



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 12:18 PM UTC

PDB ID : 8CN1 / pdb_00008cn1
Title : hDLG1-PDZ1 in complex with a TAX1 peptide from HTLV-1
Authors : Maseko, S.; Sogues, A.; Volkov, A.; Remaut, H.; Twizere, J.C.
Deposited on : 2023-02-21
Resolution : 2.09 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

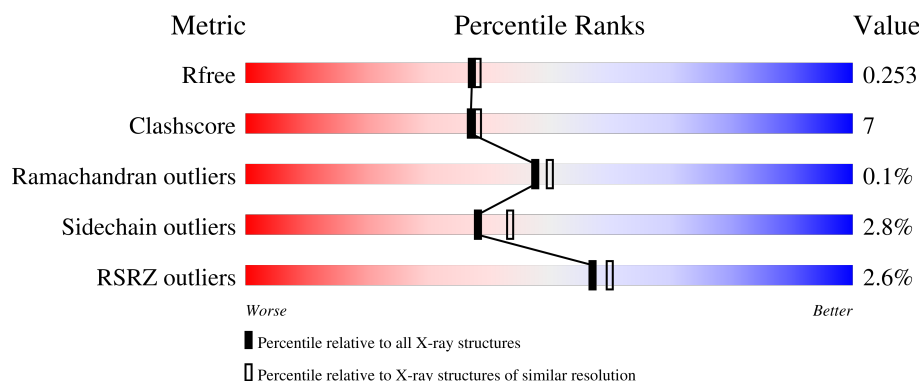
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.09 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	116	4% 74% • • 22%
1	B	116	72% 6% • 20%
1	C	116	2% 71% 7% 22%
1	D	116	• 72% 9% 20%
1	E	116	71% 7% • 21%

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Mol	Chain	Length	Quality of chain
1	F	116	
1	G	116	
1	H	116	
1	I	116	
1	J	116	
1	K	116	
1	L	116	
2	N	4	
2	O	4	
2	P	4	
2	Q	4	
2	R	4	
2	T	4	
2	U	4	
2	V	4	
2	W	4	
2	X	4	
2	Y	4	
2	Z	4	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9661 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 Disks large homolog 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	93	Total	C	N	O	S	0	0	0
			714	440	131	142	1			
1	A	91	Total	C	N	O	S	0	0	0
			676	415	122	138	1			
1	C	90	Total	C	N	O	S	0	0	0
			681	420	125	135	1			
1	D	93	Total	C	N	O	S	0	0	0
			710	437	130	142	1			
1	E	92	Total	C	N	O	S	0	0	0
			701	432	129	139	1			
1	F	89	Total	C	N	O	S	0	0	0
			677	419	124	133	1			
1	G	100	Total	C	N	O	S	0	0	0
			750	463	138	148	1			
1	H	101	Total	C	N	O	S	0	0	0
			750	461	133	155	1			
1	I	98	Total	C	N	O	S	0	0	0
			735	453	135	146	1			
1	J	99	Total	C	N	O	S	0	0	0
			733	451	137	144	1			
1	K	98	Total	C	N	O	S	0	0	0
			736	453	136	146	1			
1	L	98	Total	C	N	O	S	0	0	0
			727	448	130	148	1			

There are 276 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	GLY	-	expression tag	UNP Q12959
B	2	PRO	-	expression tag	UNP Q12959
B	3	LEU	-	expression tag	UNP Q12959
B	4	GLY	-	expression tag	UNP Q12959
B	5	SER	-	expression tag	UNP Q12959

