



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 09:56 PM UTC

PDB ID : 8TF0 / pdb_00008tf0
Title : Crystal structure of Grp94 N-terminal domain bound to the purine inhibitor PU-H36
Authors : Que, N.L.S.; Gewirth, D.T.
Deposited on : 2023-07-07
Resolution : 2.79 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

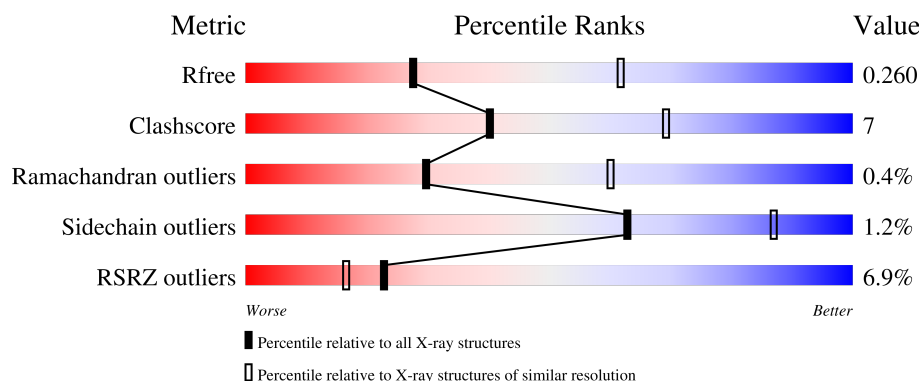
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

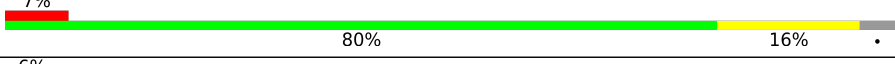
The reported resolution of this entry is 2.79 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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

Mol	Chain	Length	Quality of chain
1	A	236	
1	B	236	
1	C	236	
1	D	236	

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
6	MN	D	403	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6864 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Endoplasmin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	226	Total	C	N	O	S	0	1	0
			1726	1099	286	334	7			
1	A	226	Total	C	N	O	S	0	0	0
			1726	1096	287	336	7			
1	C	209	Total	C	N	O	S	0	0	0
			1560	992	262	301	5			
1	D	210	Total	C	N	O	S	0	0	0
			1590	1010	264	311	5			

There are 180 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	65	GLY	-	expression tag	UNP P41148
B	66	SER	-	expression tag	UNP P41148
B	67	HIS	-	expression tag	UNP P41148
B	68	MET	-	expression tag	UNP P41148
B	?	-	GLU	deletion	UNP P41148
B	?	-	THR	deletion	UNP P41148
B	?	-	VAL	deletion	UNP P41148
B	?	-	GLU	deletion	UNP P41148
B	?	-	GLU	deletion	UNP P41148
B	?	-	PRO	deletion	UNP P41148
B	?	-	MET	deletion	UNP P41148
B	?	-	GLU	deletion	UNP P41148
B	?	-	GLU	deletion	UNP P41148
B	?	-	GLU	deletion	UNP P41148
B	?	-	GLU	deletion	UNP P41148
B	?	-	ALA	deletion	UNP P41148
B	?	-	ALA	deletion	UNP P41148
B	?	-	LYS	deletion	UNP P41148
B	?	-	GLU	deletion	UNP P41148
B	?	-	GLU	deletion	UNP P41148
B	?	-	LYS	deletion	UNP P41148

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	GLU	deletion	UNP P41148
B	?	-	ASP	deletion	UNP P41148
B	?	-	SER	deletion	UNP P41148
B	?	-	ASP	deletion	UNP P41148
B	?	-	ASP	deletion	UNP P41148
B	?	-	GLU	deletion	UNP P41148
B	?	-	ALA	deletion	UNP P41148
B	?	-	ALA	deletion	UNP P41148
B	?	-	VAL	deletion	UNP P41148
B	?	-	GLU	deletion	UNP P41148
B	?	-	GLU	deletion	UNP P41148
B	?	-	GLU	deletion	UNP P41148
B	?	-	GLU	deletion	UNP P41148
B	?	-	GLU	deletion	UNP P41148
B	?	-	GLU	deletion	UNP P41148
B	?	-	LYS	deletion	UNP P41148
B	?	-	LYS	deletion	UNP P41148
B	?	-	PRO	deletion	UNP P41148
B	?	-	LYS	deletion	UNP P41148
B	?	-	THR	deletion	UNP P41148
B	324	GLY	LYS	conflict	UNP P41148
B	325	GLY	LYS	conflict	UNP P41148
B	326	GLY	VAL	conflict	UNP P41148
B	327	GLY	GLU	conflict	UNP P41148
A	65	GLY	-	expression tag	UNP P41148
A	66	SER	-	expression tag	UNP P41148
A	67	HIS	-	expression tag	UNP P41148
A	68	MET	-	expression tag	UNP P41148
A	?	-	GLU	deletion	UNP P41148
A	?	-	THR	deletion	UNP P41148
A	?	-	VAL	deletion	UNP P41148
A	?	-	GLU	deletion	UNP P41148
A	?	-	GLU	deletion	UNP P41148
A	?	-	PRO	deletion	UNP P41148
A	?	-	MET	deletion	UNP P41148
A	?	-	GLU	deletion	UNP P41148
A	?	-	GLU	deletion	UNP P41148
A	?	-	GLU	deletion	UNP P41148
A	?	-	GLU	deletion	UNP P41148
A	?	-	ALA	deletion	UNP P41148
A	?	-	ALA	deletion	UNP P41148
A	?	-	LYS	deletion	UNP P41148

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLU	deletion	UNP P41148
A	?	-	GLU	deletion	UNP P41148
A	?	-	LYS	deletion	UNP P41148
A	?	-	GLU	deletion	UNP P41148
A	?	-	ASP	deletion	UNP P41148
A	?	-	SER	deletion	UNP P41148
A	?	-	ASP	deletion	UNP P41148
A	?	-	ASP	deletion	UNP P41148
A	?	-	GLU	deletion	UNP P41148
A	?	-	ALA	deletion	UNP P41148
A	?	-	ALA	deletion	UNP P41148
A	?	-	VAL	deletion	UNP P41148
A	?	-	GLU	deletion	UNP P41148
A	?	-	GLU	deletion	UNP P41148
A	?	-	GLU	deletion	UNP P41148
A	?	-	GLU	deletion	UNP P41148
A	?	-	GLU	deletion	UNP P41148
A	?	-	GLU	deletion	UNP P41148
A	?	-	GLU	deletion	UNP P41148
A	?	-	LYS	deletion	UNP P41148
A	?	-	LYS	deletion	UNP P41148
A	?	-	PRO	deletion	UNP P41148
A	?	-	LYS	deletion	UNP P41148
A	?	-	THR	deletion	UNP P41148
A	324	GLY	LYS	conflict	UNP P41148
A	325	GLY	LYS	conflict	UNP P41148
A	326	GLY	VAL	conflict	UNP P41148
A	327	GLY	GLU	conflict	UNP P41148
C	65	GLY	-	expression tag	UNP P41148
C	66	SER	-	expression tag	UNP P41148
C	67	HIS	-	expression tag	UNP P41148
C	68	MET	-	expression tag	UNP P41148
C	?	-	GLU	deletion	UNP P41148
C	?	-	THR	deletion	UNP P41148
C	?	-	VAL	deletion	UNP P41148
C	?	-	GLU	deletion	UNP P41148
C	?	-	GLU	deletion	UNP P41148
C	?	-	PRO	deletion	UNP P41148
C	?	-	MET	deletion	UNP P41148
C	?	-	GLU	deletion	UNP P41148
C	?	-	GLU	deletion	UNP P41148
C	?	-	GLU	deletion	UNP P41148
C	?	-	GLU	deletion	UNP P41148
C	?	-	GLU	deletion	UNP P41148

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	?	-	ALA	deletion	UNP P41148
C	?	-	ALA	deletion	UNP P41148
C	?	-	LYS	deletion	UNP P41148
C	?	-	GLU	deletion	UNP P41148
C	?	-	GLU	deletion	UNP P41148
C	?	-	LYS	deletion	UNP P41148
C	?	-	GLU	deletion	UNP P41148
C	?	-	ASP	deletion	UNP P41148
C	?	-	SER	deletion	UNP P41148
C	?	-	ASP	deletion	UNP P41148
C	?	-	ASP	deletion	UNP P41148
C	?	-	GLU	deletion	UNP P41148
C	?	-	ALA	deletion	UNP P41148
C	?	-	ALA	deletion	UNP P41148
C	?	-	VAL	deletion	UNP P41148
C	?	-	GLU	deletion	UNP P41148
C	?	-	GLU	deletion	UNP P41148
C	?	-	GLU	deletion	UNP P41148
C	?	-	GLU	deletion	UNP P41148
C	?	-	GLU	deletion	UNP P41148
C	?	-	GLU	deletion	UNP P41148
C	?	-	LYS	deletion	UNP P41148
C	?	-	LYS	deletion	UNP P41148
C	?	-	PRO	deletion	UNP P41148
C	?	-	LYS	deletion	UNP P41148
C	?	-	THR	deletion	UNP P41148
C	324	GLY	LYS	conflict	UNP P41148
C	325	GLY	LYS	conflict	UNP P41148
C	326	GLY	VAL	conflict	UNP P41148
C	327	GLY	GLU	conflict	UNP P41148
D	65	GLY	-	expression tag	UNP P41148
D	66	SER	-	expression tag	UNP P41148
D	67	HIS	-	expression tag	UNP P41148
D	68	MET	-	expression tag	UNP P41148
D	?	-	GLU	deletion	UNP P41148
D	?	-	THR	deletion	UNP P41148
D	?	-	VAL	deletion	UNP P41148
D	?	-	GLU	deletion	UNP P41148
D	?	-	GLU	deletion	UNP P41148
D	?	-	PRO	deletion	UNP P41148
D	?	-	MET	deletion	UNP P41148
D	?	-	GLU	deletion	UNP P41148

Continued on next page...

