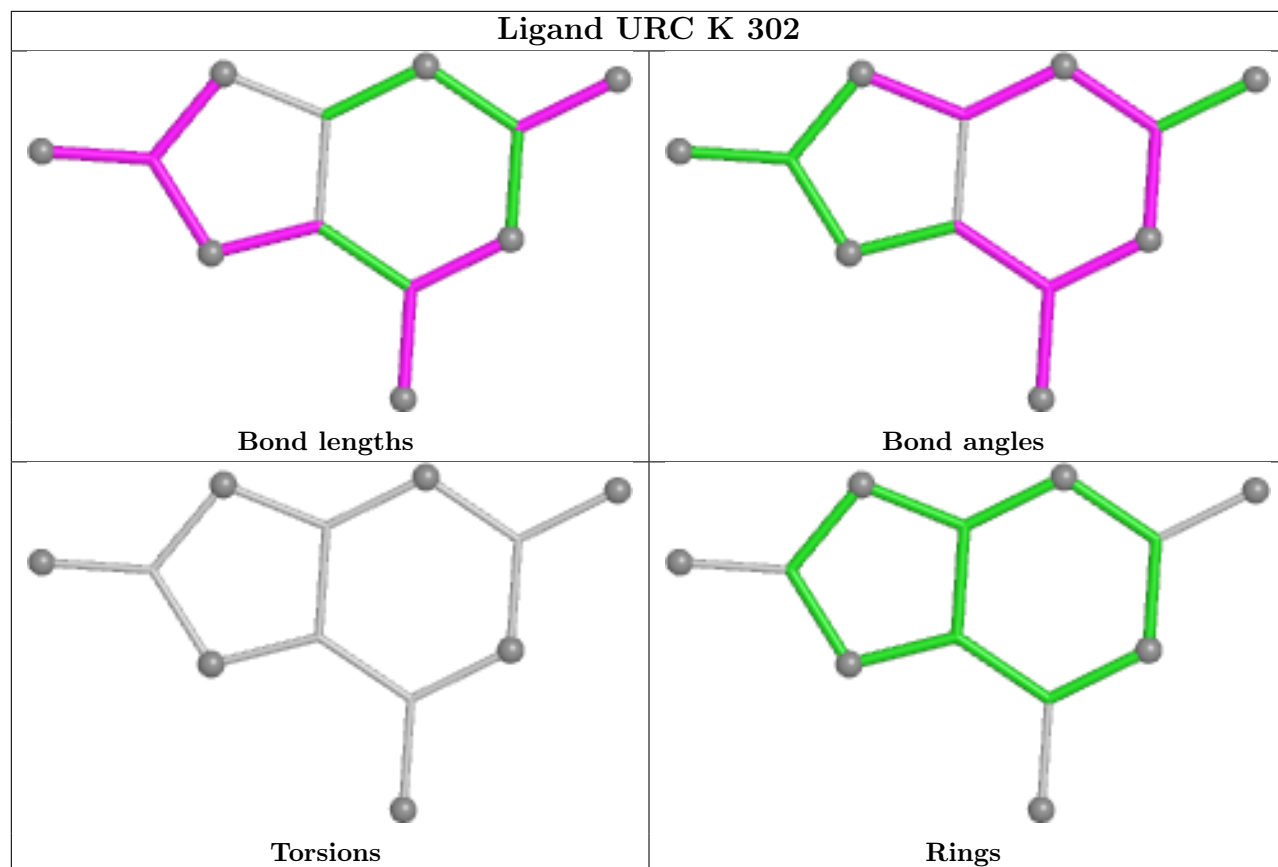
There are no ring outliers.

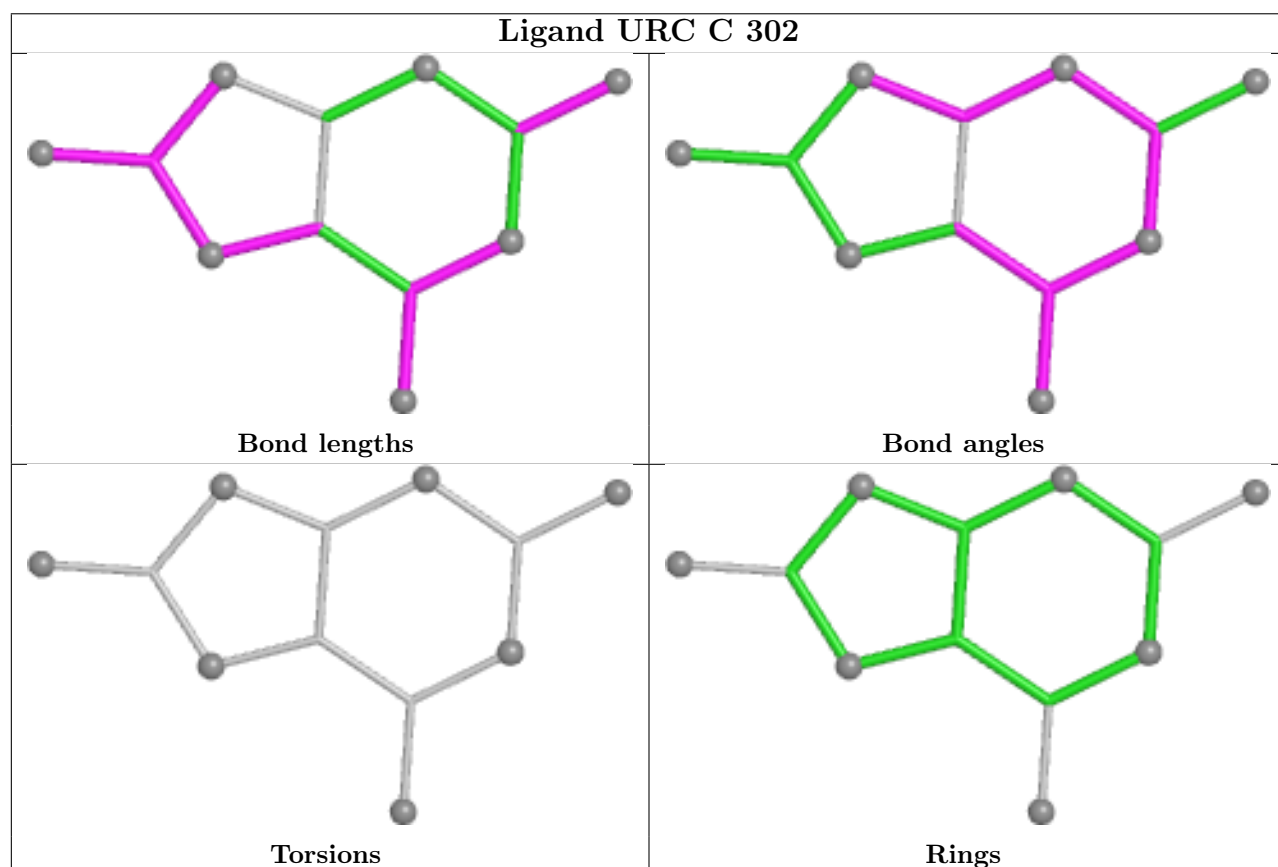
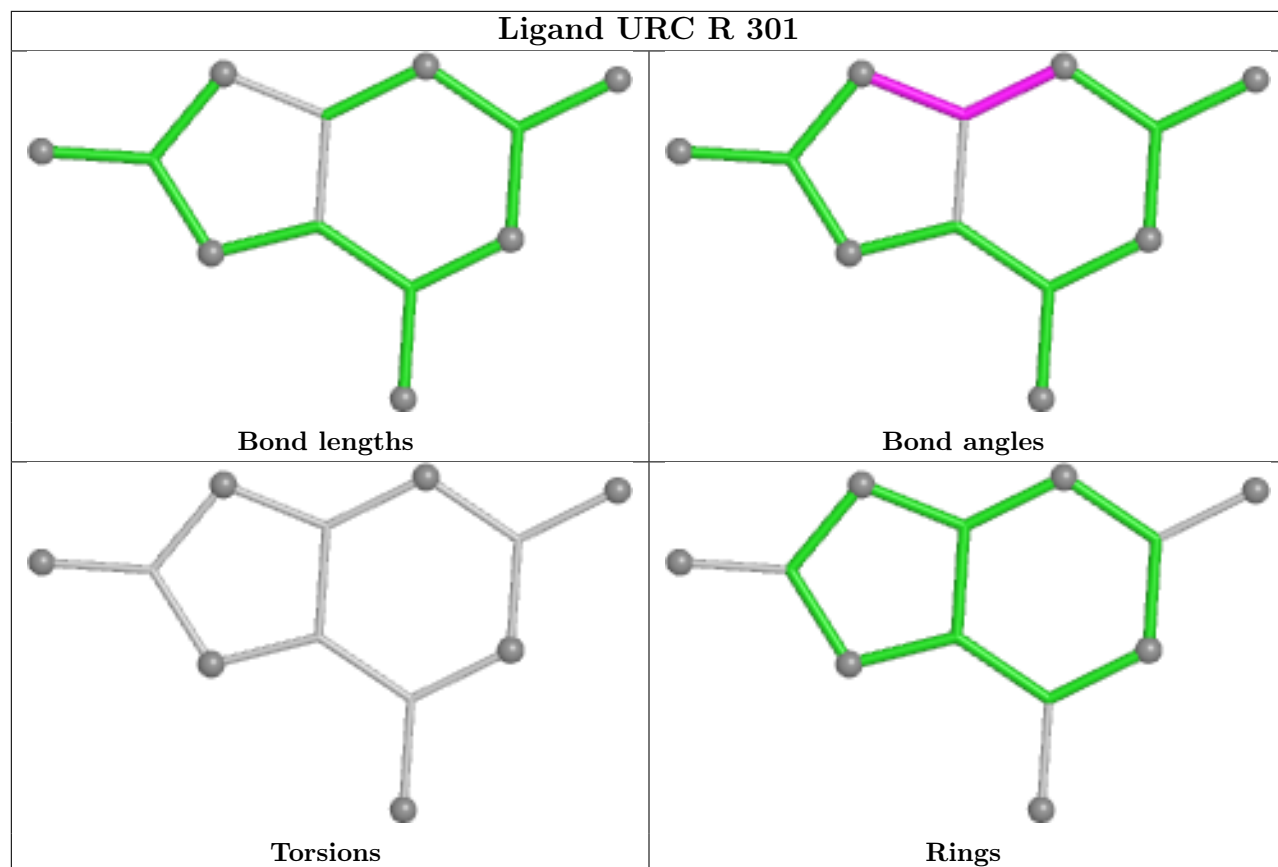
18 monomers are involved in 54 short contacts:

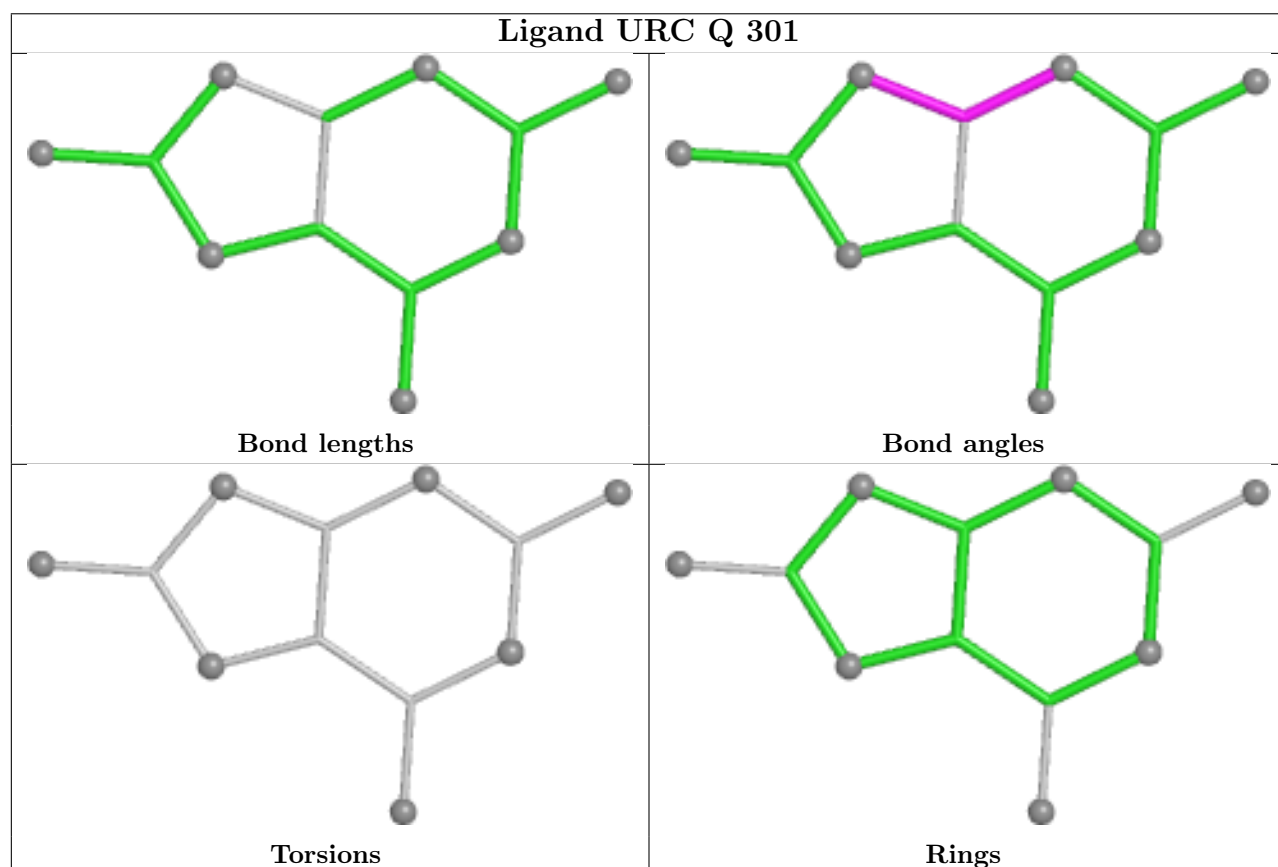
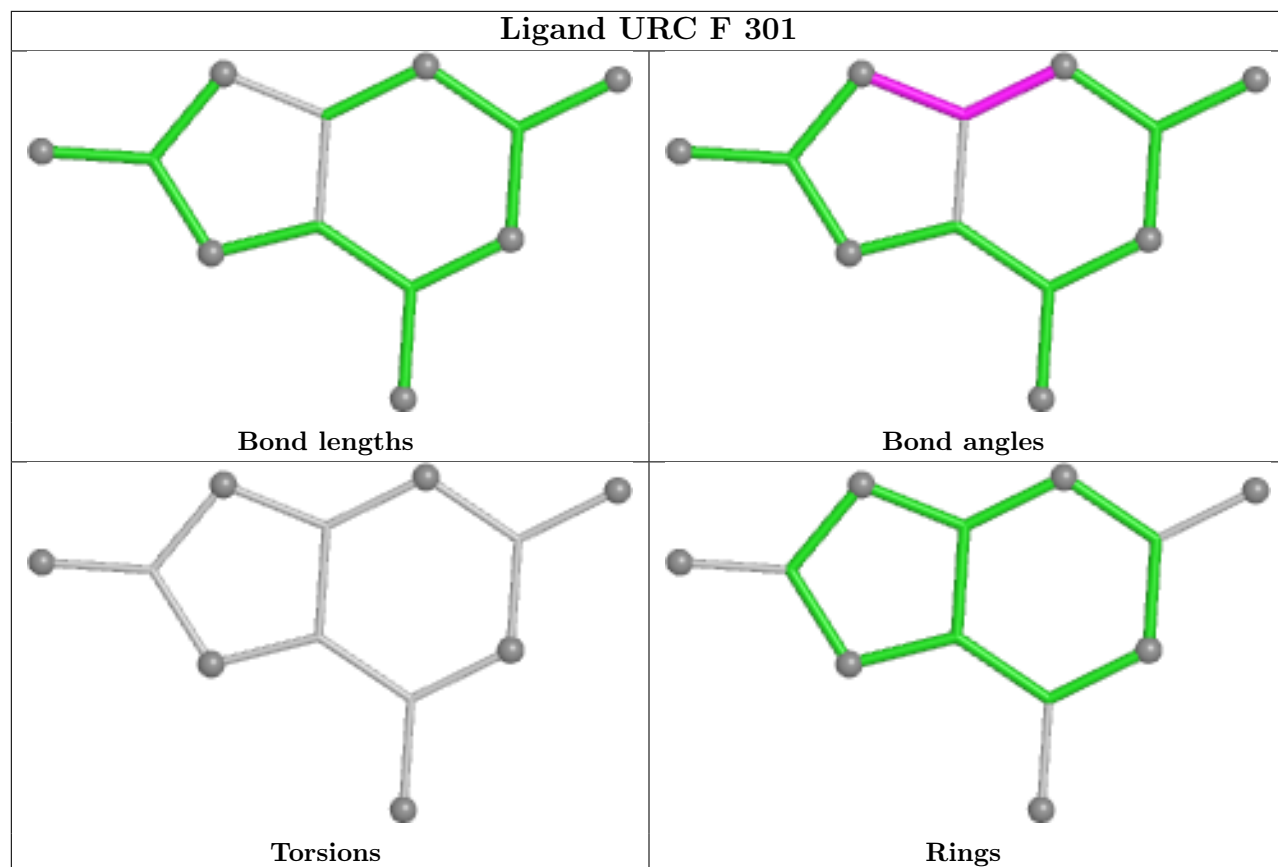
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	S	301	URC	1	0
2	C	301	URC	1	0
2	G	301	URC	1	0
2	R	301	URC	4	0
2	F	301	URC	4	0
2	Q	301	URC	4	0
2	M	301	URC	4	0
2	I	301	URC	4	0
2	O	301	URC	1	0
2	A	301	URC	4	0
2	N	301	URC	4	0
2	E	301	URC	4	0
2	B	301	URC	4	0
2	K	301	URC	1	0
2	J	301	URC	4	0
2	V	301	URC	4	0
2	U	301	URC	4	0
2	W	301	URC	1	0