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Chain	Residue	Modelled	Actual	Comment	Reference
B	6	GLU	-	expression tag	UNP Q12959
B	7	THR	-	expression tag	UNP Q12959
B	8	PRO	-	expression tag	UNP Q12959
B	9	THR	-	expression tag	UNP Q12959
B	10	TYR	-	expression tag	UNP Q12959
B	11	VAL	-	expression tag	UNP Q12959
B	12	ASN	-	expression tag	UNP Q12959
B	13	GLY	-	expression tag	UNP Q12959
B	14	THR	-	expression tag	UNP Q12959
B	15	ASP	-	expression tag	UNP Q12959
B	16	ALA	-	expression tag	UNP Q12959
B	110	PRO	-	expression tag	UNP Q12959
B	111	VAL	-	expression tag	UNP Q12959
B	112	SER	-	expression tag	UNP Q12959
B	113	GLU	-	expression tag	UNP Q12959
B	114	LYS	-	expression tag	UNP Q12959
B	115	ILE	-	expression tag	UNP Q12959
B	116	MET	-	expression tag	UNP Q12959
A	203	GLY	-	expression tag	UNP Q12959
A	204	PRO	-	expression tag	UNP Q12959
A	205	LEU	-	expression tag	UNP Q12959
A	206	GLY	-	expression tag	UNP Q12959
A	207	SER	-	expression tag	UNP Q12959
A	208	GLU	-	expression tag	UNP Q12959
A	209	THR	-	expression tag	UNP Q12959
A	210	PRO	-	expression tag	UNP Q12959
A	211	THR	-	expression tag	UNP Q12959
A	212	TYR	-	expression tag	UNP Q12959
A	213	VAL	-	expression tag	UNP Q12959
A	214	ASN	-	expression tag	UNP Q12959
A	215	GLY	-	expression tag	UNP Q12959
A	216	THR	-	expression tag	UNP Q12959
A	217	ASP	-	expression tag	UNP Q12959
A	218	ALA	-	expression tag	UNP Q12959
A	312	PRO	-	expression tag	UNP Q12959
A	313	VAL	-	expression tag	UNP Q12959
A	314	SER	-	expression tag	UNP Q12959
A	315	GLU	-	expression tag	UNP Q12959
A	316	LYS	-	expression tag	UNP Q12959
A	317	ILE	-	expression tag	UNP Q12959
A	318	MET	-	expression tag	UNP Q12959
C	203	GLY	-	expression tag	UNP Q12959

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Chain	Residue	Modelled	Actual	Comment	Reference
C	204	PRO	-	expression tag	UNP Q12959
C	205	LEU	-	expression tag	UNP Q12959
C	206	GLY	-	expression tag	UNP Q12959
C	207	SER	-	expression tag	UNP Q12959
C	208	GLU	-	expression tag	UNP Q12959
C	209	THR	-	expression tag	UNP Q12959
C	210	PRO	-	expression tag	UNP Q12959
C	211	THR	-	expression tag	UNP Q12959
C	212	TYR	-	expression tag	UNP Q12959
C	213	VAL	-	expression tag	UNP Q12959
C	214	ASN	-	expression tag	UNP Q12959
C	215	GLY	-	expression tag	UNP Q12959
C	216	THR	-	expression tag	UNP Q12959
C	217	ASP	-	expression tag	UNP Q12959
C	218	ALA	-	expression tag	UNP Q12959
C	312	PRO	-	expression tag	UNP Q12959
C	313	VAL	-	expression tag	UNP Q12959
C	314	SER	-	expression tag	UNP Q12959
C	315	GLU	-	expression tag	UNP Q12959
C	316	LYS	-	expression tag	UNP Q12959
C	317	ILE	-	expression tag	UNP Q12959
C	318	MET	-	expression tag	UNP Q12959
D	203	GLY	-	expression tag	UNP Q12959
D	204	PRO	-	expression tag	UNP Q12959
D	205	LEU	-	expression tag	UNP Q12959
D	206	GLY	-	expression tag	UNP Q12959
D	207	SER	-	expression tag	UNP Q12959
D	208	GLU	-	expression tag	UNP Q12959
D	209	THR	-	expression tag	UNP Q12959
D	210	PRO	-	expression tag	UNP Q12959
D	211	THR	-	expression tag	UNP Q12959
D	212	TYR	-	expression tag	UNP Q12959
D	213	VAL	-	expression tag	UNP Q12959
D	214	ASN	-	expression tag	UNP Q12959
D	215	GLY	-	expression tag	UNP Q12959
D	216	THR	-	expression tag	UNP Q12959
D	217	ASP	-	expression tag	UNP Q12959
D	218	ALA	-	expression tag	UNP Q12959
D	312	PRO	-	expression tag	UNP Q12959
D	313	VAL	-	expression tag	UNP Q12959
D	314	SER	-	expression tag	UNP Q12959
D	315	GLU	-	expression tag	UNP Q12959