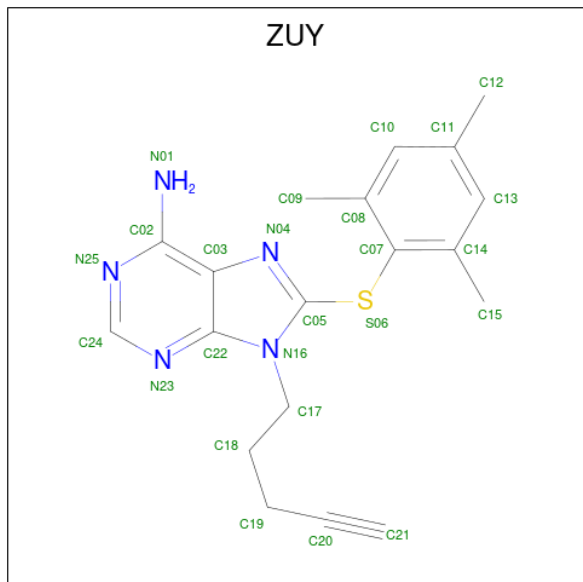
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	?	-	GLU	deletion	UNP P41148
D	?	-	GLU	deletion	UNP P41148
D	?	-	GLU	deletion	UNP P41148
D	?	-	ALA	deletion	UNP P41148
D	?	-	ALA	deletion	UNP P41148
D	?	-	LYS	deletion	UNP P41148
D	?	-	GLU	deletion	UNP P41148
D	?	-	GLU	deletion	UNP P41148
D	?	-	LYS	deletion	UNP P41148
D	?	-	GLU	deletion	UNP P41148
D	?	-	ASP	deletion	UNP P41148
D	?	-	SER	deletion	UNP P41148
D	?	-	ASP	deletion	UNP P41148
D	?	-	ASP	deletion	UNP P41148
D	?	-	GLU	deletion	UNP P41148
D	?	-	ALA	deletion	UNP P41148
D	?	-	ALA	deletion	UNP P41148
D	?	-	VAL	deletion	UNP P41148
D	?	-	GLU	deletion	UNP P41148
D	?	-	GLU	deletion	UNP P41148
D	?	-	GLU	deletion	UNP P41148
D	?	-	GLU	deletion	UNP P41148
D	?	-	GLU	deletion	UNP P41148
D	?	-	GLU	deletion	UNP P41148
D	?	-	GLU	deletion	UNP P41148
D	?	-	LYS	deletion	UNP P41148
D	?	-	LYS	deletion	UNP P41148
D	?	-	PRO	deletion	UNP P41148
D	?	-	LYS	deletion	UNP P41148
D	?	-	THR	deletion	UNP P41148
D	324	GLY	LYS	conflict	UNP P41148
D	325	GLY	LYS	conflict	UNP P41148
D	326	GLY	VAL	conflict	UNP P41148
D	327	GLY	GLU	conflict	UNP P41148

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

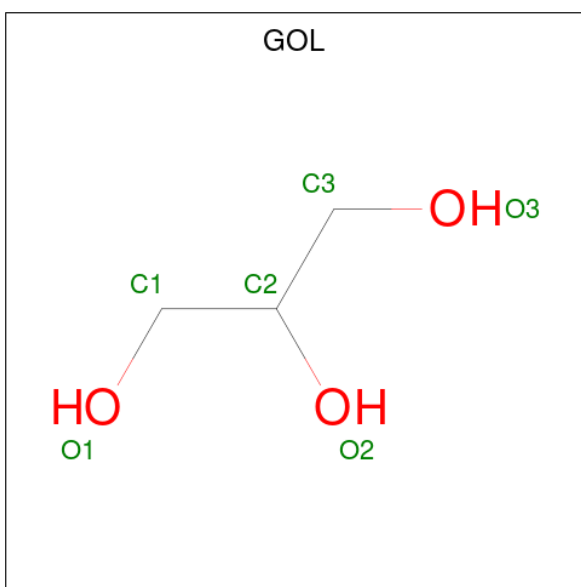
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	3	Total Mg 3 3	0	0
2	A	4	Total Mg 4 4	0	0
2	D	4	Total Mg 4 4	0	0

- Molecule 3 is 9-(pent-4-yn-1-yl)-8-[(2,4,6-trimethylphenyl)sulfanyl]-9H-purin-6-amine (CCD ID: ZUY) (formula: $C_{19}H_{21}N_5S$) (labeled as "Ligand of Interest" by depositor).



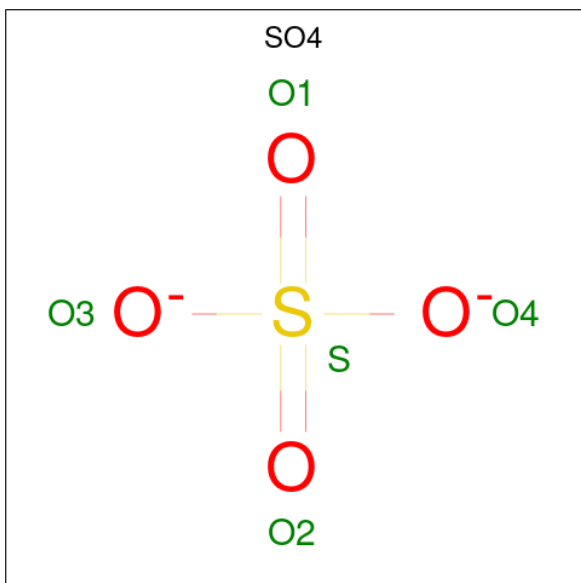
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	S	0	0
			25	19	5	1		
3	A	1	Total	C	N	S	0	0
			25	19	5	1		
3	C	1	Total	C	N	S	0	0
			25	19	5	1		
3	D	1	Total	C	N	S	0	0
			25	19	5	1		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 6 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	D	1	Total Mn 1 1	0	0

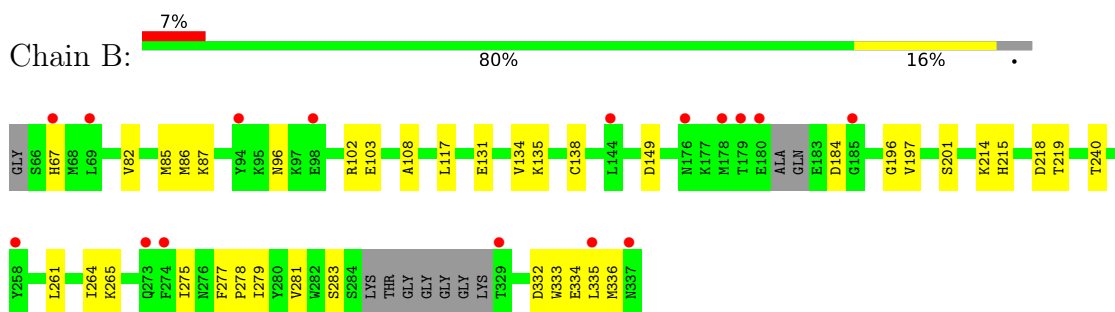
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	31	Total O 31 31	0	0
7	A	9	Total O 9 9	0	0
7	C	10	Total O 10 10	0	0
7	D	11	Total O 11 11	0	0

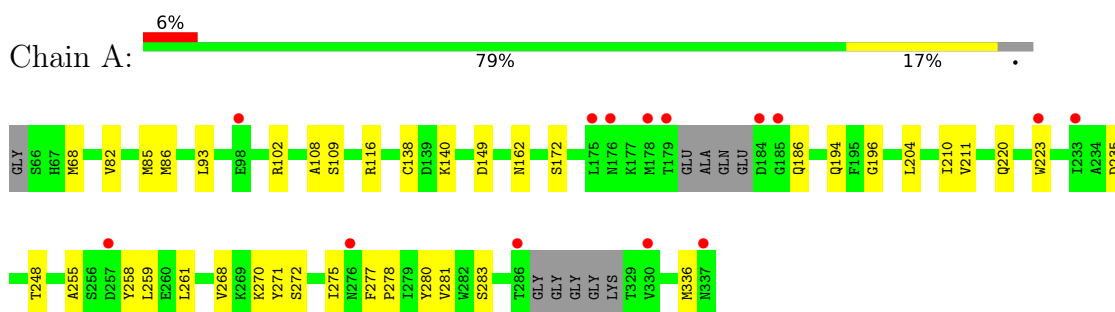
3 Residue-property plots [i](#)