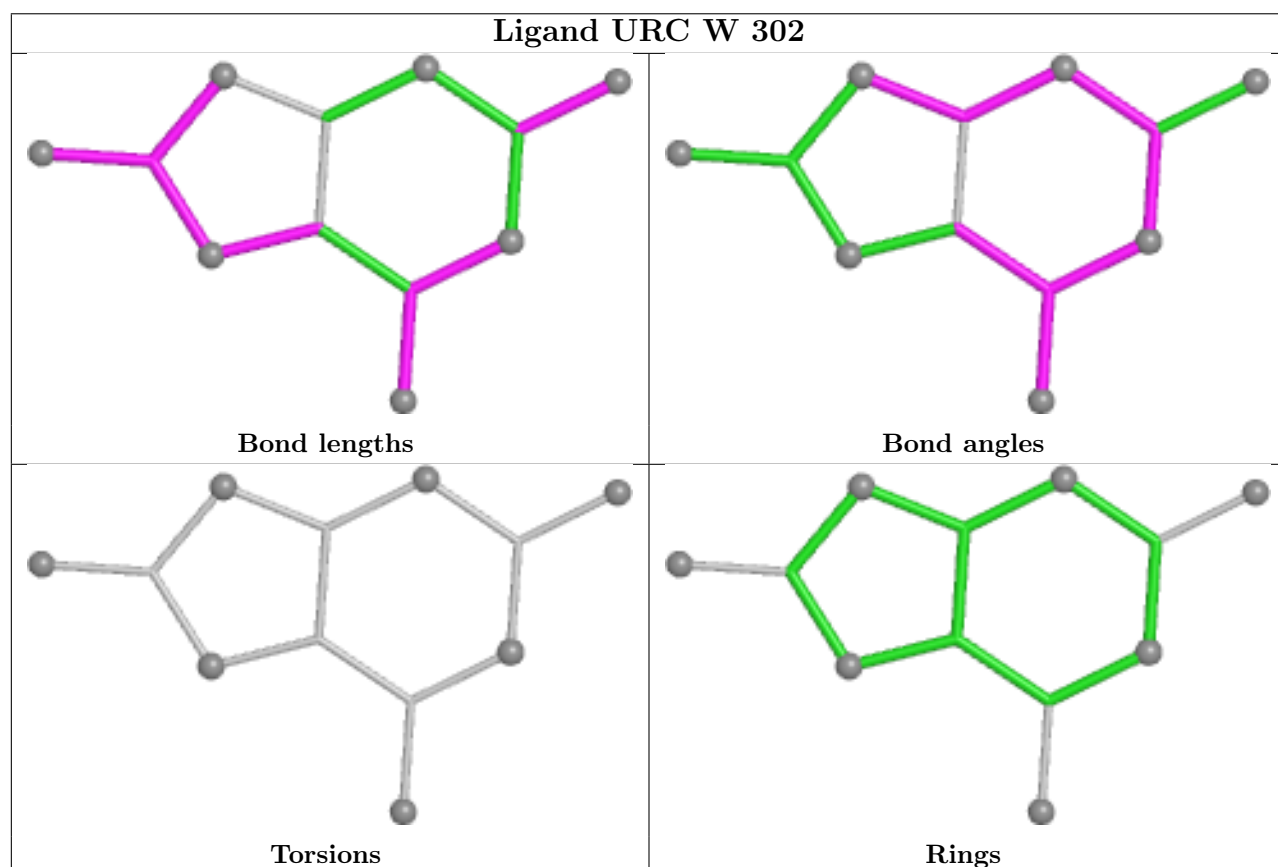
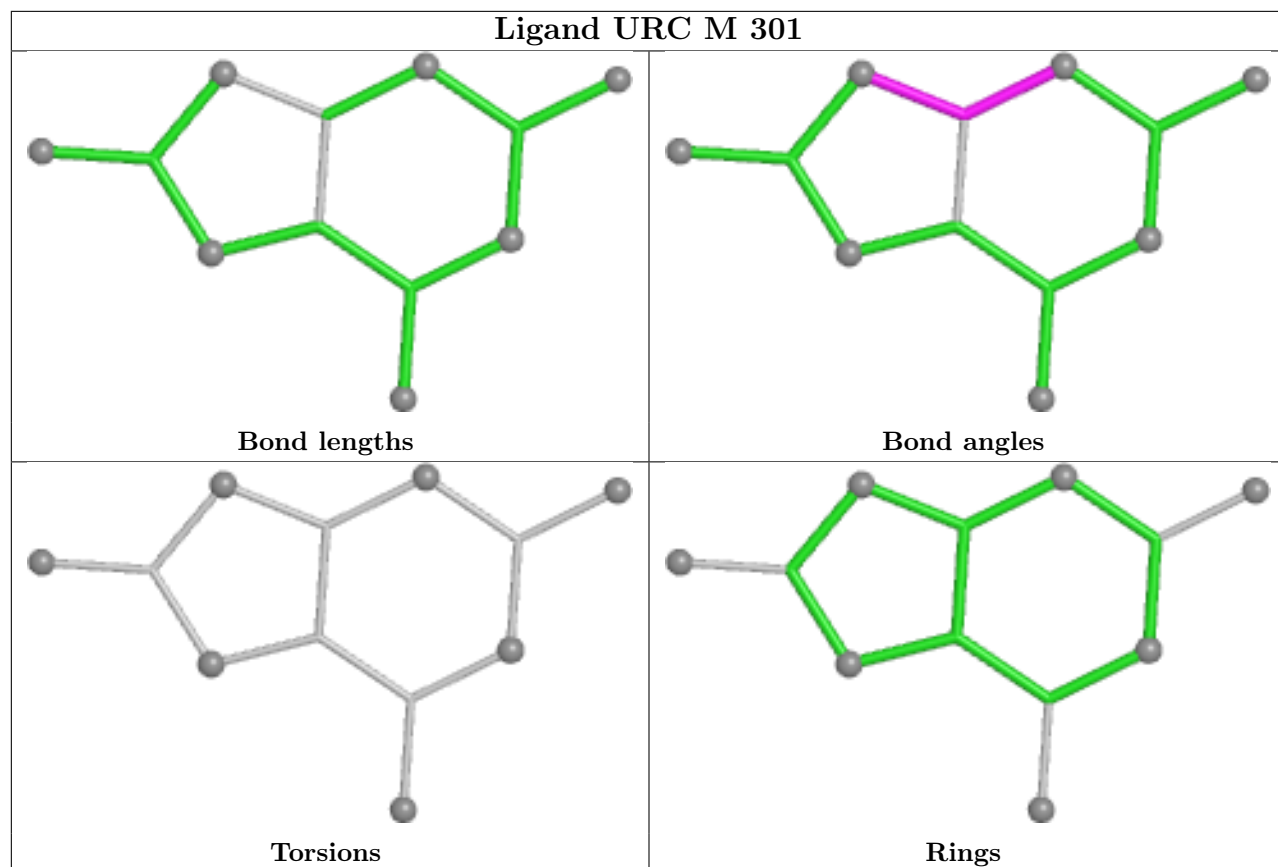
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

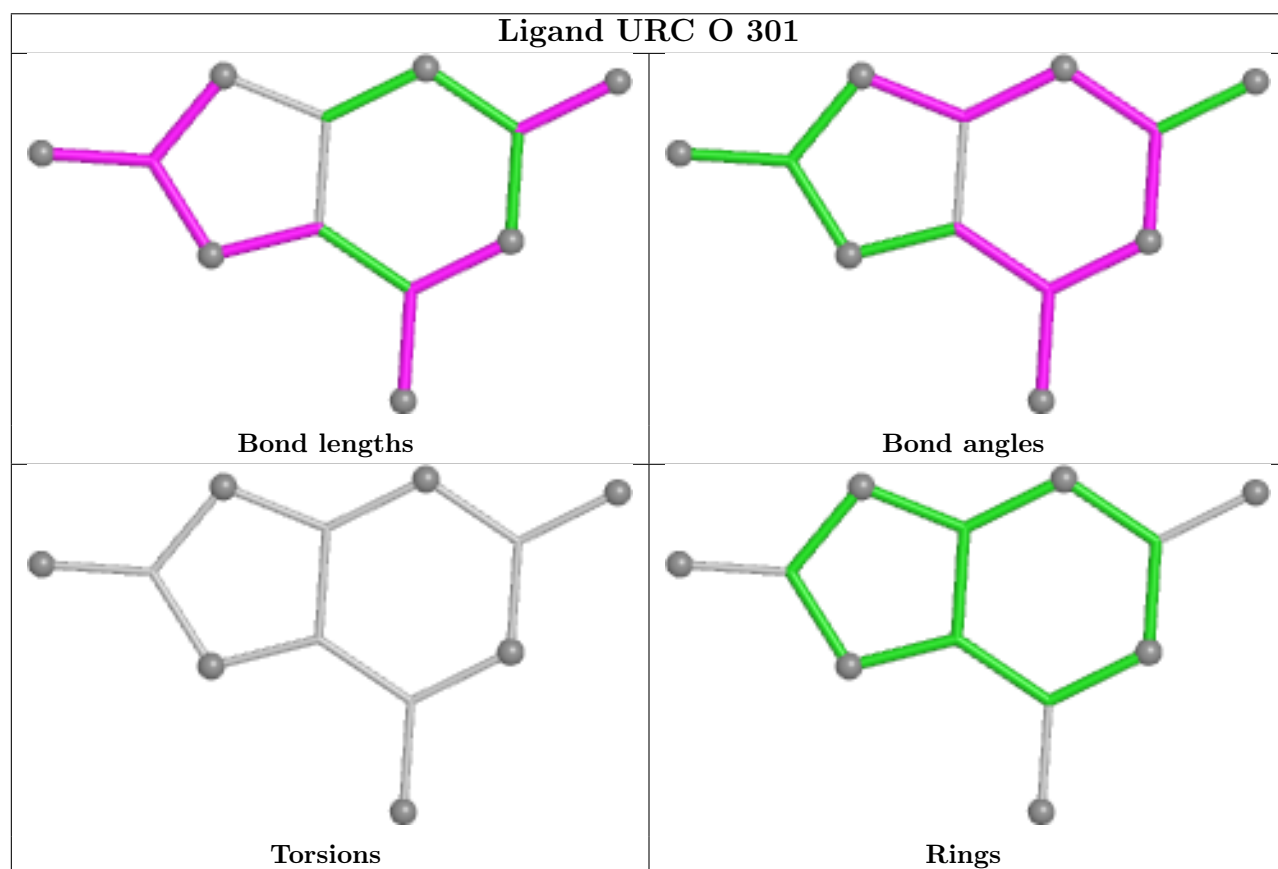
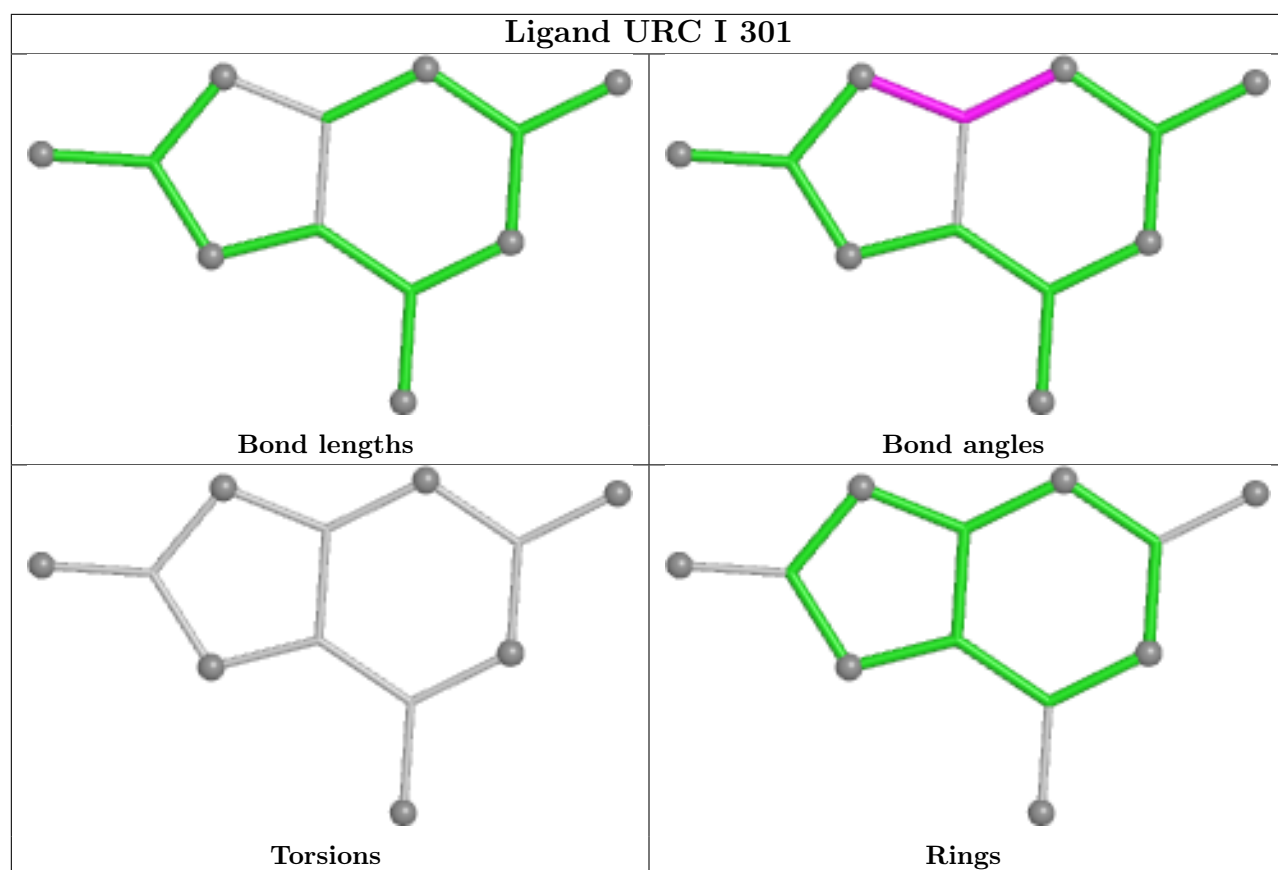