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Chain	Residue	Modelled	Actual	Comment	Reference
D	316	LYS	-	expression tag	UNP Q12959
D	317	ILE	-	expression tag	UNP Q12959
D	318	MET	-	expression tag	UNP Q12959
E	203	GLY	-	expression tag	UNP Q12959
E	204	PRO	-	expression tag	UNP Q12959
E	205	LEU	-	expression tag	UNP Q12959
E	206	GLY	-	expression tag	UNP Q12959
E	207	SER	-	expression tag	UNP Q12959
E	208	GLU	-	expression tag	UNP Q12959
E	209	THR	-	expression tag	UNP Q12959
E	210	PRO	-	expression tag	UNP Q12959
E	211	THR	-	expression tag	UNP Q12959
E	212	TYR	-	expression tag	UNP Q12959
E	213	VAL	-	expression tag	UNP Q12959
E	214	ASN	-	expression tag	UNP Q12959
E	215	GLY	-	expression tag	UNP Q12959
E	216	THR	-	expression tag	UNP Q12959
E	217	ASP	-	expression tag	UNP Q12959
E	218	ALA	-	expression tag	UNP Q12959
E	312	PRO	-	expression tag	UNP Q12959
E	313	VAL	-	expression tag	UNP Q12959
E	314	SER	-	expression tag	UNP Q12959
E	315	GLU	-	expression tag	UNP Q12959
E	316	LYS	-	expression tag	UNP Q12959
E	317	ILE	-	expression tag	UNP Q12959
E	318	MET	-	expression tag	UNP Q12959
F	203	GLY	-	expression tag	UNP Q12959
F	204	PRO	-	expression tag	UNP Q12959
F	205	LEU	-	expression tag	UNP Q12959
F	206	GLY	-	expression tag	UNP Q12959
F	207	SER	-	expression tag	UNP Q12959
F	208	GLU	-	expression tag	UNP Q12959
F	209	THR	-	expression tag	UNP Q12959
F	210	PRO	-	expression tag	UNP Q12959
F	211	THR	-	expression tag	UNP Q12959
F	212	TYR	-	expression tag	UNP Q12959
F	213	VAL	-	expression tag	UNP Q12959
F	214	ASN	-	expression tag	UNP Q12959
F	215	GLY	-	expression tag	UNP Q12959
F	216	THR	-	expression tag	UNP Q12959
F	217	ASP	-	expression tag	UNP Q12959
F	218	ALA	-	expression tag	UNP Q12959

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Chain	Residue	Modelled	Actual	Comment	Reference
F	312	PRO	-	expression tag	UNP Q12959
F	313	VAL	-	expression tag	UNP Q12959
F	314	SER	-	expression tag	UNP Q12959
F	315	GLU	-	expression tag	UNP Q12959
F	316	LYS	-	expression tag	UNP Q12959
F	317	ILE	-	expression tag	UNP Q12959
F	318	MET	-	expression tag	UNP Q12959
G	203	GLY	-	expression tag	UNP Q12959
G	204	PRO	-	expression tag	UNP Q12959
G	205	LEU	-	expression tag	UNP Q12959
G	206	GLY	-	expression tag	UNP Q12959
G	207	SER	-	expression tag	UNP Q12959
G	208	GLU	-	expression tag	UNP Q12959
G	209	THR	-	expression tag	UNP Q12959
G	210	PRO	-	expression tag	UNP Q12959
G	211	THR	-	expression tag	UNP Q12959
G	212	TYR	-	expression tag	UNP Q12959
G	213	VAL	-	expression tag	UNP Q12959
G	214	ASN	-	expression tag	UNP Q12959
G	215	GLY	-	expression tag	UNP Q12959
G	216	THR	-	expression tag	UNP Q12959
G	217	ASP	-	expression tag	UNP Q12959
G	218	ALA	-	expression tag	UNP Q12959
G	312	PRO	-	expression tag	UNP Q12959
G	313	VAL	-	expression tag	UNP Q12959
G	314	SER	-	expression tag	UNP Q12959
G	315	GLU	-	expression tag	UNP Q12959
G	316	LYS	-	expression tag	UNP Q12959
G	317	ILE	-	expression tag	UNP Q12959
G	318	MET	-	expression tag	UNP Q12959
H	203	GLY	-	expression tag	UNP Q12959
H	204	PRO	-	expression tag	UNP Q12959
H	205	LEU	-	expression tag	UNP Q12959
H	206	GLY	-	expression tag	UNP Q12959
H	207	SER	-	expression tag	UNP Q12959
H	208	GLU	-	expression tag	UNP Q12959
H	209	THR	-	expression tag	UNP Q12959
H	210	PRO	-	expression tag	UNP Q12959
H	211	THR	-	expression tag	UNP Q12959
H	212	TYR	-	expression tag	UNP Q12959
H	213	VAL	-	expression tag	UNP Q12959
H	214	ASN	-	expression tag	UNP Q12959