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

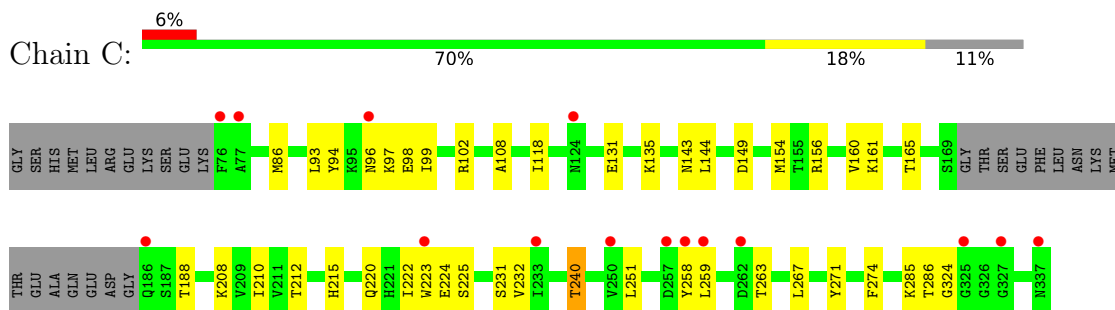
• Molecule 1: Endoplasmin



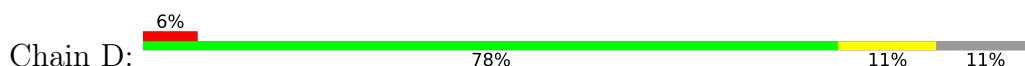
• Molecule 1: Endoplasmin

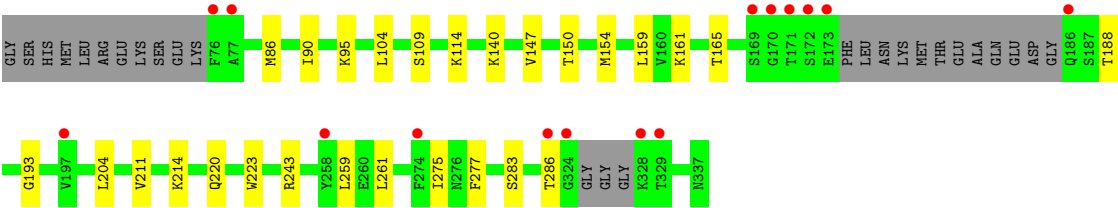


• Molecule 1: Endoplasmin



• Molecule 1: Endoplasmin





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	96.28Å 104.39Å 172.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.89 – 2.79 36.89 – 2.79	Depositor EDS
% Data completeness (in resolution range)	99.5 (36.89-2.79) 99.5 (36.89-2.79)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.58 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.228 , 0.260 0.228 , 0.260	Depositor DCC
R_{free} test set	2192 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	78.5	Xtriage
Anisotropy	0.401	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 62.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6864	wwPDB-VP
Average B, all atoms (Å ²)	82.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.58% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZUY, GOL, MG, MN, SO4

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	0.09	0/1752	0.28	0/2374
1	B	0.08	0/1753	0.25	0/2376
1	C	0.10	0/1584	0.29	0/2149
1	D	0.09	0/1613	0.27	0/2189
All	All	0.09	0/6702	0.27	0/9088

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 [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1726	0	1650	24	0
1	B	1726	0	1631	21	0
1	C	1560	0	1487	29	0
1	D	1590	0	1508	17	0
2	A	4	0	0	0	0
2	B	3	0	0	0	0
2	D	4	0	0	0	0
3	A	25	0	0	0	0
3	B	25	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	25	0	0	0	0
3	D	25	0	0	0	0
4	A	12	0	16	0	0
4	B	6	0	8	0	0
4	D	6	0	8	0	0
5	A	15	0	0	0	0
5	B	25	0	0	0	0
5	C	10	0	0	0	0
5	D	15	0	0	0	0
6	D	1	0	0	0	0
7	A	9	0	0	1	0
7	B	31	0	0	0	0
7	C	10	0	0	0	0
7	D	11	0	0	1	0
All	All	6864	0	6308	86	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 7.

All (86) 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:C:210:ILE:HG23	1:C:224:GLU:HG2	1.71	0.72
1:A:281:VAL:HB	1:A:336:MET:HE3	1.72	0.70
1:B:131:GLU:OE2	1:B:135:LYS:NZ	2.27	0.68
1:B:134:VAL:HB	1:B:279:ILE:HG12	1.75	0.67
1:A:162:ASN:HD21	1:A:186:GLN:HE21	1.43	0.66
1:C:208:LYS:NZ	1:C:224:GLU:OE1	2.22	0.65
1:D:154:MET:HE2	1:D:159:LEU:HD23	1.80	0.64
1:B:332:ASP:OD2	1:B:333:TRP:N	2.31	0.64
1:A:85:MET:HE2	1:A:196:GLY:HA3	1.80	0.63
1:C:220:GLN:HE22	1:C:240:THR:HB	1.65	0.62
1:A:270:LYS:HE2	1:A:271:TYR:CZ	2.35	0.61
1:D:261:LEU:HD21	1:D:283:SER:HA	1.80	0.61
1:B:82:VAL:HG12	1:B:86:MET:HE2	1.85	0.59
1:D:109:SER:HB2	1:D:275:ILE:HG23	1.83	0.58
1:B:214:LYS:NZ	1:B:215:HIS:O	2.36	0.58
1:B:85:MET:HE2	1:B:196:GLY:HA3	1.86	0.57
1:B:87:LYS:HG2	1:D:193:GLY:HA2	1.87	0.57
1:B:261:LEU:HD21	1:B:283:SER:HA	1.87	0.56
1:D:140:LYS:HA	1:D:259:LEU:HD13	1.88	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:281:VAL:HG23	1:B:336:MET:HG3	1.90	0.53
1:D:86:MET:O	1:D:90:ILE:HG13	2.09	0.53
1:C:285:LYS:O	1:C:324:GLY:N	2.35	0.53
1:B:102:ARG:NH1	1:B:103:GLU:OE2	2.43	0.52
1:D:86:MET:HB3	1:D:204:LEU:HD11	1.91	0.52
1:A:93:LEU:HD21	1:A:204:LEU:HD22	1.91	0.52
1:C:99:ILE:HG13	1:C:102:ARG:HH12	1.75	0.52
1:C:156:ARG:O	1:C:160:VAL:HG23	2.09	0.52
1:A:102:ARG:HB2	1:A:271:TYR:CE2	2.45	0.52
1:B:275:ILE:HG22	1:B:277:PHE:H	1.75	0.52
1:C:102:ARG:HG3	1:C:271:TYR:CD1	2.46	0.50
1:B:278:PRO:HB3	1:C:118:ILE:HG12	1.95	0.49
1:A:255:ALA:HB1	1:A:258:TYR:HD2	1.77	0.49
1:A:68:MET:HG2	1:C:274:PHE:O	2.13	0.48
1:A:172:SER:N	1:C:93:LEU:O	2.46	0.48
1:C:251:LEU:HD21	1:C:258:TYR:HB2	1.95	0.48
1:B:108:ALA:HB1	1:B:149:ASP:HB3	1.96	0.48
1:A:268:VAL:O	1:A:272:SER:OG	2.28	0.47
1:C:131:GLU:OE2	1:C:135:LYS:NZ	2.46	0.47
1:A:255:ALA:HB1	1:A:258:TYR:CD2	2.50	0.47
1:D:114:LYS:HB2	1:D:114:LYS:HE3	1.57	0.47
1:C:86:MET:HA	1:C:86:MET:HE2	1.98	0.46
1:C:96:ASN:C	1:C:98:GLU:H	2.24	0.46
1:A:275:ILE:HG22	1:A:277:PHE:H	1.81	0.46
1:D:95:LYS:NZ	7:D:501:HOH:O	2.26	0.46
1:B:335:LEU:HD21	1:C:118:ILE:HD13	1.96	0.46
1:C:223:TRP:CH2	1:C:225:SER:HB3	2.51	0.46
1:A:210:ILE:HB	1:A:248:THR:HB	1.97	0.46
1:D:150:THR:O	1:D:243:ARG:NH2	2.47	0.46
1:C:99:ILE:HG13	1:C:102:ARG:NH1	2.31	0.46
1:B:197:VAL:O	1:B:201:SER:OG	2.25	0.45
1:B:218:ASP:OD1	1:B:219:THR:N	2.48	0.45
1:A:194:GLN:NE2	7:A:501:HOH:O	2.33	0.45
1:D:275:ILE:HG22	1:D:277:PHE:H	1.82	0.45
1:C:161:LYS:O	1:C:165:THR:OG1	2.32	0.45
1:D:161:LYS:O	1:D:165:THR:OG1	2.32	0.45
1:D:214:LYS:HB2	1:D:220:GLN:HB2	1.99	0.45
1:C:212:THR:HG23	1:C:222:ILE:HG12	1.99	0.45
1:C:263:THR:O	1:C:267:LEU:HG	2.17	0.45
1:B:117:LEU:HD23	1:B:117:LEU:HA	1.88	0.44
1:A:138:CYS:HB3	1:A:259:LEU:HD22	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:85:MET:HE2	1:A:196:GLY:CA	2.47	0.43
1:A:82:VAL:HG12	1:A:86:MET:HE2	2.01	0.43
1:A:140:LYS:HA	1:A:259:LEU:HD13	2.01	0.43
1:C:165:THR:HG21	1:C:188:THR:HG22	2.01	0.43
1:A:108:ALA:HB1	1:A:149:ASP:HB3	2.01	0.42
1:C:160:VAL:HG22	1:C:232:VAL:HG11	2.00	0.42
1:A:261:LEU:HD12	1:A:261:LEU:HA	1.86	0.42
1:A:211:VAL:HB	1:A:223:TRP:HB3	2.02	0.42
1:A:278:PRO:HB2	1:A:280:TYR:CE1	2.55	0.41
1:D:104:LEU:HD13	1:D:147:VAL:HG21	2.02	0.41
1:A:261:LEU:HD21	1:A:283:SER:HA	2.02	0.41
1:A:220:GLN:NE2	1:A:235:ASP:OD2	2.43	0.41
1:B:264:ILE:HD13	1:B:264:ILE:HA	1.88	0.41
1:B:265:LYS:NZ	1:B:334:GLU:OE1	2.43	0.41
1:D:165:THR:HG22	1:D:188:THR:HG23	2.02	0.41
1:D:211:VAL:HB	1:D:223:TRP:HB3	2.03	0.41
1:C:94:TYR:CG	1:C:99:ILE:HD11	2.56	0.41
1:B:138:CYS:SG	1:B:264:ILE:HG13	2.61	0.40
1:C:143:ASN:ND2	1:C:251:LEU:O	2.53	0.40
1:C:154:MET:C	1:C:215:HIS:HB2	2.46	0.40
1:D:86:MET:HE2	1:D:86:MET:HA	2.03	0.40
1:C:108:ALA:HB1	1:C:149:ASP:HB3	2.03	0.40
1:C:143:ASN:OD1	1:C:259:LEU:HD11	2.22	0.40
1:C:208:LYS:HE2	1:C:224:GLU:HB3	2.02	0.40
1:C:143:ASN:O	1:C:144:LEU:HD23	2.22	0.40
1:B:135:LYS:HB3	1:B:333:TRP:CH2	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	220/236 (93%)	210 (96%)	10 (4%)	0	100	100
1	B	221/236 (94%)	209 (95%)	11 (5%)	1 (0%)	24	55
1	C	205/236 (87%)	193 (94%)	10 (5%)	2 (1%)	12	38
1	D	204/236 (86%)	195 (96%)	9 (4%)	0	100	100
All	All	850/944 (90%)	807 (95%)	40 (5%)	3 (0%)	30	60