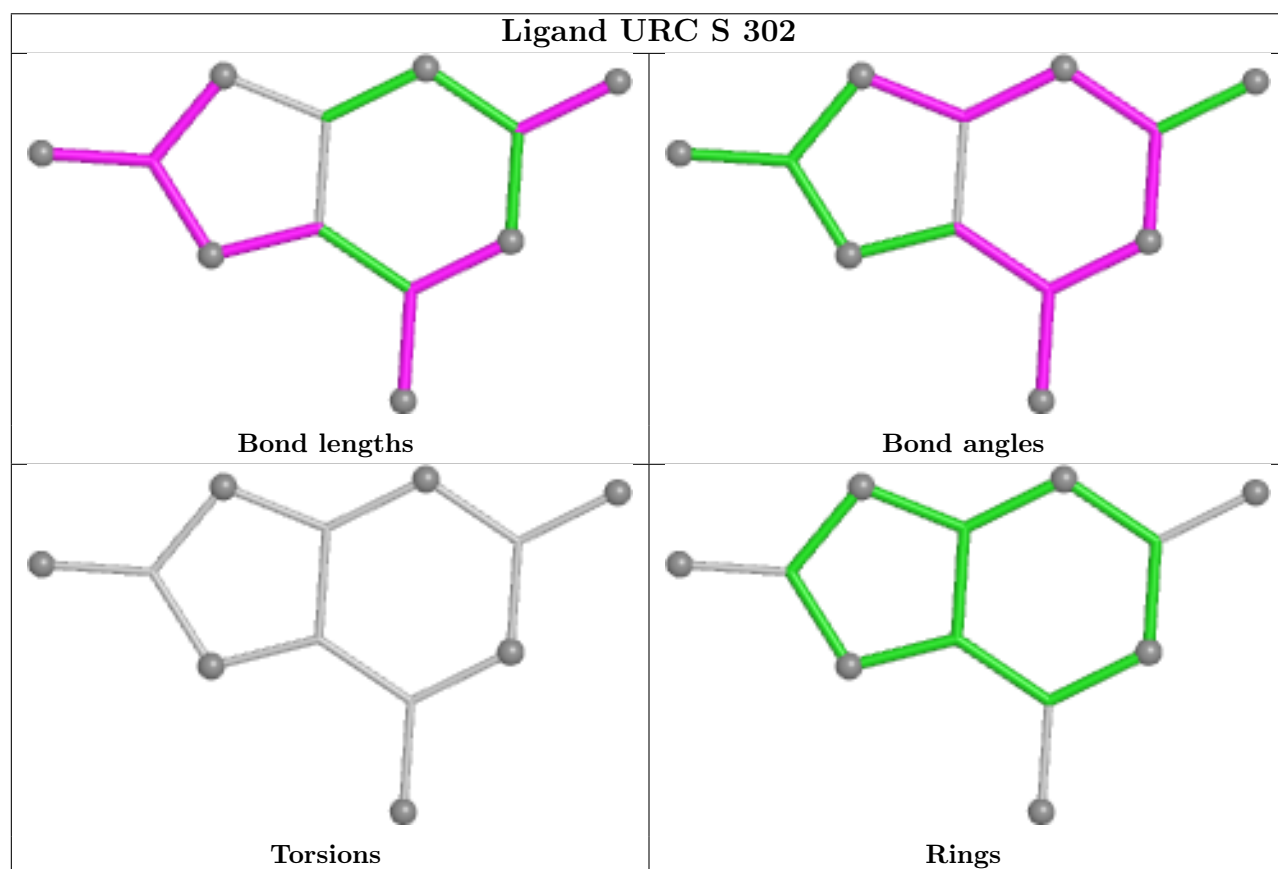
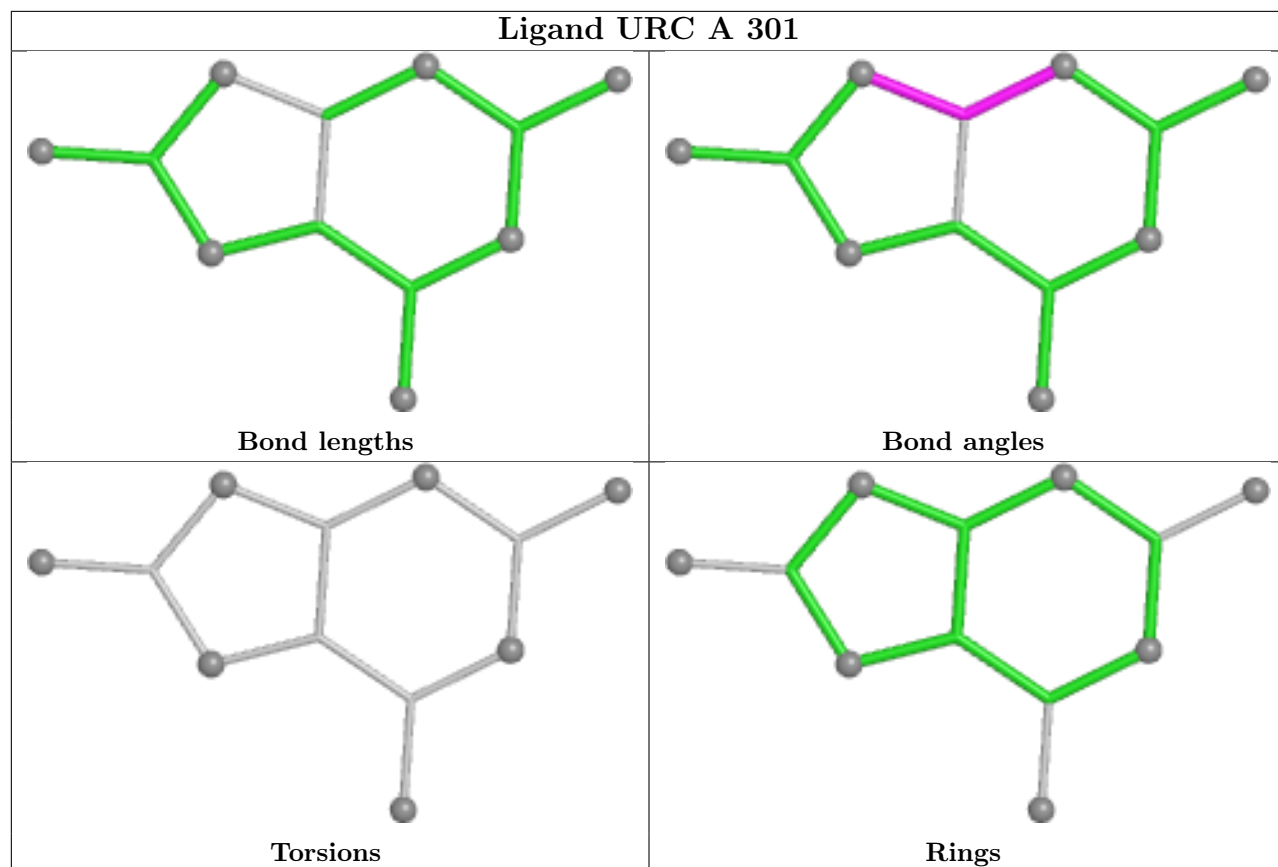


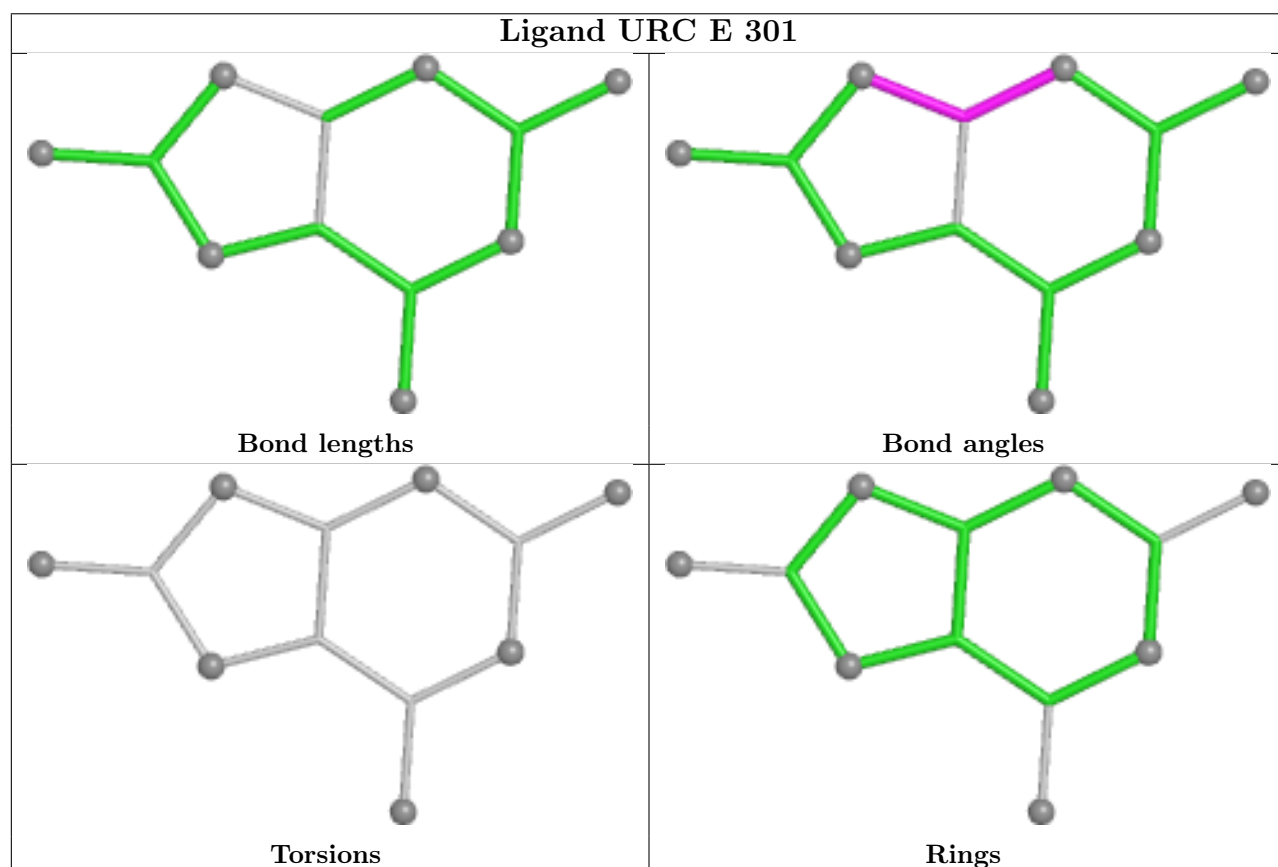
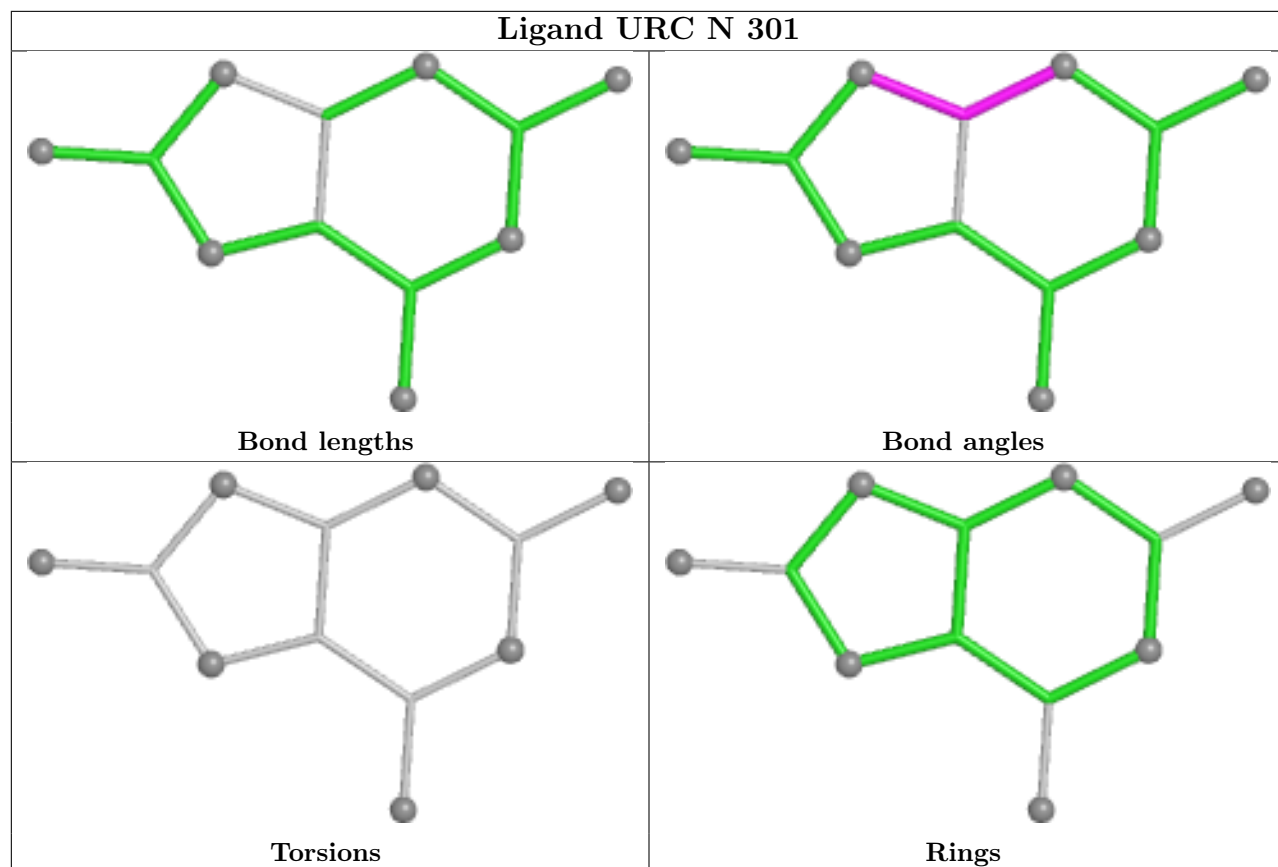