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Chain	Residue	Modelled	Actual	Comment	Reference
H	215	GLY	-	expression tag	UNP Q12959
H	216	THR	-	expression tag	UNP Q12959
H	217	ASP	-	expression tag	UNP Q12959
H	218	ALA	-	expression tag	UNP Q12959
H	312	PRO	-	expression tag	UNP Q12959
H	313	VAL	-	expression tag	UNP Q12959
H	314	SER	-	expression tag	UNP Q12959
H	315	GLU	-	expression tag	UNP Q12959
H	316	LYS	-	expression tag	UNP Q12959
H	317	ILE	-	expression tag	UNP Q12959
H	318	MET	-	expression tag	UNP Q12959
I	203	GLY	-	expression tag	UNP Q12959
I	204	PRO	-	expression tag	UNP Q12959
I	205	LEU	-	expression tag	UNP Q12959
I	206	GLY	-	expression tag	UNP Q12959
I	207	SER	-	expression tag	UNP Q12959
I	208	GLU	-	expression tag	UNP Q12959
I	209	THR	-	expression tag	UNP Q12959
I	210	PRO	-	expression tag	UNP Q12959
I	211	THR	-	expression tag	UNP Q12959
I	212	TYR	-	expression tag	UNP Q12959
I	213	VAL	-	expression tag	UNP Q12959
I	214	ASN	-	expression tag	UNP Q12959
I	215	GLY	-	expression tag	UNP Q12959
I	216	THR	-	expression tag	UNP Q12959
I	217	ASP	-	expression tag	UNP Q12959
I	218	ALA	-	expression tag	UNP Q12959
I	312	PRO	-	expression tag	UNP Q12959
I	313	VAL	-	expression tag	UNP Q12959
I	314	SER	-	expression tag	UNP Q12959
I	315	GLU	-	expression tag	UNP Q12959
I	316	LYS	-	expression tag	UNP Q12959
I	317	ILE	-	expression tag	UNP Q12959
I	318	MET	-	expression tag	UNP Q12959
J	203	GLY	-	expression tag	UNP Q12959
J	204	PRO	-	expression tag	UNP Q12959
J	205	LEU	-	expression tag	UNP Q12959
J	206	GLY	-	expression tag	UNP Q12959
J	207	SER	-	expression tag	UNP Q12959
J	208	GLU	-	expression tag	UNP Q12959
J	209	THR	-	expression tag	UNP Q12959
J	210	PRO	-	expression tag	UNP Q12959

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Chain	Residue	Modelled	Actual	Comment	Reference
J	211	THR	-	expression tag	UNP Q12959
J	212	TYR	-	expression tag	UNP Q12959
J	213	VAL	-	expression tag	UNP Q12959
J	214	ASN	-	expression tag	UNP Q12959
J	215	GLY	-	expression tag	UNP Q12959
J	216	THR	-	expression tag	UNP Q12959
J	217	ASP	-	expression tag	UNP Q12959
J	218	ALA	-	expression tag	UNP Q12959
J	312	PRO	-	expression tag	UNP Q12959
J	313	VAL	-	expression tag	UNP Q12959
J	314	SER	-	expression tag	UNP Q12959
J	315	GLU	-	expression tag	UNP Q12959
J	316	LYS	-	expression tag	UNP Q12959
J	317	ILE	-	expression tag	UNP Q12959
J	318	MET	-	expression tag	UNP Q12959
K	203	GLY	-	expression tag	UNP Q12959
K	204	PRO	-	expression tag	UNP Q12959
K	205	LEU	-	expression tag	UNP Q12959
K	206	GLY	-	expression tag	UNP Q12959
K	207	SER	-	expression tag	UNP Q12959
K	208	GLU	-	expression tag	UNP Q12959
K	209	THR	-	expression tag	UNP Q12959
K	210	PRO	-	expression tag	UNP Q12959
K	211	THR	-	expression tag	UNP Q12959
K	212	TYR	-	expression tag	UNP Q12959
K	213	VAL	-	expression tag	UNP Q12959
K	214	ASN	-	expression tag	UNP Q12959
K	215	GLY	-	expression tag	UNP Q12959
K	216	THR	-	expression tag	UNP Q12959
K	217	ASP	-	expression tag	UNP Q12959
K	218	ALA	-	expression tag	UNP Q12959
K	312	PRO	-	expression tag	UNP Q12959
K	313	VAL	-	expression tag	UNP Q12959
K	314	SER	-	expression tag	UNP Q12959
K	315	GLU	-	expression tag	UNP Q12959
K	316	LYS	-	expression tag	UNP Q12959
K	317	ILE	-	expression tag	UNP Q12959
K	318	MET	-	expression tag	UNP Q12959
L	203	GLY	-	expression tag	UNP Q12959
L	204	PRO	-	expression tag	UNP Q12959
L	205	LEU	-	expression tag	UNP Q12959
L	206	GLY	-	expression tag	UNP Q12959