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	286	THR
1	B	96	ASN
1	C	97	LYS

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	181/207 (87%)	179 (99%)	2 (1%)	65	87
1	B	177/207 (86%)	173 (98%)	4 (2%)	44	78
1	C	158/207 (76%)	156 (99%)	2 (1%)	61	86
1	D	164/207 (79%)	163 (99%)	1 (1%)	78	92
All	All	680/828 (82%)	671 (99%)	9 (1%)	63	86

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	67[A]	HIS
1	B	67[B]	HIS
1	B	184	ASP
1	B	240	THR
1	A	109	SER
1	A	116	ARG
1	C	231	SER
1	C	240	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	286	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	79	GLN
1	A	146	HIS
1	A	162	ASN
1	C	107	ASN
1	D	96	ASN
1	D	143	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 33 ligands modelled in this entry, 12 are monoatomic - leaving 21 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	SO4	B	406	-	4,4,4	0.24	0	6,6,6	0.07	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	ZUY	C	401	-	27,27,27	1.62	3 (11%)	35,38,38	2.50	13 (37%)
5	SO4	B	410	-	4,4,4	0.23	0	6,6,6	0.09	0
4	GOL	D	402	-	5,5,5	0.91	0	5,5,5	1.15	0
3	ZUY	A	402	-	27,27,27	1.62	3 (11%)	35,38,38	2.31	10 (28%)
5	SO4	B	409	-	4,4,4	0.23	0	6,6,6	0.08	0
5	SO4	D	409	-	4,4,4	0.24	0	6,6,6	0.07	0
5	SO4	A	409	-	4,4,4	0.24	0	6,6,6	0.08	0
5	SO4	C	402	-	4,4,4	0.23	0	6,6,6	0.07	0
4	GOL	B	403	-	5,5,5	0.94	0	5,5,5	1.05	0
5	SO4	C	403	-	4,4,4	0.24	0	6,6,6	0.07	0
5	SO4	B	408	-	4,4,4	0.23	0	6,6,6	0.09	0
4	GOL	A	404	-	5,5,5	0.95	0	5,5,5	1.04	0
5	SO4	B	407	-	4,4,4	0.24	0	6,6,6	0.08	0
5	SO4	A	408	-	4,4,4	0.23	0	6,6,6	0.08	0
5	SO4	A	410	-	4,4,4	0.24	0	6,6,6	0.11	0
5	SO4	D	408	-	4,4,4	0.23	0	6,6,6	0.07	0
5	SO4	D	410	-	4,4,4	0.24	0	6,6,6	0.09	0
3	ZUY	D	401	-	27,27,27	1.63	4 (14%)	35,38,38	2.40	11 (31%)
3	ZUY	B	402	-	27,27,27	1.60	3 (11%)	35,38,38	2.29	10 (28%)
4	GOL	A	403	-	5,5,5	0.96	0	5,5,5	1.05	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	A	404	-	-	2/4/4/4	-
3	ZUY	C	401	-	-	5/8/9/9	0/3/3/3
4	GOL	B	403	-	-	1/4/4/4	-
4	GOL	D	402	-	-	0/4/4/4	-
3	ZUY	D	401	-	-	4/8/9/9	0/3/3/3
3	ZUY	B	402	-	-	1/8/9/9	0/3/3/3
3	ZUY	A	402	-	-	1/8/9/9	0/3/3/3
4	GOL	A	403	-	-	0/4/4/4	-

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	401	ZUY	C02-N01	4.51	1.45	1.34
3	B	402	ZUY	C02-N01	4.48	1.45	1.34

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	402	ZUY	C02-N01	4.47	1.45	1.34
3	C	401	ZUY	C02-N01	4.42	1.45	1.34
3	C	401	ZUY	C05-S06	4.24	1.82	1.75
3	D	401	ZUY	C05-S06	4.21	1.82	1.75
3	A	402	ZUY	C05-S06	4.17	1.82	1.75
3	B	402	ZUY	C05-S06	4.11	1.82	1.75
3	C	401	ZUY	C07-S06	3.37	1.82	1.77
3	D	401	ZUY	C07-S06	3.21	1.82	1.77
3	A	402	ZUY	C07-S06	3.13	1.82	1.77
3	B	402	ZUY	C07-S06	3.04	1.82	1.77
3	D	401	ZUY	C05-N16	-2.03	1.33	1.37

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	401	ZUY	C03-C22-N23	-6.37	117.94	126.72
3	C	401	ZUY	N23-C22-N16	6.12	135.08	125.09
3	D	401	ZUY	C03-C22-N23	-6.09	118.34	126.72
3	D	401	ZUY	N23-C22-N16	5.91	134.73	125.09
3	A	402	ZUY	N16-C05-N04	-5.58	108.37	113.97
3	B	402	ZUY	C03-C22-N23	-5.51	119.12	126.72
3	A	402	ZUY	C03-C22-N23	-5.50	119.15	126.72
3	B	402	ZUY	N16-C05-N04	-5.28	108.67	113.97
3	B	402	ZUY	N23-C22-N16	5.13	133.46	125.09
3	A	402	ZUY	N23-C22-N16	5.10	133.41	125.09
3	C	401	ZUY	N25-C24-N23	-4.95	121.09	128.58
3	A	402	ZUY	N25-C24-N23	-4.88	121.19	128.58
3	B	402	ZUY	N25-C24-N23	-4.87	121.20	128.58
3	D	401	ZUY	N25-C24-N23	-4.84	121.25	128.58
3	C	401	ZUY	N16-C05-N04	-4.83	109.13	113.97
3	D	401	ZUY	N16-C05-N04	-4.80	109.15	113.97
3	C	401	ZUY	C24-N23-C22	4.23	122.15	111.83
3	D	401	ZUY	C24-N23-C22	4.01	121.62	111.83
3	B	402	ZUY	C24-N23-C22	3.85	121.23	111.83
3	A	402	ZUY	C24-N23-C22	3.83	121.19	111.83
3	A	402	ZUY	C22-C03-N04	-3.67	107.16	110.91
3	B	402	ZUY	C22-C03-N04	-3.55	107.28	110.91
3	C	401	ZUY	C22-C03-N04	-3.29	107.54	110.91
3	D	401	ZUY	C22-C03-N04	-3.26	107.58	110.91
3	C	401	ZUY	C14-C07-S06	3.26	123.03	119.00
3	A	402	ZUY	C02-C03-N04	3.11	134.81	131.72
3	B	402	ZUY	C02-C03-N04	3.03	134.73	131.72