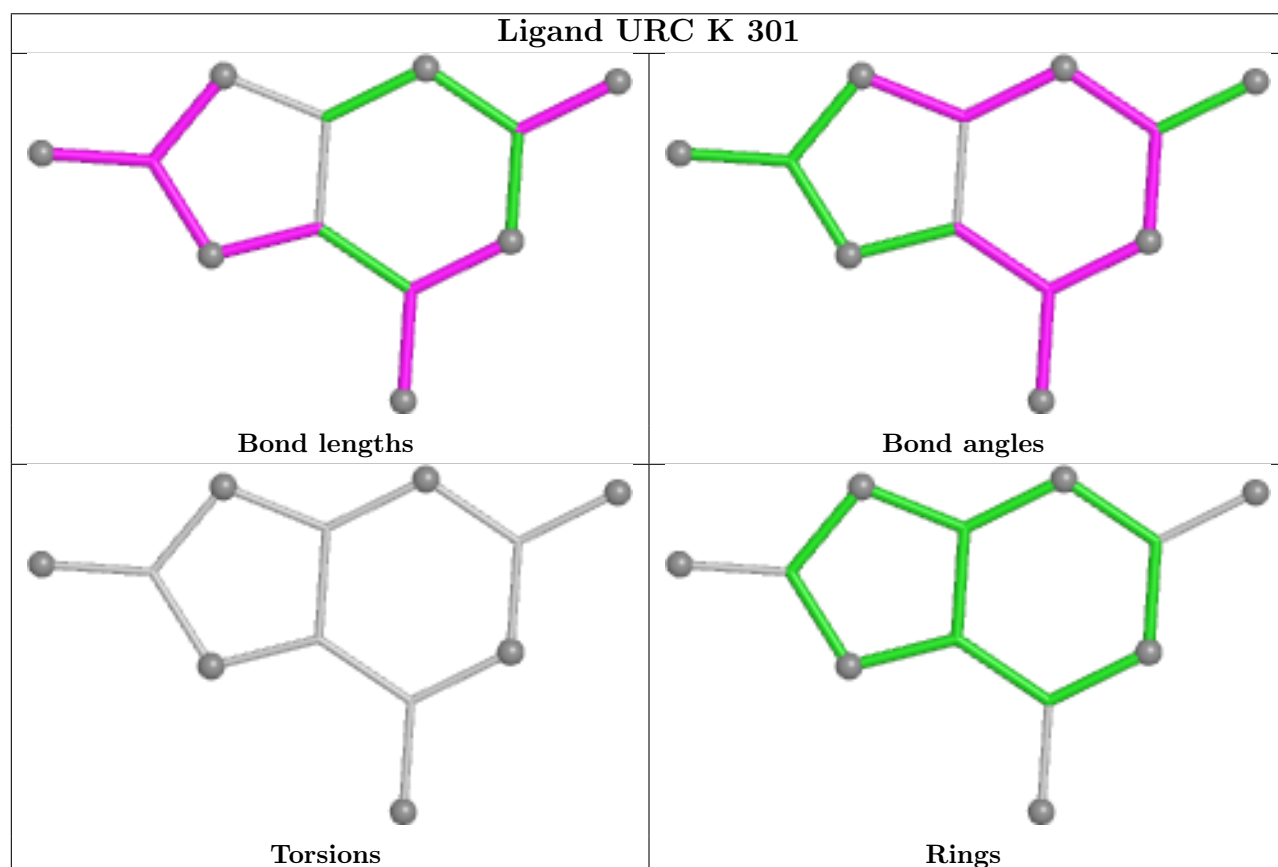
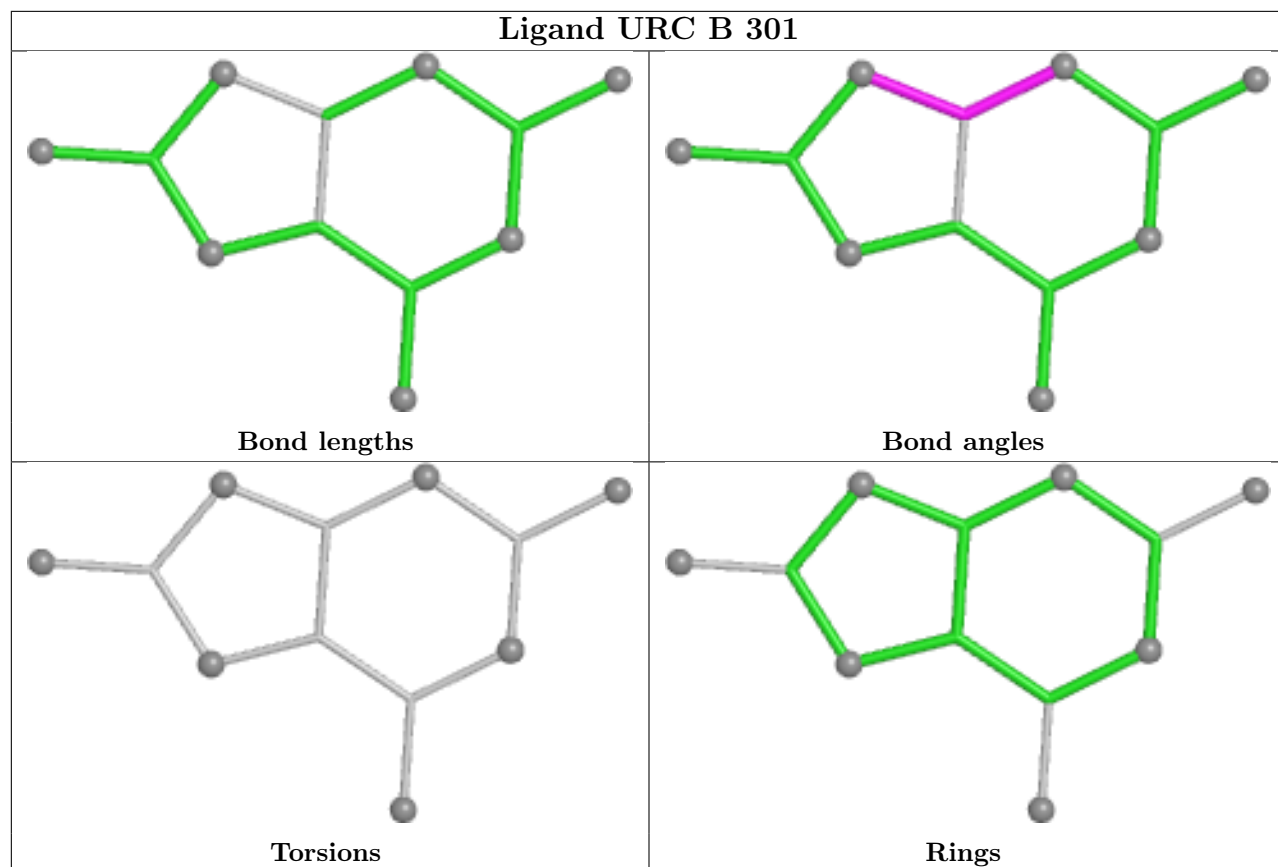


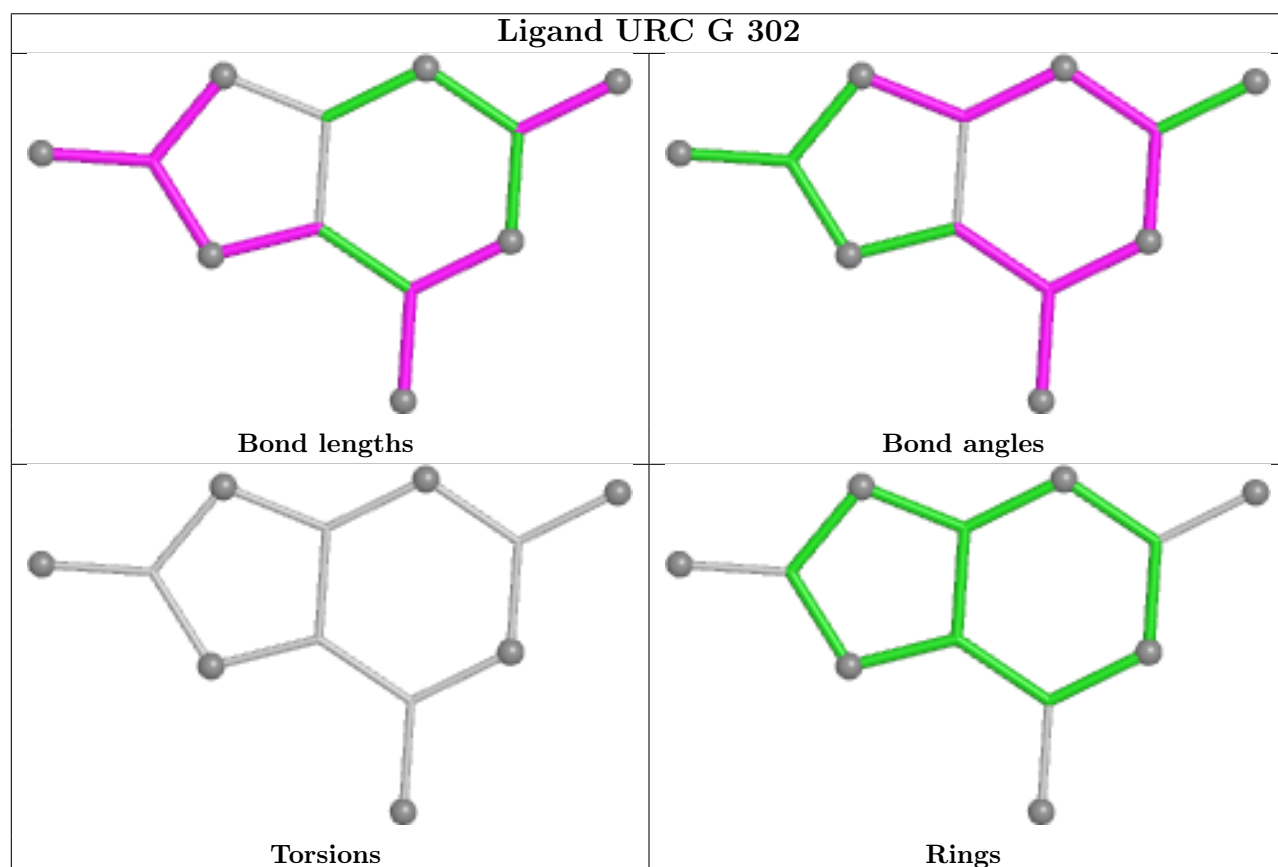
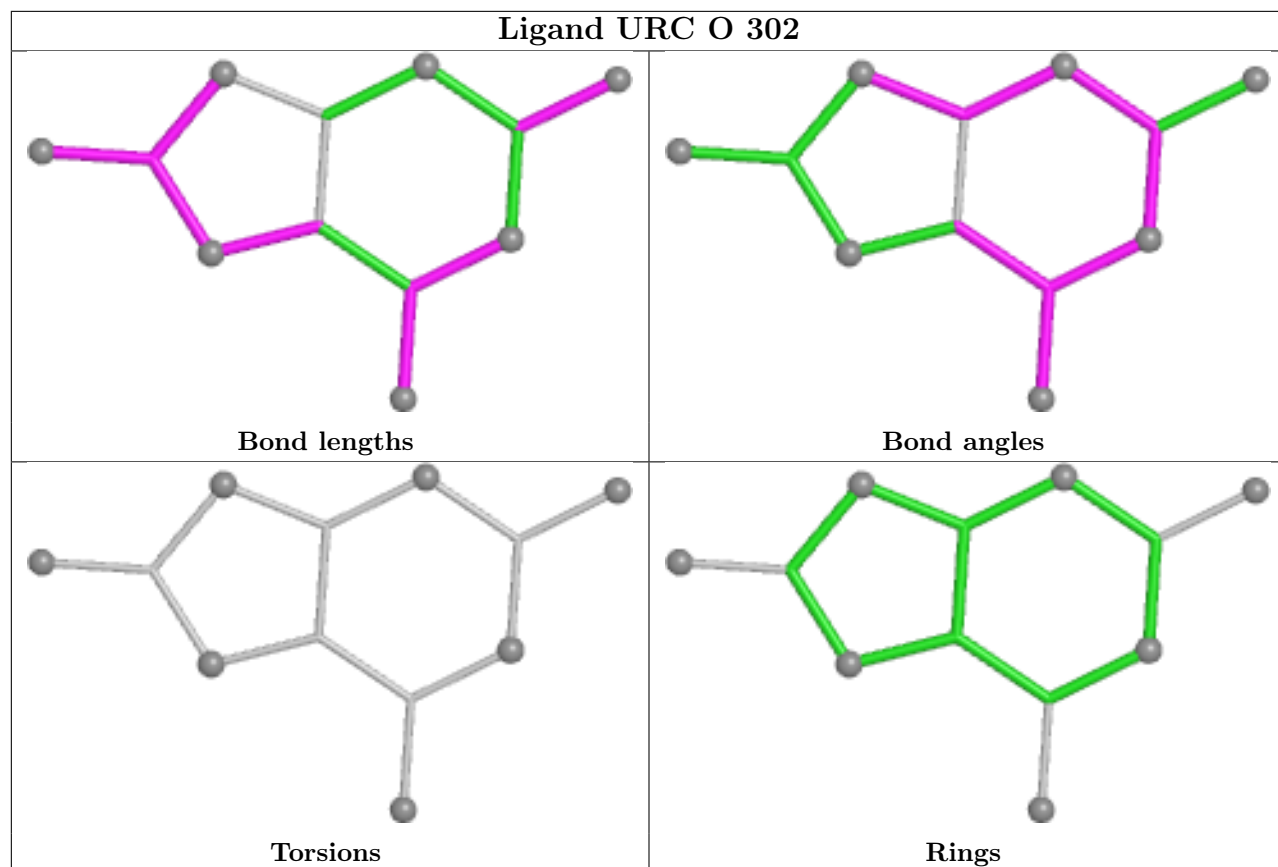