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Chain	Residue	Modelled	Actual	Comment	Reference
L	207	SER	-	expression tag	UNP Q12959
L	208	GLU	-	expression tag	UNP Q12959
L	209	THR	-	expression tag	UNP Q12959
L	210	PRO	-	expression tag	UNP Q12959
L	211	THR	-	expression tag	UNP Q12959
L	212	TYR	-	expression tag	UNP Q12959
L	213	VAL	-	expression tag	UNP Q12959
L	214	ASN	-	expression tag	UNP Q12959
L	215	GLY	-	expression tag	UNP Q12959
L	216	THR	-	expression tag	UNP Q12959
L	217	ASP	-	expression tag	UNP Q12959
L	218	ALA	-	expression tag	UNP Q12959
L	312	PRO	-	expression tag	UNP Q12959
L	313	VAL	-	expression tag	UNP Q12959
L	314	SER	-	expression tag	UNP Q12959
L	315	GLU	-	expression tag	UNP Q12959
L	316	LYS	-	expression tag	UNP Q12959
L	317	ILE	-	expression tag	UNP Q12959
L	318	MET	-	expression tag	UNP Q12959

- Molecule 2 is a protein called GLU-THR-GLU-VAL.

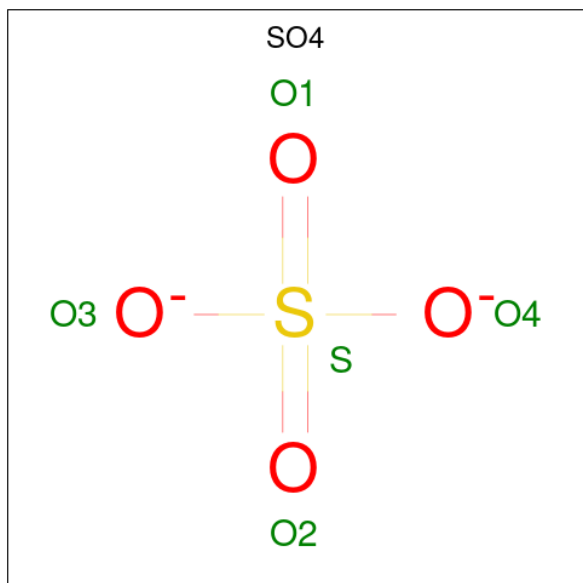
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	V	4	Total	C	N	O	0	1	0
			39	23	4	12			
2	W	4	Total	C	N	O	0	0	0
			33	19	4	10			
2	X	4	Total	C	N	O	0	0	0
			29	17	4	8			
2	Y	4	Total	C	N	O	0	0	0
			33	19	4	10			
2	N	4	Total	C	N	O	0	0	0
			33	19	4	10			
2	O	4	Total	C	N	O	0	0	0
			33	19	4	10			
2	P	4	Total	C	N	O	0	0	0
			33	19	4	10			
2	Q	4	Total	C	N	O	0	0	0
			33	19	4	10			
2	R	4	Total	C	N	O	0	0	0
			33	19	4	10			
2	T	4	Total	C	N	O	0	0	0
			33	19	4	10			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	Z	4	Total	C	N	O	0	0	0
			33	19	4	10			
2	U	4	Total	C	N	O	0	0	0
			33	19	4	10			