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	401	ZUY	C17-N16-C22	2.74	129.78	125.00
3	C	401	ZUY	C08-C10-C11	-2.70	119.56	122.13
3	C	401	ZUY	C17-N16-C22	2.66	129.65	125.00
3	A	402	ZUY	C22-N16-C05	2.47	108.37	105.93
3	C	401	ZUY	C02-C03-N04	2.42	134.12	131.72
3	D	401	ZUY	C14-C07-S06	2.39	121.95	119.00
3	C	401	ZUY	C10-C08-C07	2.37	120.87	118.64
3	B	402	ZUY	C22-N16-C05	2.34	108.25	105.93
3	D	401	ZUY	C02-C03-N04	2.30	134.01	131.72
3	D	401	ZUY	C08-C10-C11	-2.30	119.95	122.13
3	B	402	ZUY	C08-C10-C11	-2.29	119.95	122.13
3	D	401	ZUY	C22-N16-C05	2.28	108.19	105.93
3	C	401	ZUY	C09-C08-C07	-2.28	119.17	121.99
3	A	402	ZUY	C08-C10-C11	-2.15	120.09	122.13
3	A	402	ZUY	C14-C13-C11	-2.15	120.09	122.13
3	B	402	ZUY	C14-C13-C11	-2.14	120.10	122.13
3	C	401	ZUY	C22-N16-C05	2.12	108.03	105.93

There are no chirality outliers.

All (14) torsion outliers are listed below:

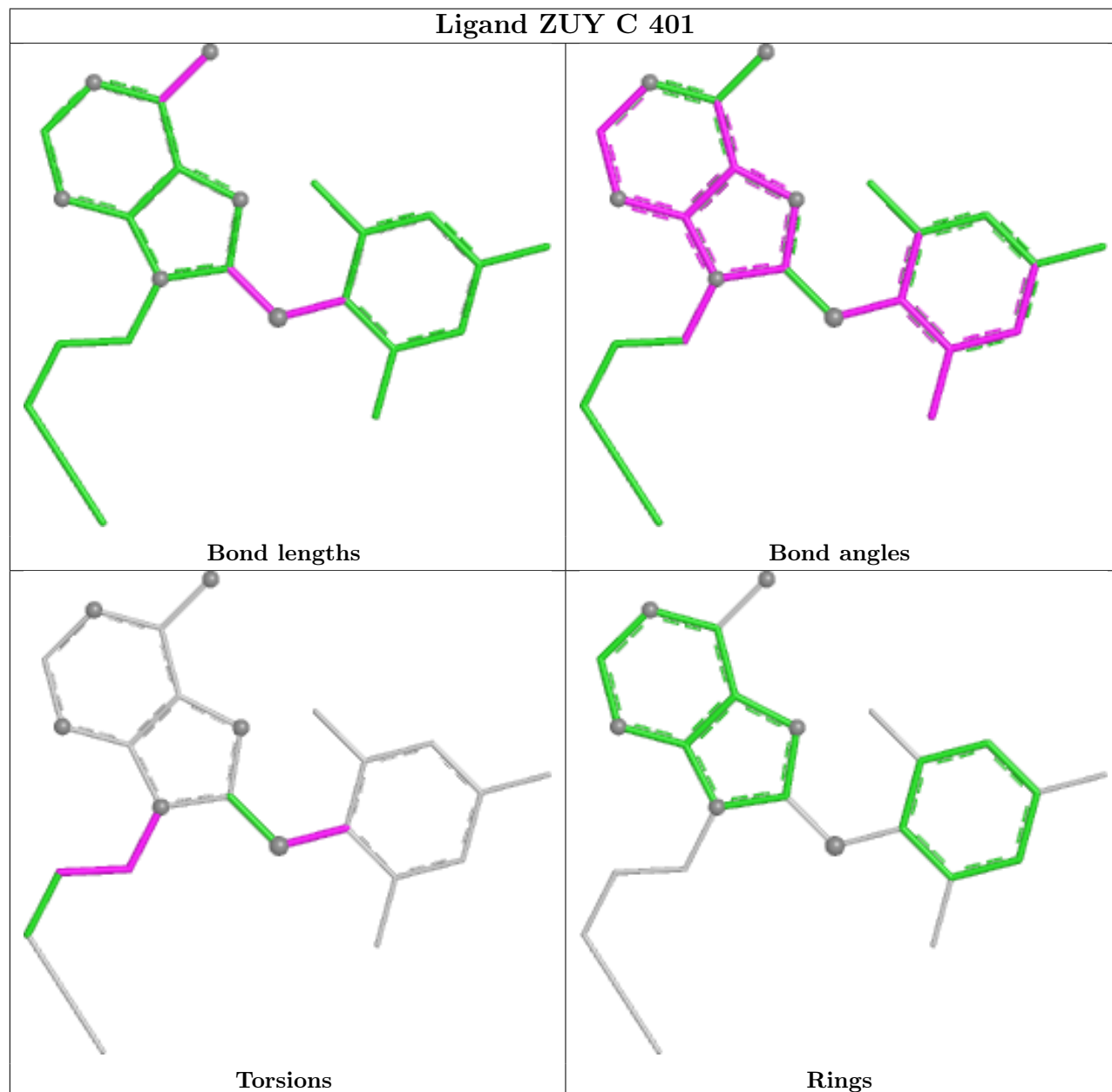
Mol	Chain	Res	Type	Atoms
3	C	401	ZUY	C18-C17-N16-C22
3	C	401	ZUY	C18-C17-N16-C05
3	C	401	ZUY	C14-C07-S06-C05
3	D	401	ZUY	C18-C17-N16-C22
3	D	401	ZUY	C18-C17-N16-C05
4	A	404	GOL	O1-C1-C2-C3
3	C	401	ZUY	N16-C17-C18-C19
3	B	402	ZUY	C17-C18-C19-C20
3	A	402	ZUY	C17-C18-C19-C20
3	C	401	ZUY	C08-C07-S06-C05
3	D	401	ZUY	C14-C07-S06-C05
4	A	404	GOL	O1-C1-C2-O2
4	B	403	GOL	O1-C1-C2-C3
3	D	401	ZUY	N16-C17-C18-C19