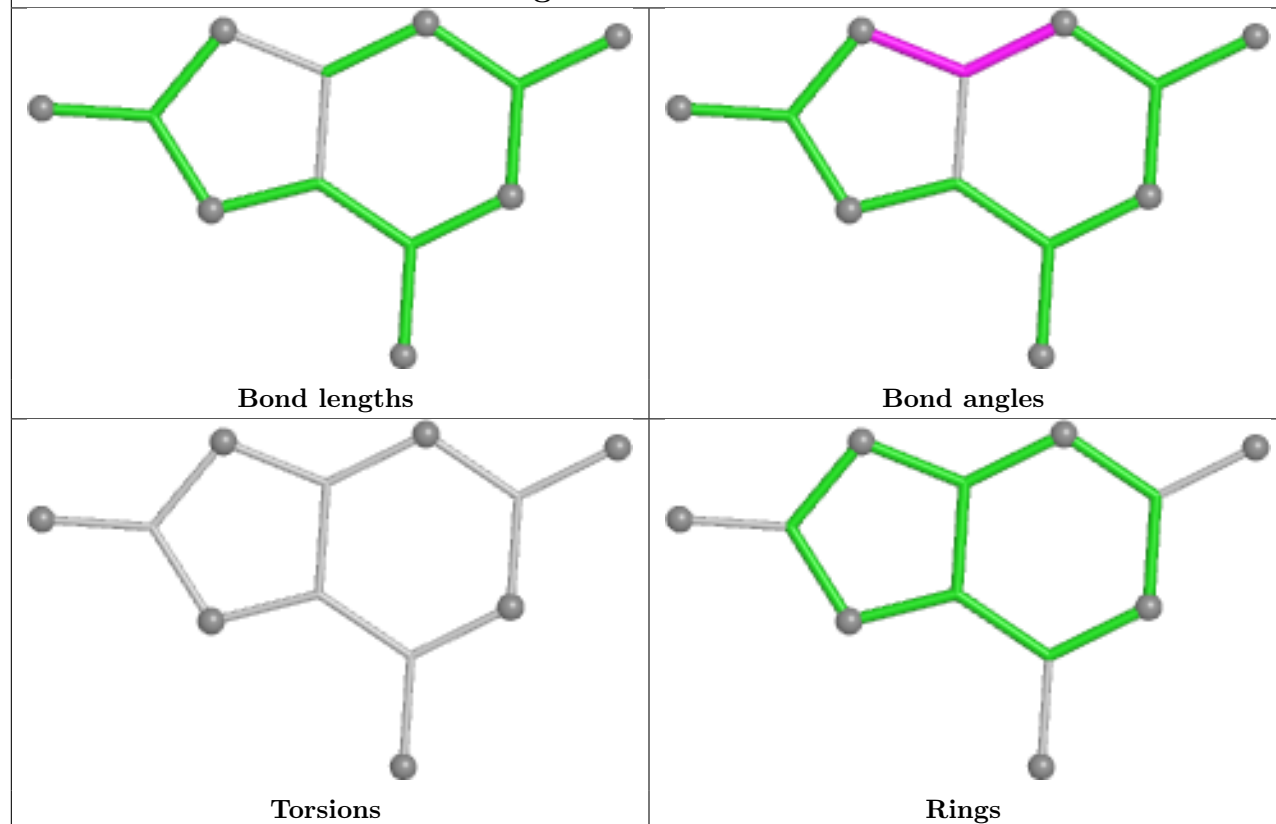




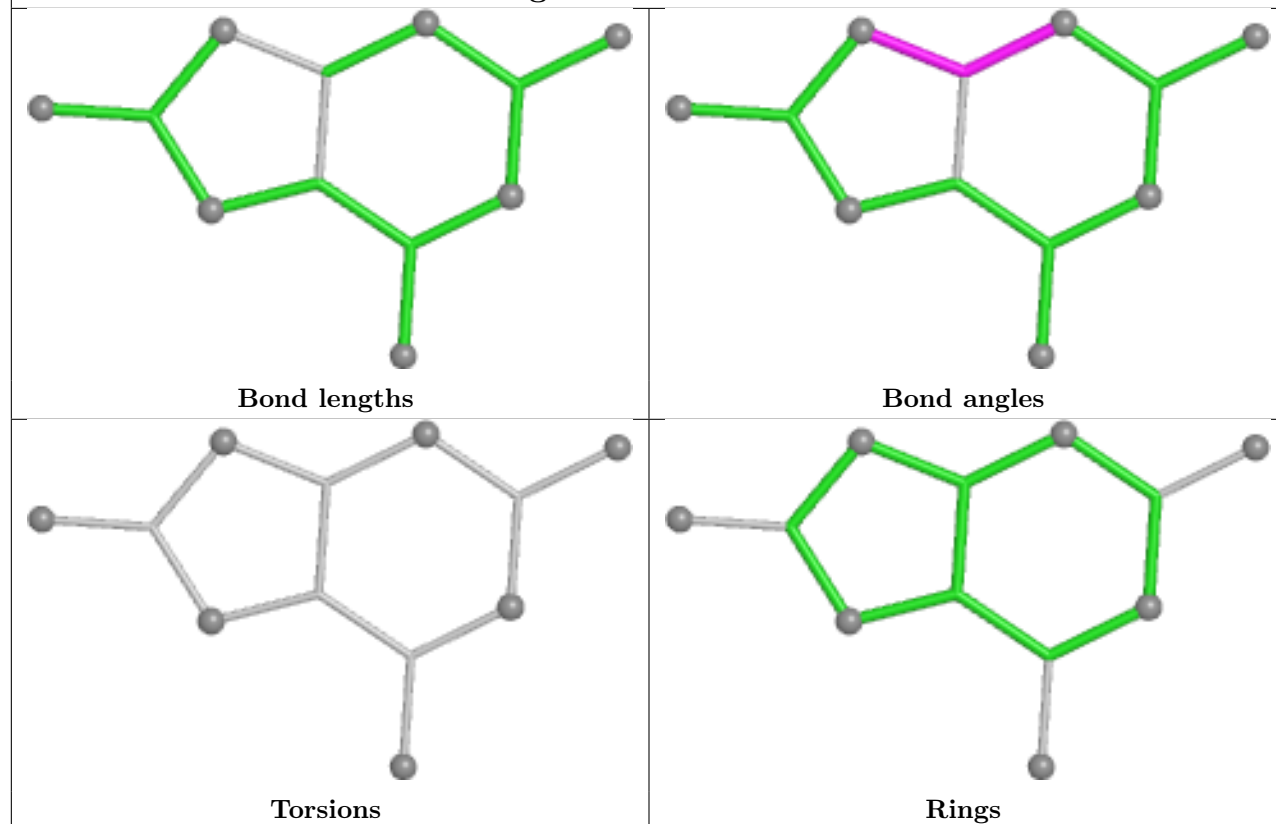


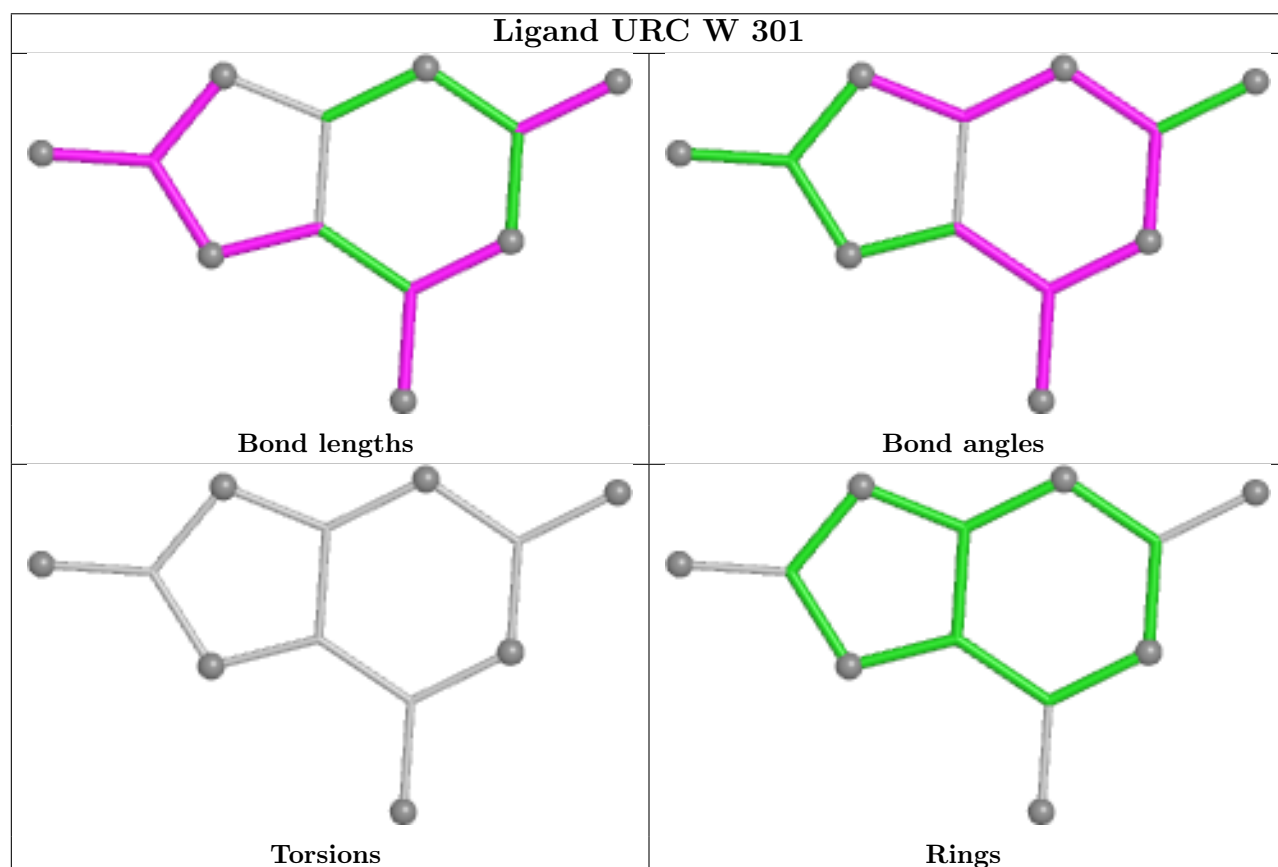
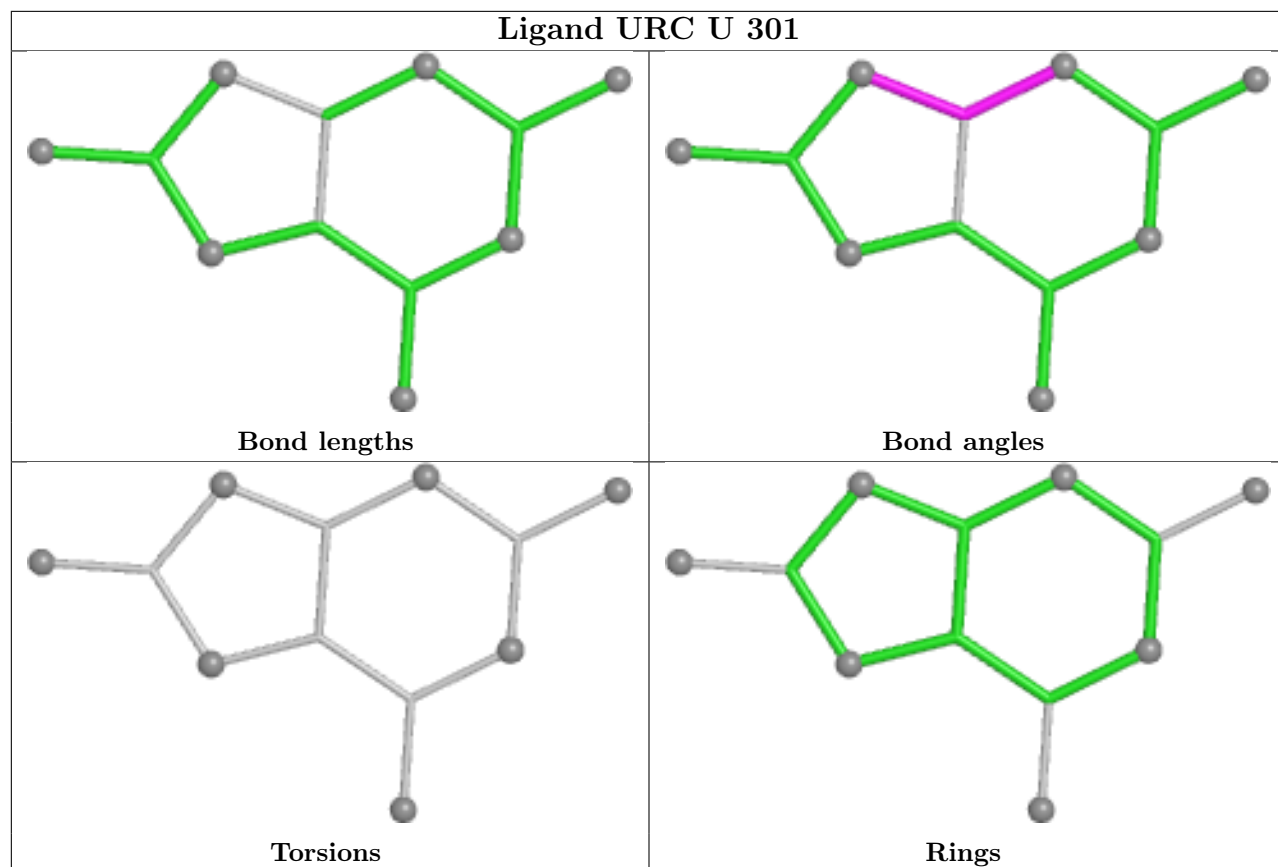


Ligand URC J 301



Ligand URC V 301





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.