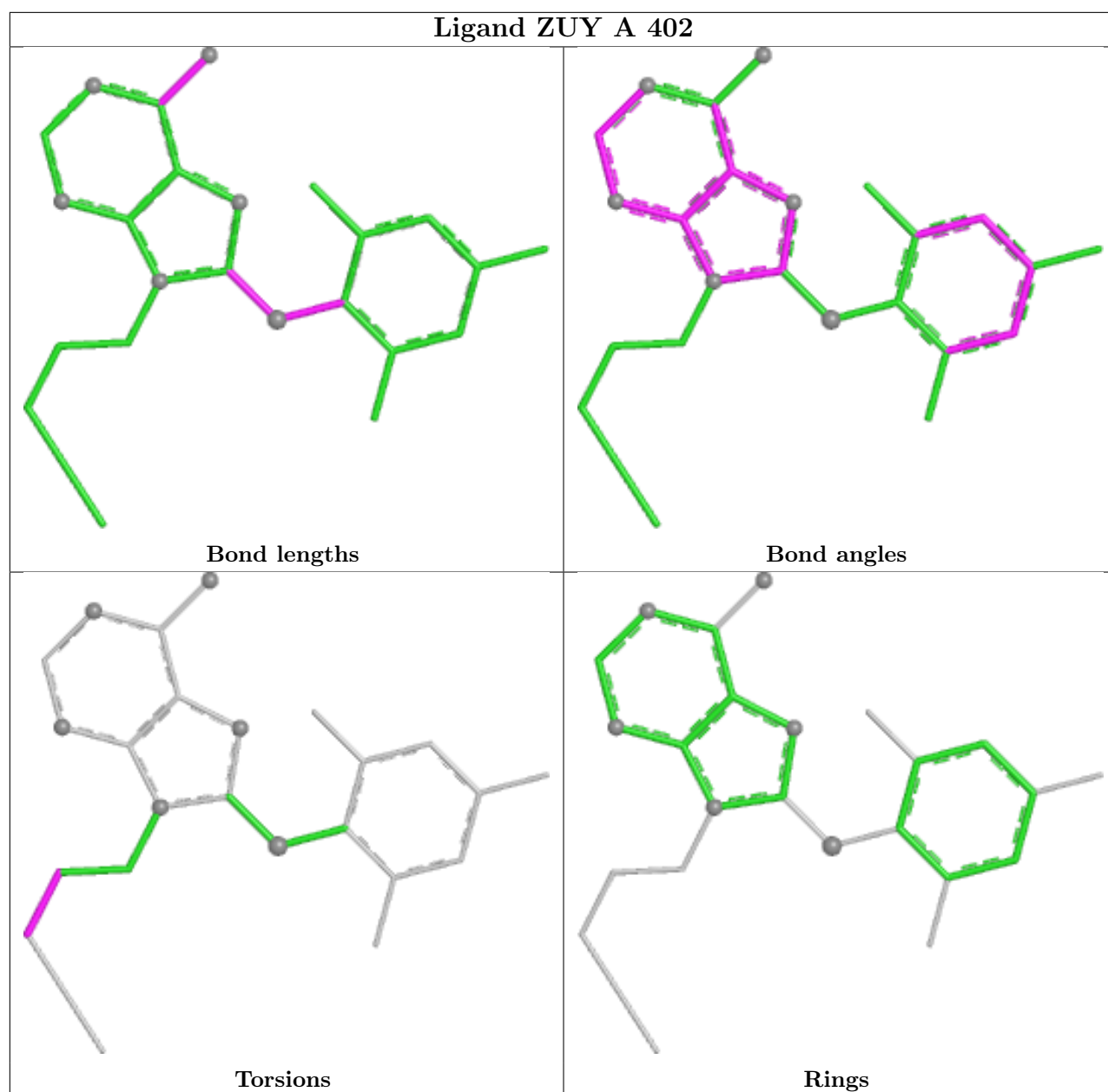
There are no ring outliers.

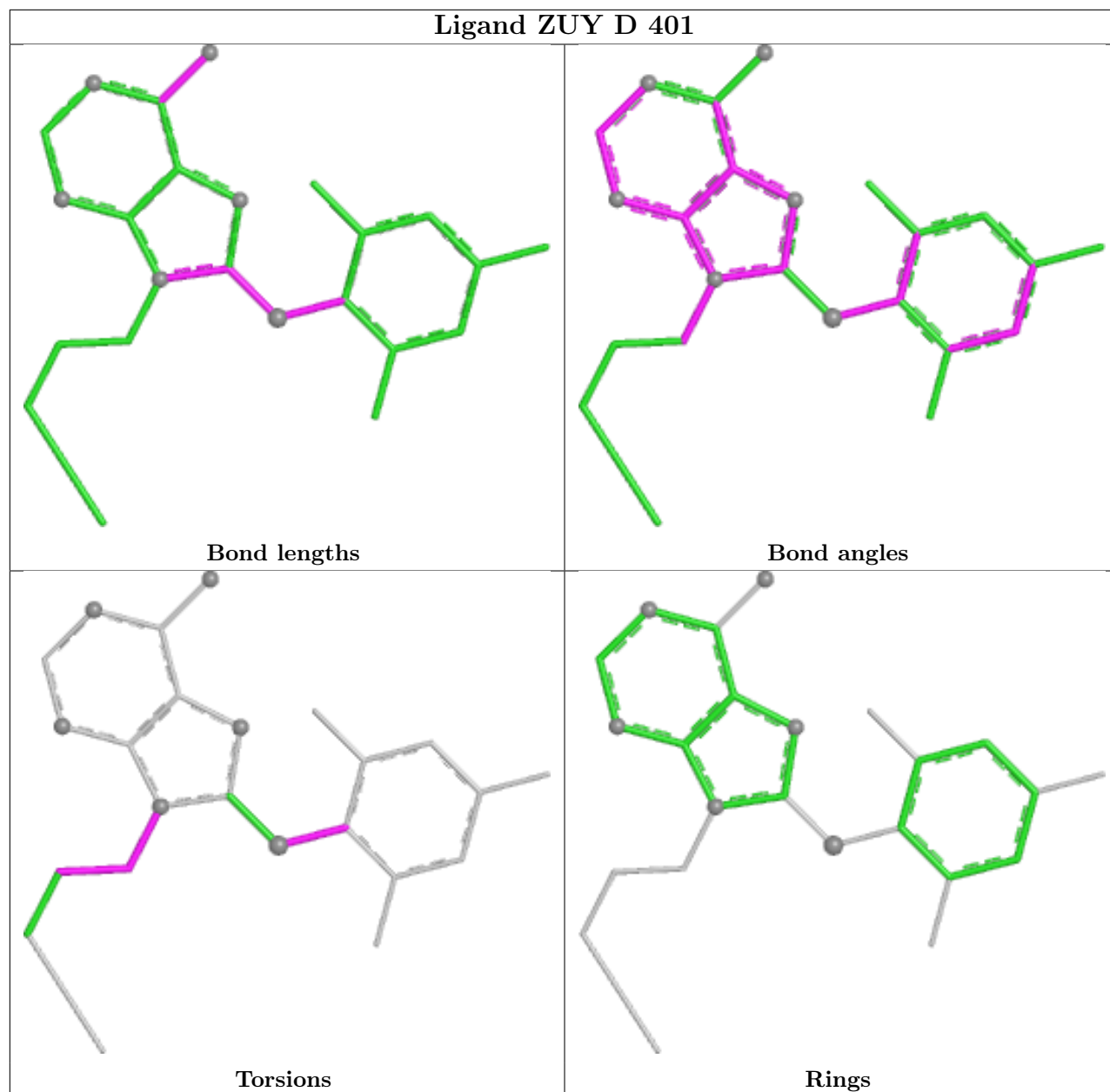
No monomer is involved in short contacts.

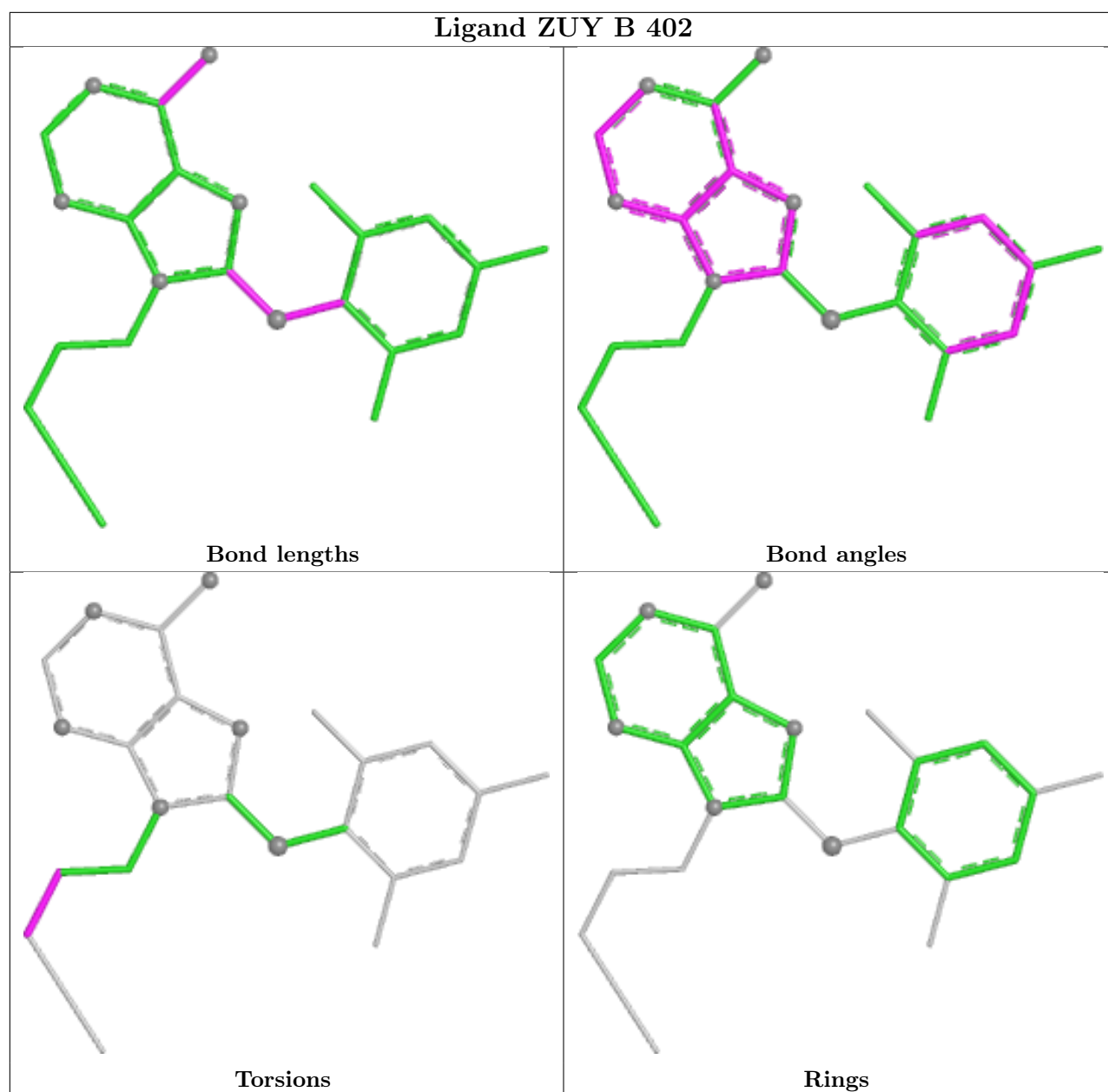
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.









5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å ²)	Q<0.9
1	A	226/236 (95%)	0.45	14 (6%)	26 20	58, 81, 115, 140	0
1	B	226/236 (95%)	0.43	16 (7%)	22 16	54, 74, 114, 126	1 (0%)
1	C	209/236 (88%)	0.60	15 (7%)	21 16	56, 81, 111, 130	0
1	D	210/236 (88%)	0.36	15 (7%)	22 16	54, 78, 115, 160	0
All	All	871/944 (92%)	0.46	60 (6%)	23 16	54, 79, 115, 160	1 (0%)

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	176	ASN	5.3
1	B	67[A]	HIS	4.8
1	C	233	ILE	4.3
1	C	337	ASN	3.9
1	B	98	GLU	3.9
1	C	186	GLN	3.8
1	D	172	SER	3.6
1	A	330	VAL	3.5
1	A	179	THR	3.4
1	C	257	ASP	3.3
1	C	258	TYR	3.3
1	C	327	GLY	3.2
1	B	337	ASN	3.2
1	A	175	LEU	3.2
1	C	250	VAL	3.1
1	D	169	SER	3.1
1	C	262	ASP	3.1
1	A	178	MET	3.0
1	D	76	PHE	3.0
1	D	171	THR	2.9
1	B	178	MET	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	76	PHE	2.9
1	B	179	THR	2.7
1	A	184	ASP	2.7
1	B	180	GLU	2.6
1	D	286	THR	2.6
1	B	335	LEU	2.6
1	A	98	GLU	2.6
1	A	286	THR	2.5
1	C	124	ASN	2.5
1	D	170	GLY	2.5
1	D	186	GLN	2.5
1	B	69	LEU	2.5
1	C	325	GLY	2.5
1	A	233	ILE	2.4
1	A	257	ASP	2.4
1	B	273	GLN	2.4
1	A	337	ASN	2.4
1	C	259	LEU	2.3
1	D	258	TYR	2.3
1	D	329	THR	2.3
1	A	276	ASN	2.3
1	D	173	GLU	2.3
1	B	274	PHE	2.2
1	A	185	GLY	2.2
1	D	324	GLY	2.2
1	B	94	TYR	2.1
1	D	328	LYS	2.1
1	B	185	GLY	2.1
1	C	77	ALA	2.1
1	A	223	TRP	2.1
1	C	223	TRP	2.1
1	D	197	VAL	2.1
1	B	329	THR	2.1
1	B	258	TYR	2.1
1	D	77	ALA	2.0
1	D	274	PHE	2.0
1	B	144	LEU	2.0
1	B	176	ASN	2.0
1	C	96	ASN	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

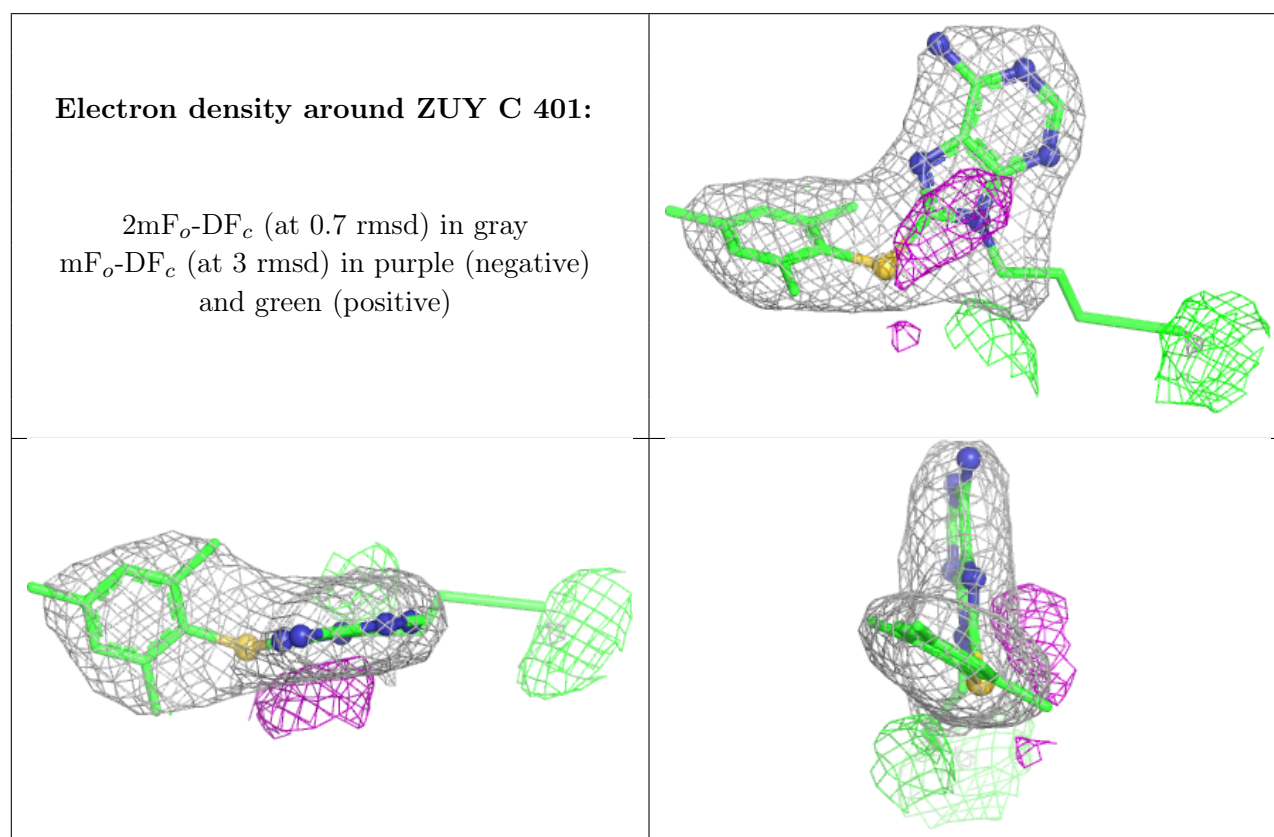
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	GOL	A	404	6/6	0.43	0.20	89,100,107,118	0
5	SO4	A	409	5/5	0.61	0.12	125,133,151,162	0
4	GOL	B	403	6/6	0.62	0.21	76,84,95,101	0
5	SO4	A	410	5/5	0.66	0.09	126,126,150,253	0
4	GOL	A	403	6/6	0.67	0.24	78,95,112,114	0
5	SO4	B	407	5/5	0.67	0.09	121,124,150,154	0
5	SO4	D	410	5/5	0.68	0.11	81,86,149,180	0
6	MN	D	403	1/1	0.68	0.42	204,204,204,204	0
5	SO4	D	409	5/5	0.72	0.08	138,147,175,176	0
5	SO4	B	406	5/5	0.73	0.08	126,132,150,154	0
5	SO4	B	410	5/5	0.74	0.28	92,123,124,141	0
5	SO4	D	408	5/5	0.75	0.10	118,119,135,156	0
2	MG	B	405	1/1	0.81	0.17	75,75,75,75	0
5	SO4	A	408	5/5	0.82	0.08	112,118,134,138	0
2	MG	D	407	1/1	0.83	0.24	93,93,93,93	0
5	SO4	B	409	5/5	0.83	0.21	98,106,135,139	0
5	SO4	C	403	5/5	0.86	0.14	95,106,134,139	0
2	MG	D	404	1/1	0.87	0.12	89,89,89,89	0
4	GOL	D	402	6/6	0.87	0.13	89,99,102,106	0
2	MG	A	406	1/1	0.89	0.15	88,88,88,88	0
5	SO4	C	402	5/5	0.90	0.13	99,99,115,121	0
2	MG	D	405	1/1	0.91	0.25	88,88,88,88	0
2	MG	A	407	1/1	0.91	0.10	84,84,84,84	0
3	ZUY	C	401	25/25	0.91	0.17	58,72,104,113	0
2	MG	B	404	1/1	0.91	0.13	74,74,74,74	0
5	SO4	B	408	5/5	0.92	0.08	73,80,94,104	0
3	ZUY	D	401	25/25	0.94	0.15	56,73,97,116	0

Continued on next page...