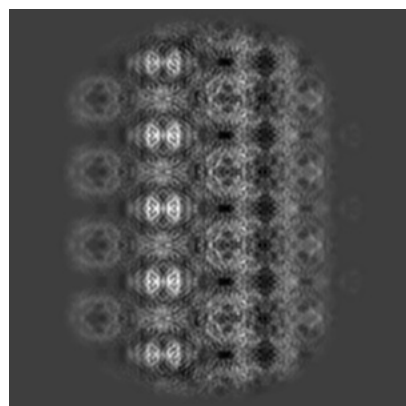
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-81807. These allow visual inspection of the internal detail of the map and identification of artifacts.

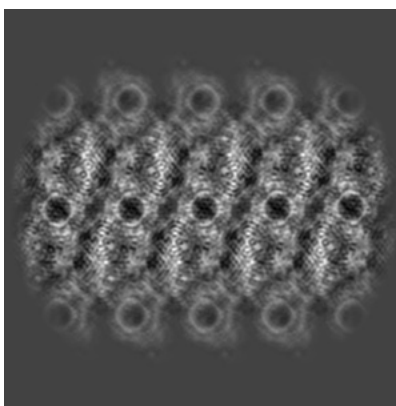
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

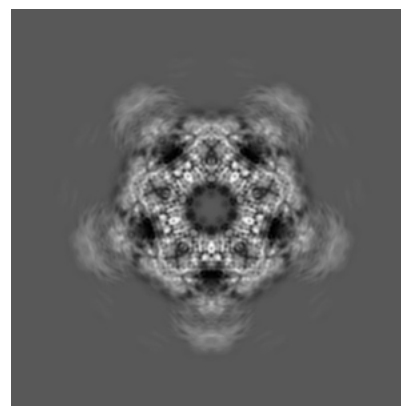
6.1.1 Primary map



X

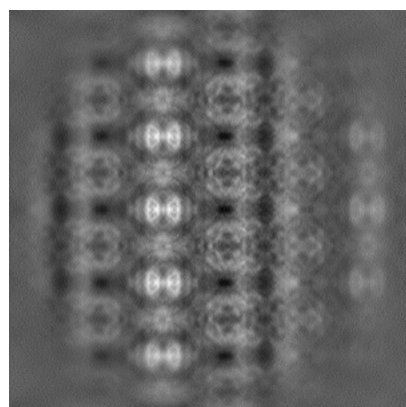


Y

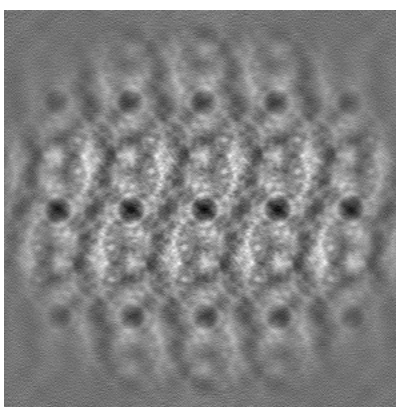


Z

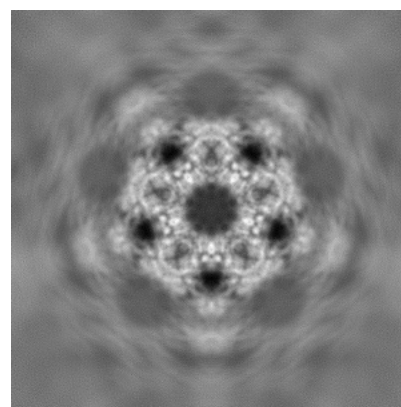
6.1.2 Raw map



X



Y

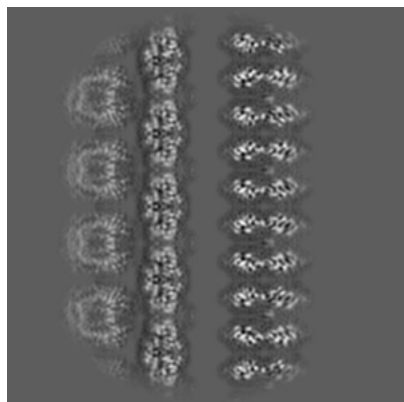


Z

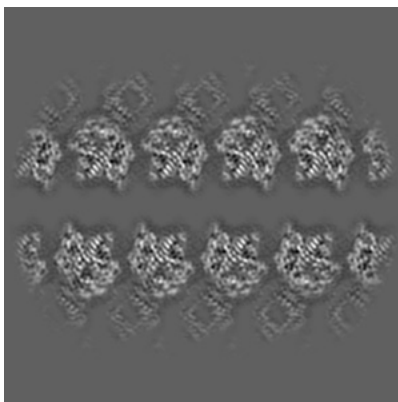
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

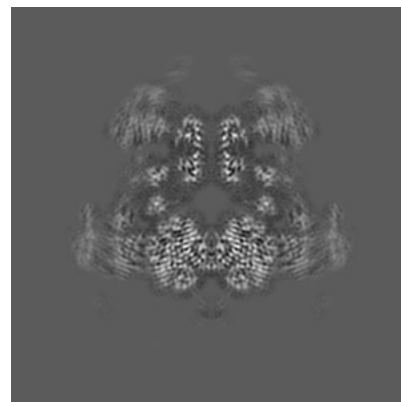
6.2.1 Primary map



X Index: 228

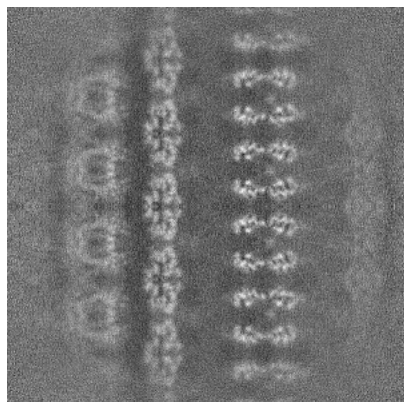


Y Index: 228

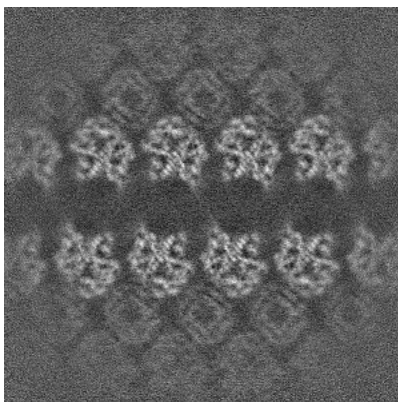


Z Index: 228

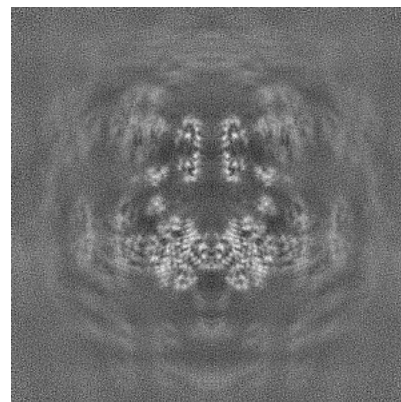
6.2.2 Raw map



X Index: 228



Y Index: 228

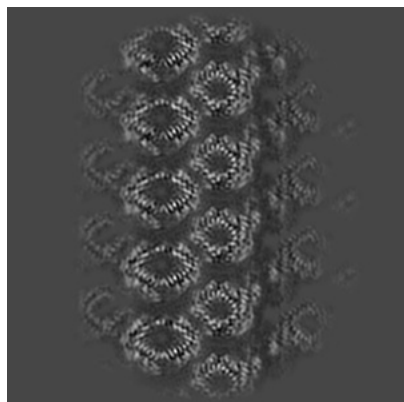


Z Index: 228

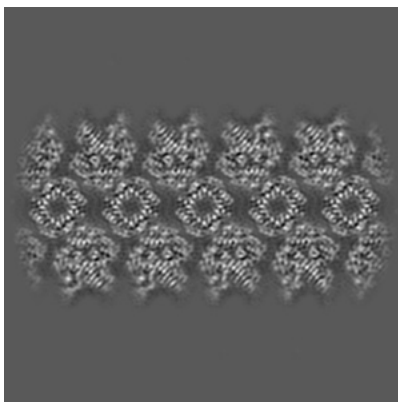
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

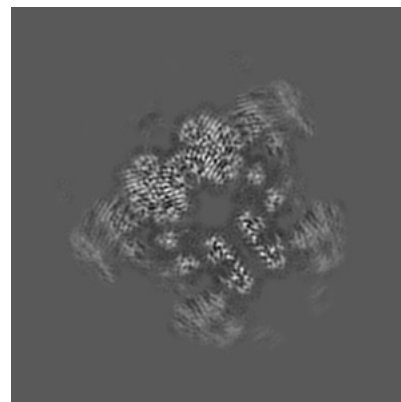
6.3.1 Primary map



X Index: 266

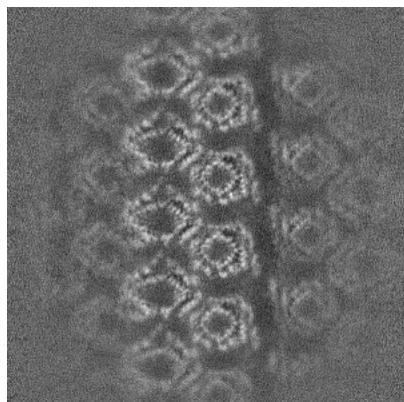


Y Index: 267

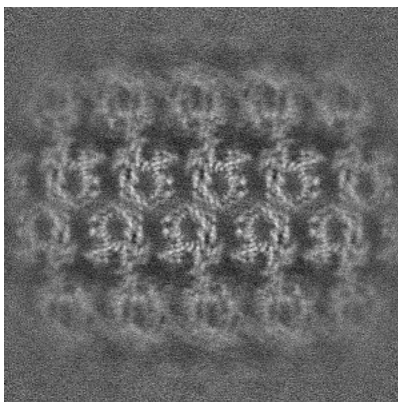


Z Index: 161

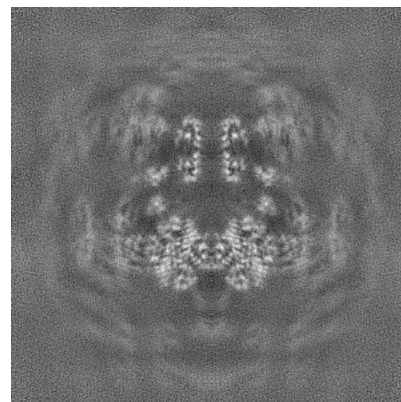
6.3.2 Raw map



X Index: 187



Y Index: 192

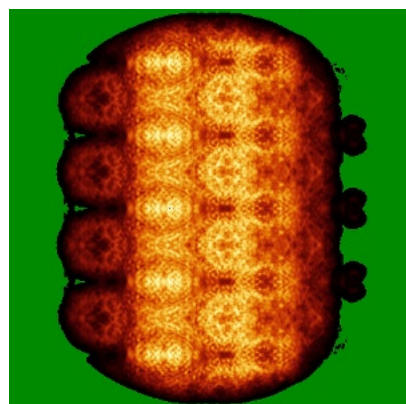


Z Index: 228

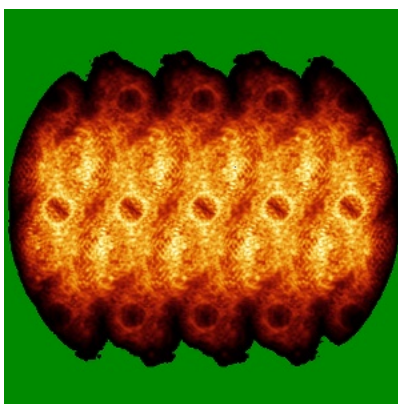
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