Continued from previous page...

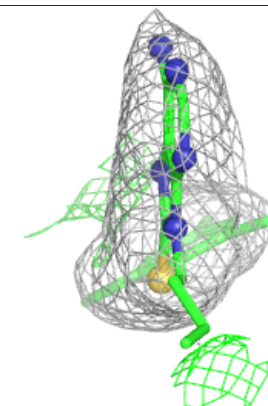
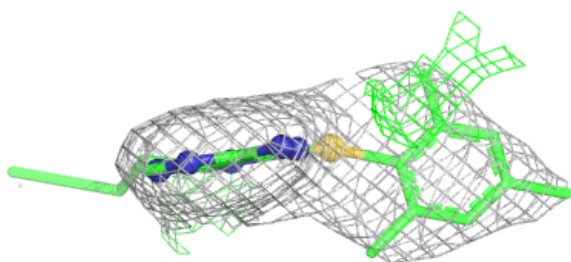
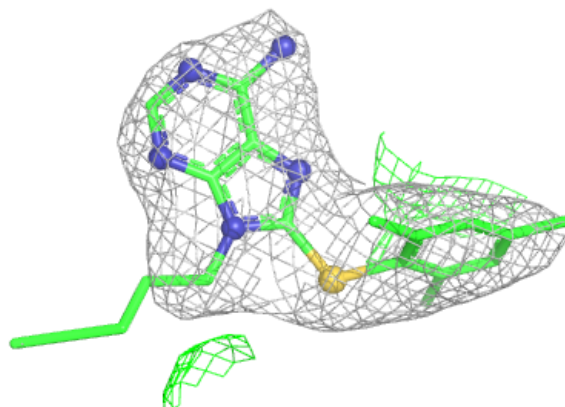
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MG	D	406	1/1	0.96	0.22	76,76,76,76	0
3	ZUY	A	402	25/25	0.96	0.11	55,66,72,75	0
3	ZUY	B	402	25/25	0.97	0.08	45,59,66,69	0
2	MG	B	401	1/1	0.97	0.07	93,93,93,93	0
2	MG	A	405	1/1	0.98	0.07	80,80,80,80	0
2	MG	A	401	1/1	0.99	0.04	56,56,56,56	0

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



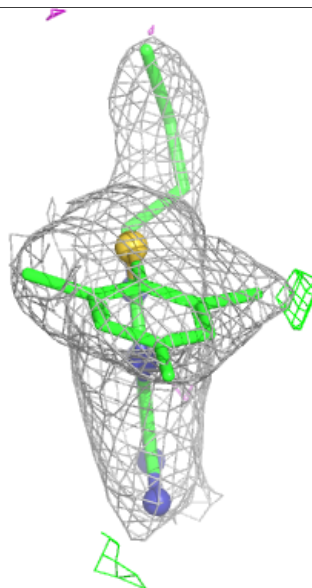
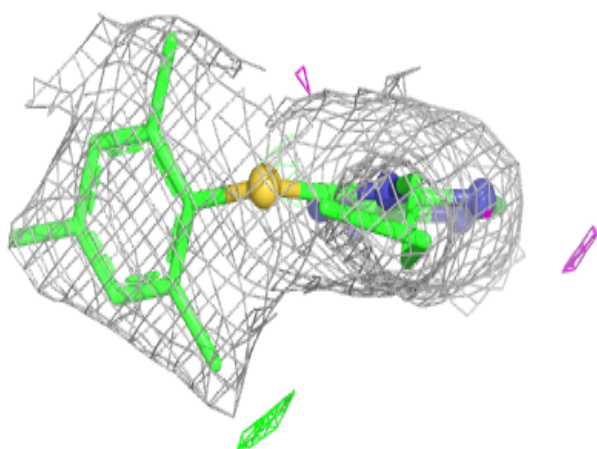
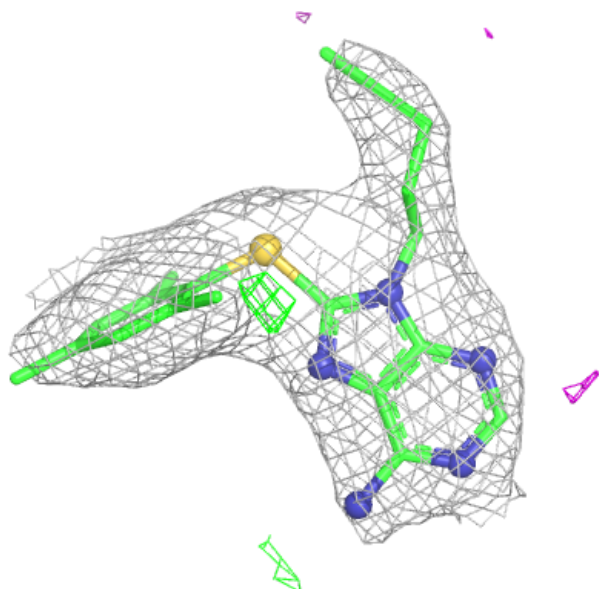
Electron density around ZUY D 401:

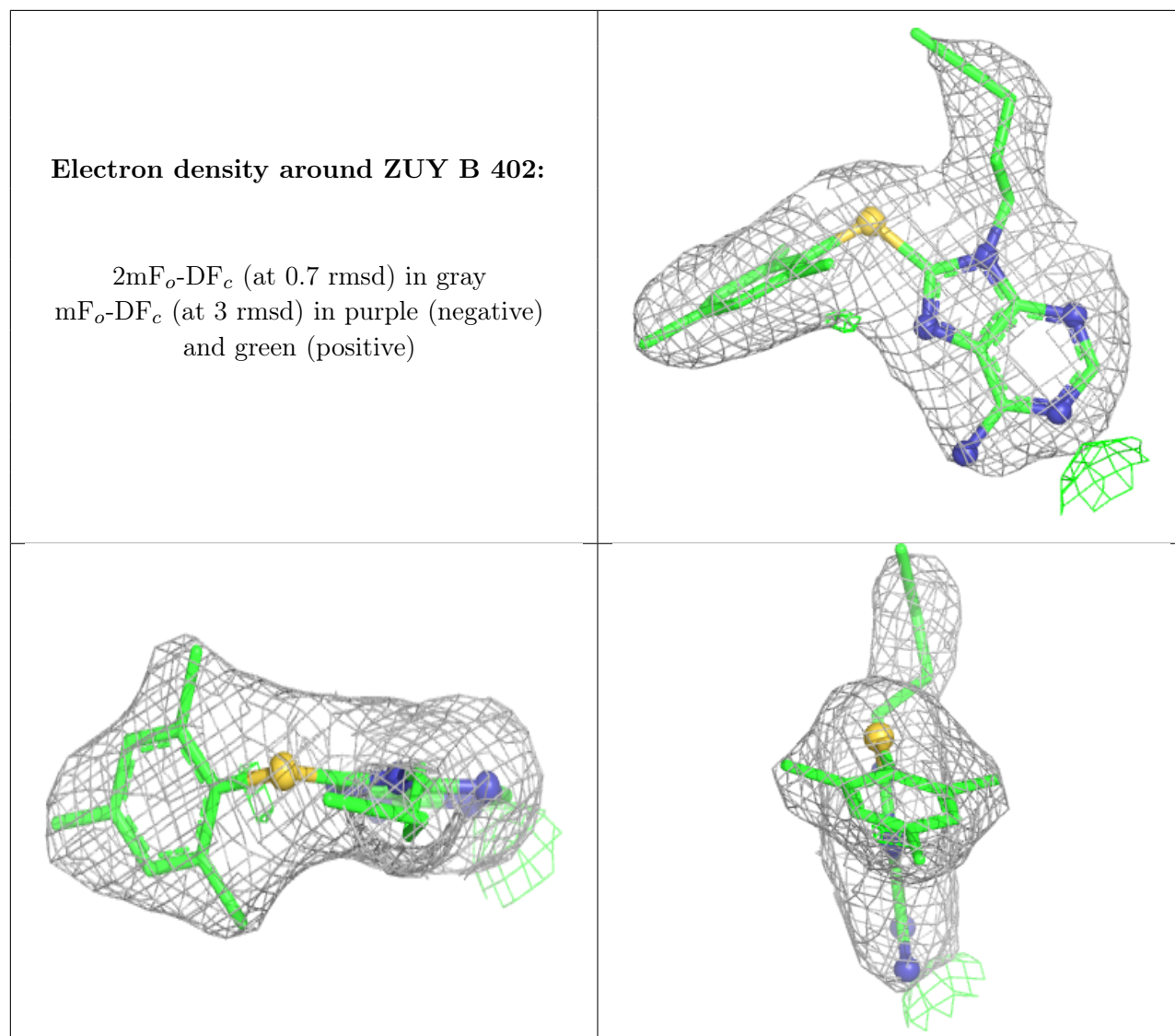
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ZUY A 402:

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





6.5 Other polymers [i](#)

There are no such residues in this entry.