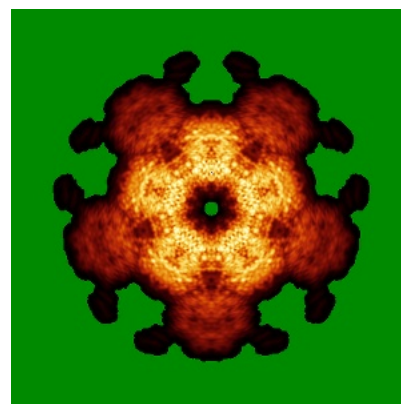
6.4.1 Primary map



X

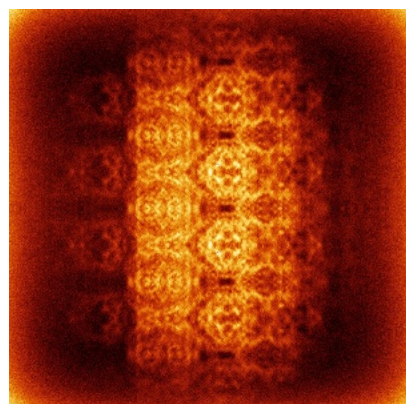


Y

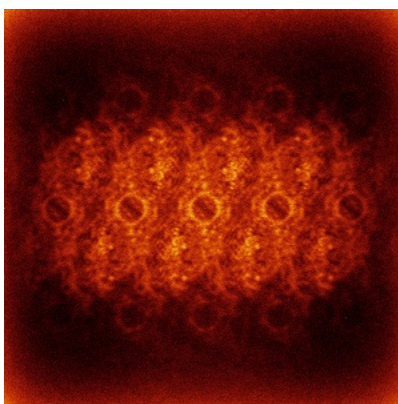


Z

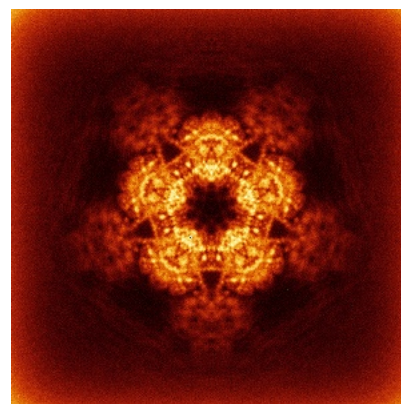
6.4.2 Raw map



X



Y

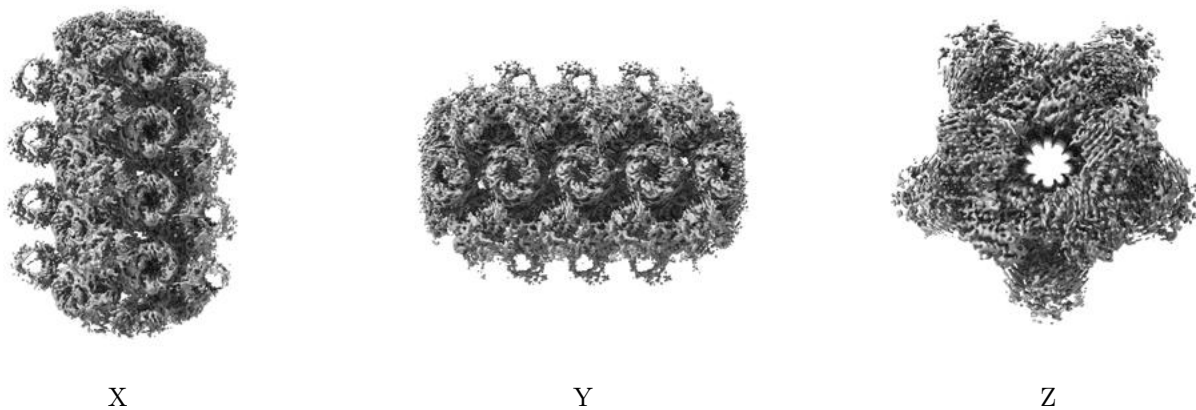


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

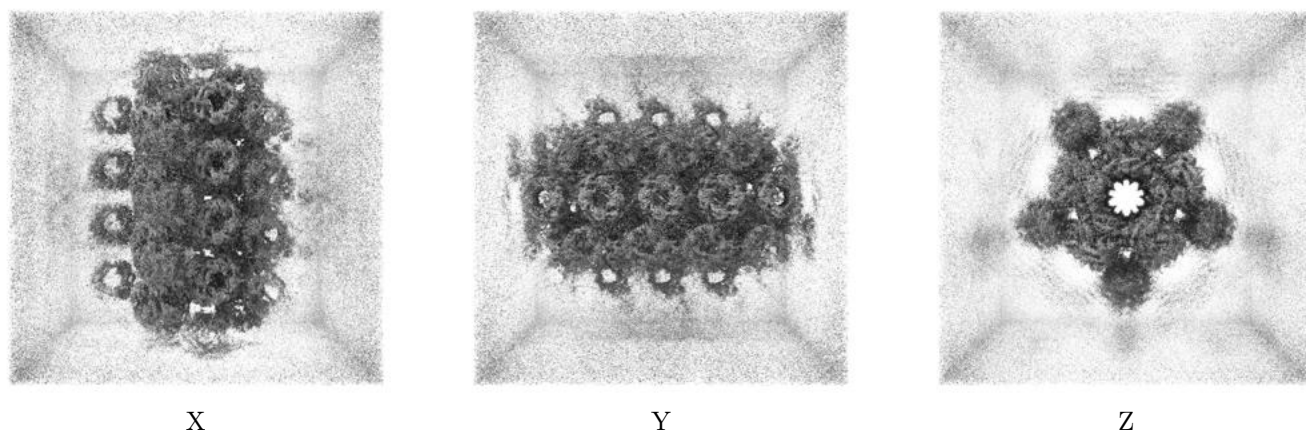
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.017. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

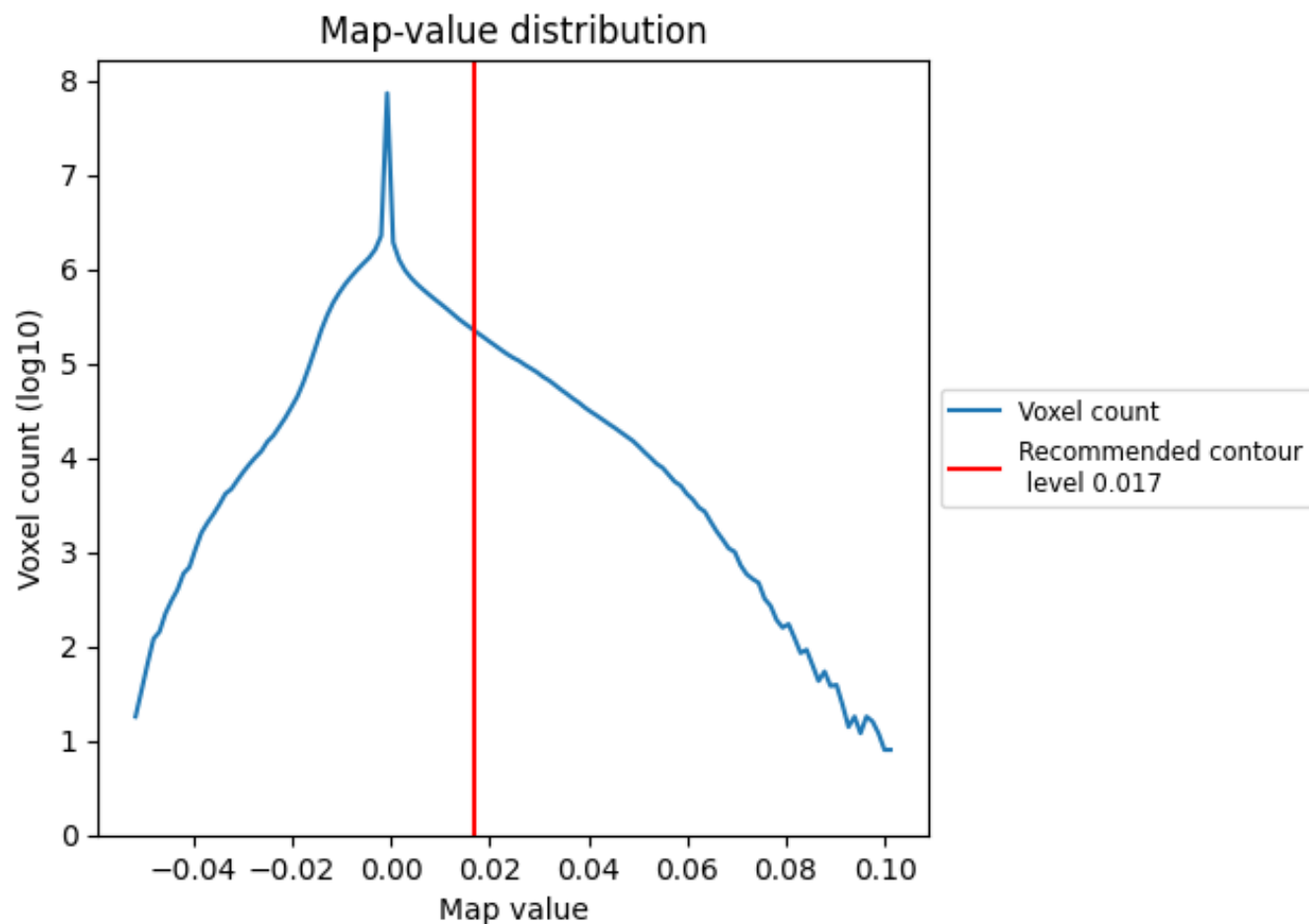
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

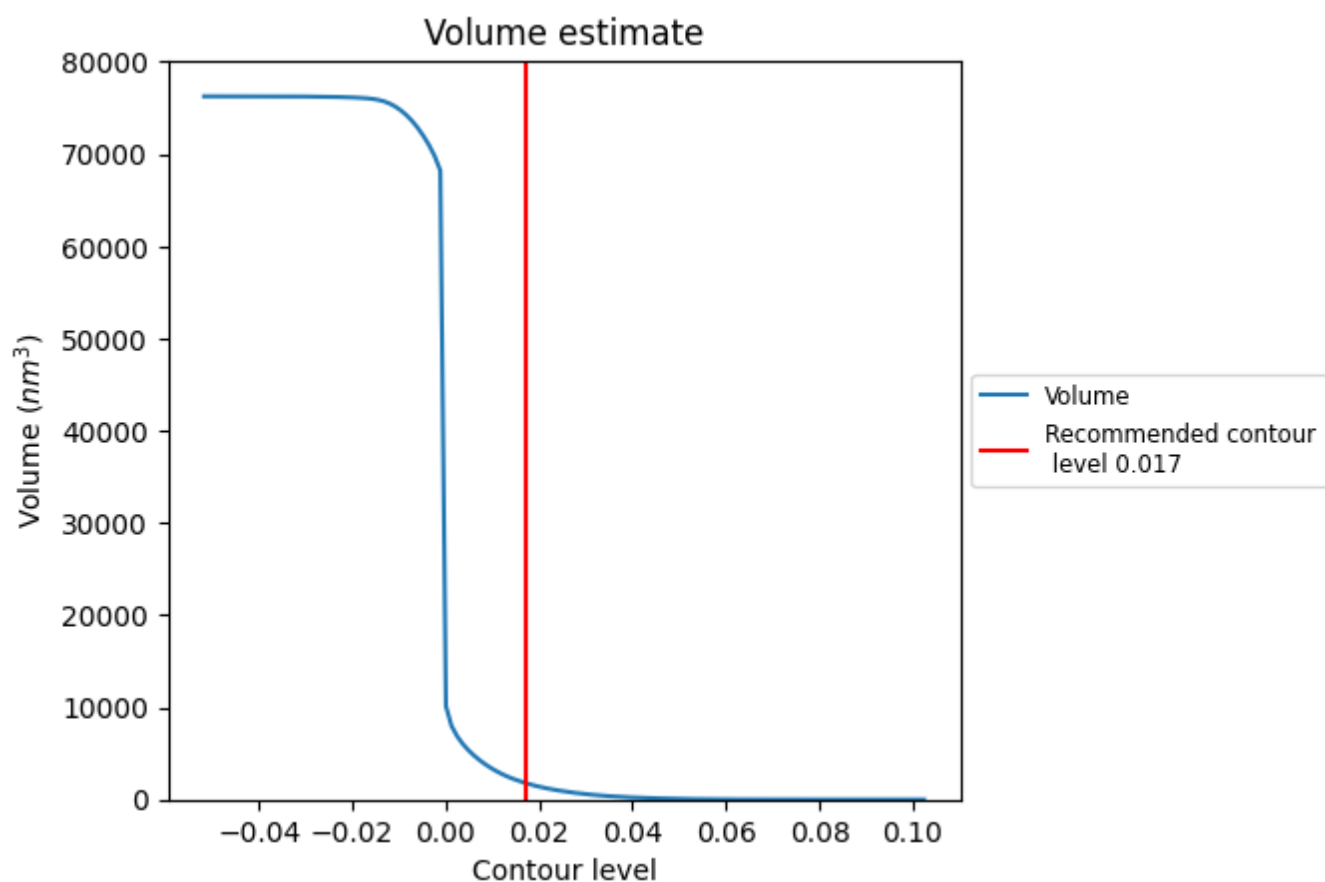
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

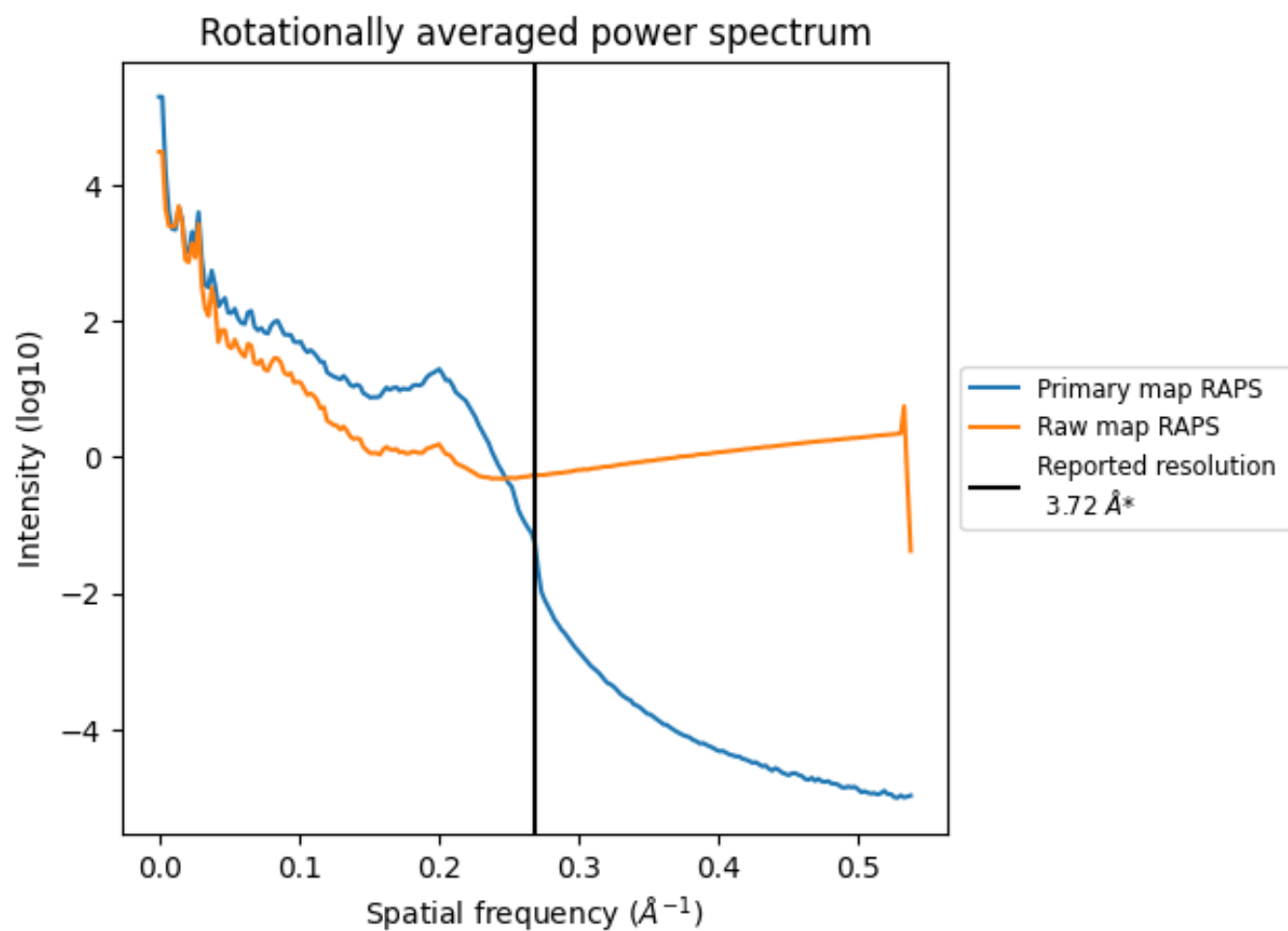
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1804 nm³; this corresponds to an approximate mass of 1630 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

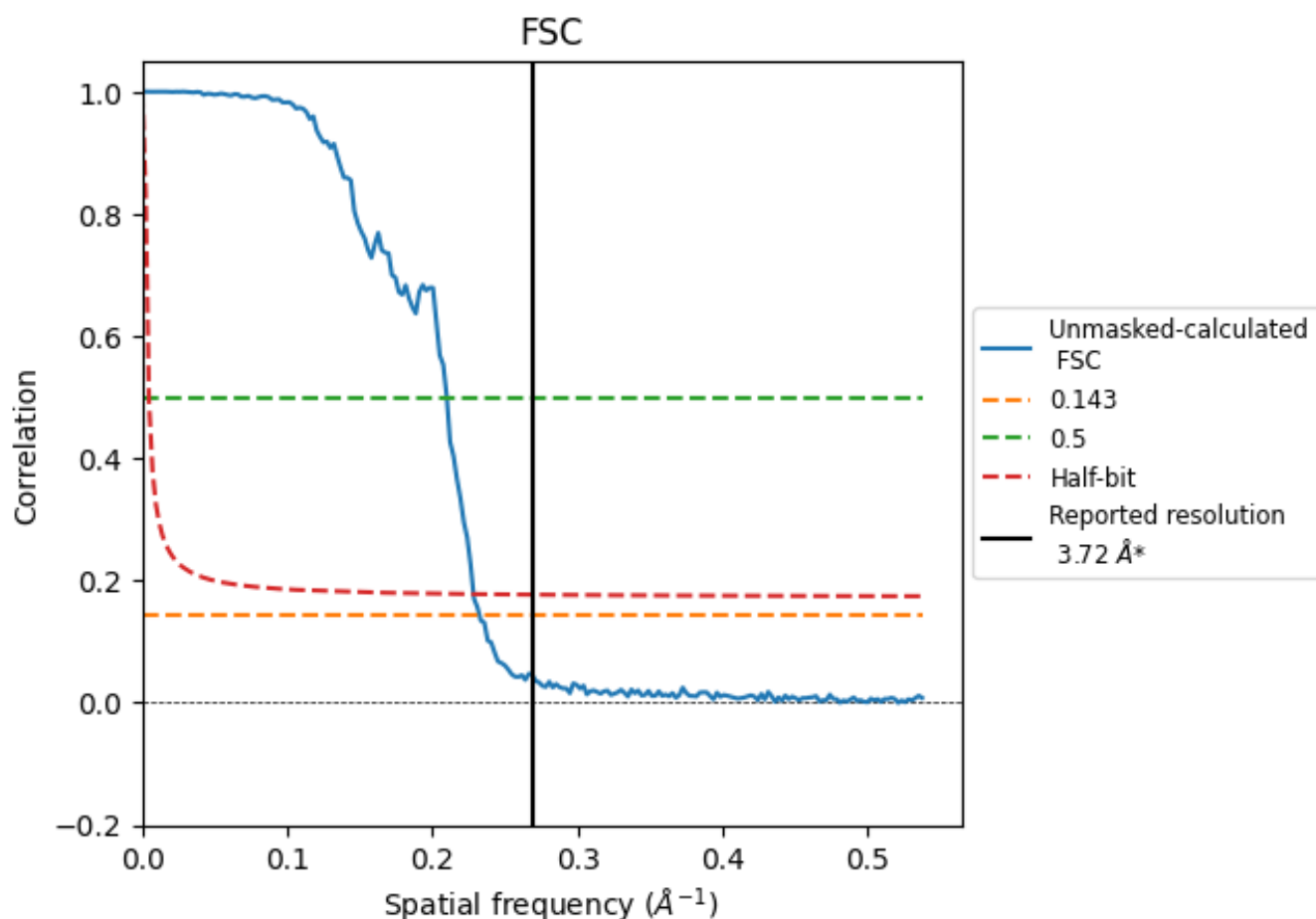


*Reported resolution corresponds to spatial frequency of 0.269 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of $0.269 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

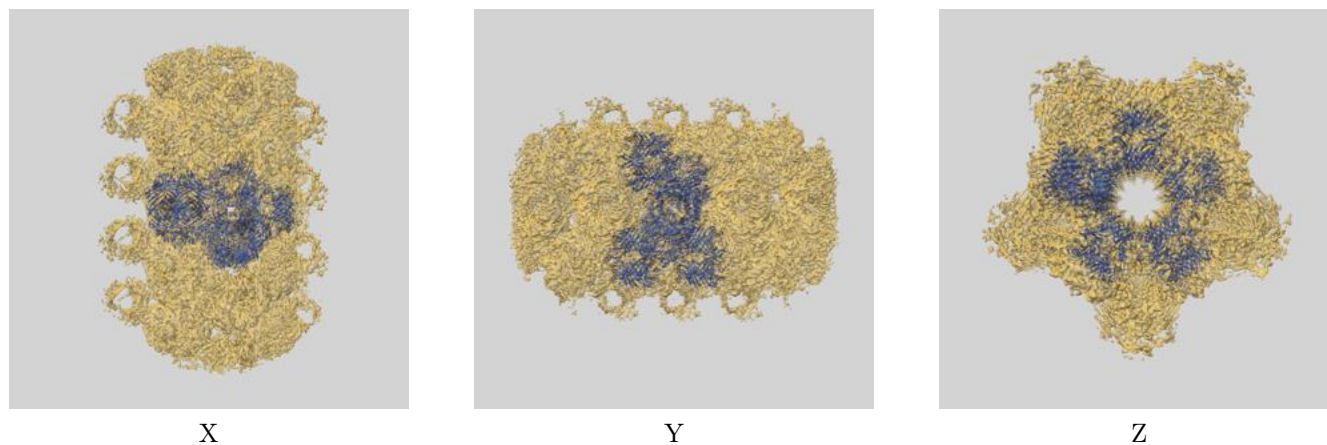
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.72	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.30	4.76	4.38

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.30 differs from the reported value 3.72 by more than 10 %

9 Map-model fit [i](#)

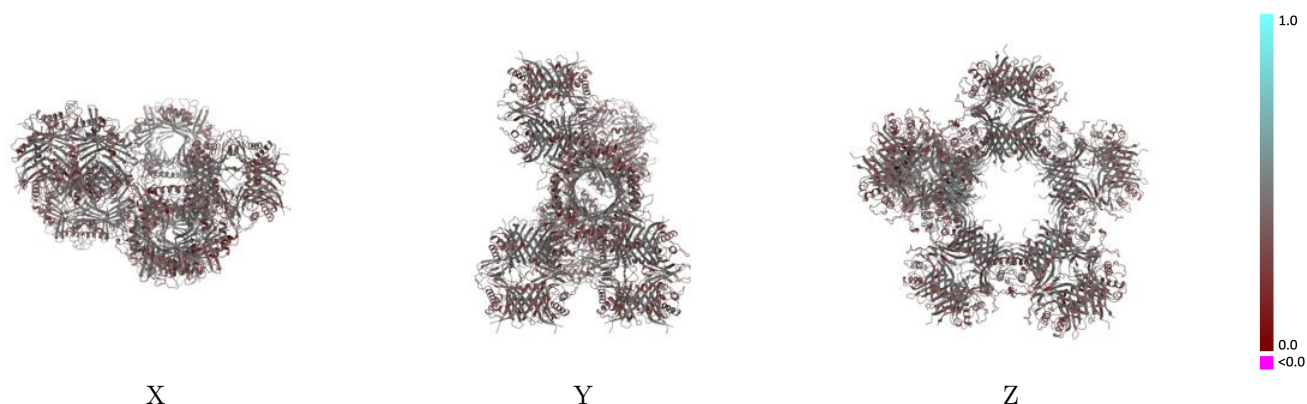
This section contains information regarding the fit between EMDB map EMD-81807 and PDB model 43DY. Per-residue inclusion information can be found in section [3](#) on page [8](#).

9.1 Map-model overlay [i](#)



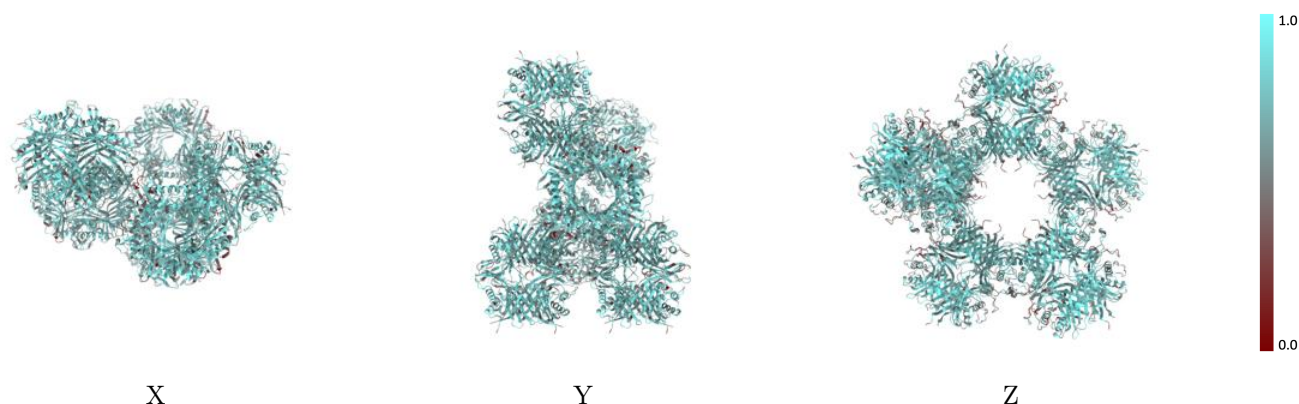
The images above show the 3D surface view of the map at the recommended contour level 0.017 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



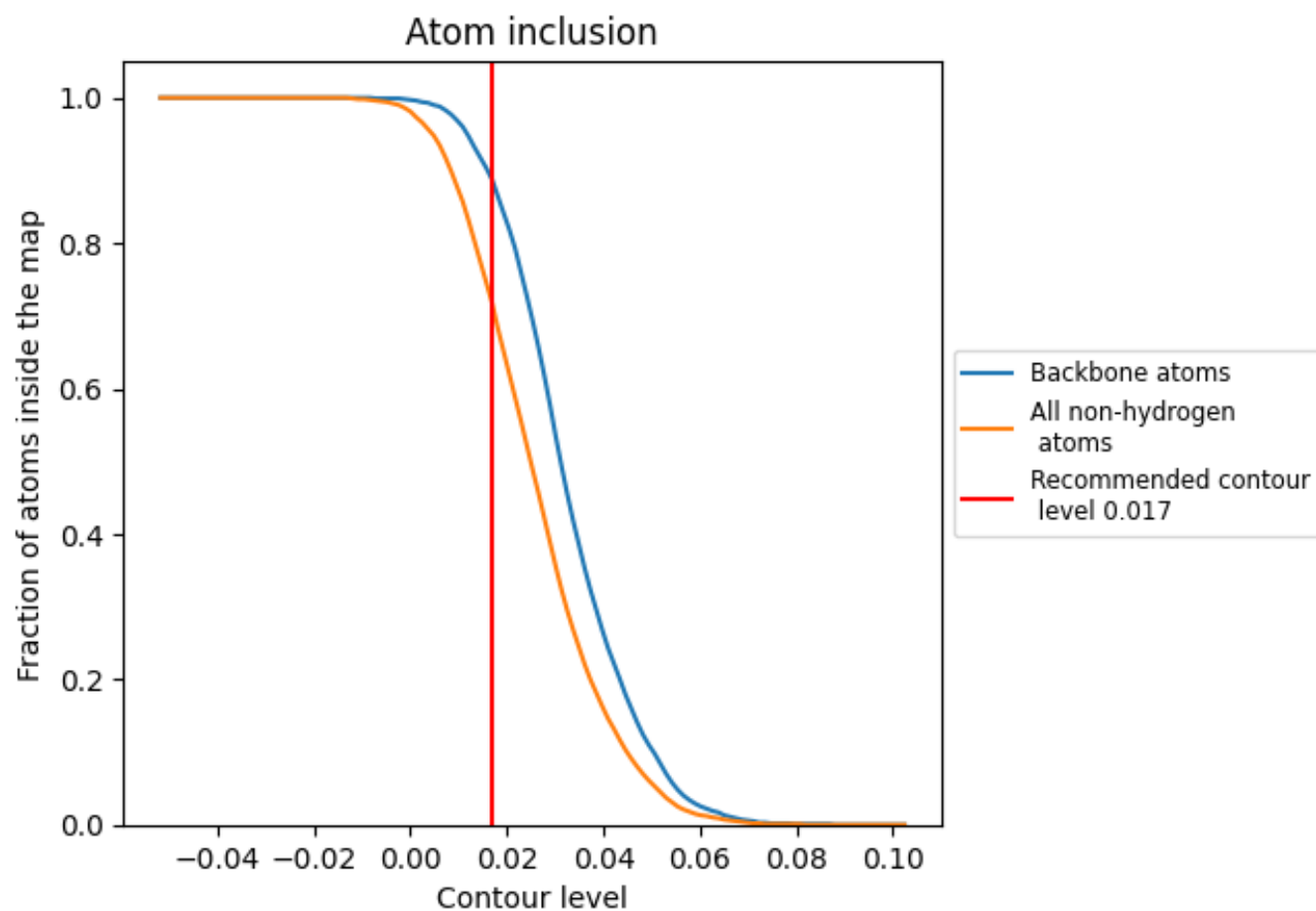
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.017).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 72% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.017) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7170	 0.3980
A	 0.7140	 0.4100
B	 0.7130	 0.4140
C	 0.7210	 0.3870
D	 0.7170	 0.3860
E	 0.7140	 0.4080
F	 0.7150	 0.4140
G	 0.7230	 0.3860
H	 0.7180	 0.3850
I	 0.7130	 0.4100
J	 0.7160	 0.4120
K	 0.7250	 0.3840
L	 0.7170	 0.3850
M	 0.7120	 0.4080
N	 0.7150	 0.4120
O	 0.7240	 0.3840
P	 0.7190	 0.3850
Q	 0.7120	 0.4100
R	 0.7190	 0.4130
S	 0.7230	 0.3870
T	 0.7190	 0.3850
U	 0.7100	 0.4080
V	 0.7160	 0.4130
W	 0.7190	 0.3870
X	 0.7140	 0.3840