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	66	Total O 66 66	0	0
4	A	53	Total O 53 53	0	0
4	C	55	Total O 55 55	0	0
4	D	54	Total O 54 54	0	0
4	E	58	Total O 58 58	0	0
4	F	41	Total O 41 41	0	0
4	G	59	Total O 59 59	0	0
4	H	51	Total O 51 51	0	0
4	I	47	Total O 47 47	0	0
4	J	40	Total O 40 40	0	0
4	K	35	Total O 35 35	0	0
4	L	34	Total O 34 34	0	0
4	V	6	Total O 6 6	0	0
4	W	4	Total O 4 4	0	0
4	X	2	Total O 2 2	0	0
4	Y	8	Total O 8 8	0	0
4	N	1	Total O 1 1	0	0
4	O	2	Total O 2 2	0	0
4	P	2	Total O 2 2	0	0
4	R	4	Total O 4 4	0	0
4	T	1	Total O 1 1	0	0

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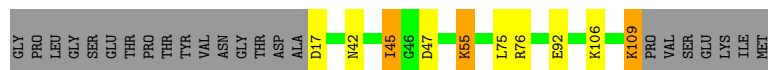
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	Z	3	Total	O	0	0
			3	3		
4	U	2	Total	O	0	0
			2	2		

3 Residue-property plots [i](#)

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

- Molecule 1: Disks large homolog 1

Chain B: 



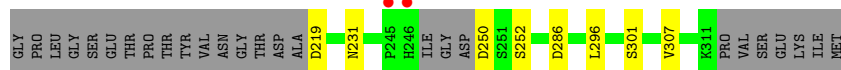
- Molecule 1: Disks large homolog 1

Chain A: 



- Molecule 1: Disks large homolog 1

Chain C: 



- Molecule 1: Disks large homolog 1

Chain D: 

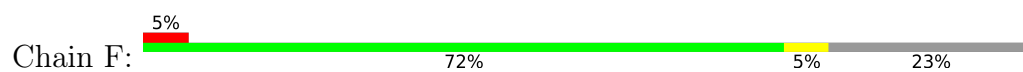


- Molecule 1: Disks large homolog 1

Chain E: 



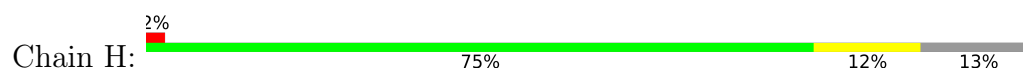
- Molecule 1: Disks large homolog 1



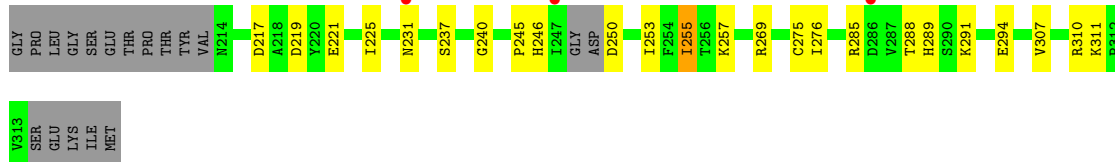
- Molecule 1: Disks large homolog 1



- Molecule 1: Disks large homolog 1



- Molecule 1: Disks large homolog 1



- Molecule 1: Disks large homolog 1

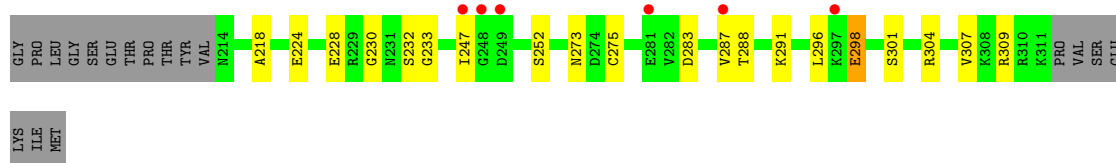


- Molecule 1: Disks large homolog 1



- Molecule 1: Disks large homolog 1





- Molecule 2: GLU-THR-GLU-VAL

Chain V: 50% 50%



- Molecule 2: GLU-THR-GLU-VAL

Chain W: 100%

There are no outlier residues recorded for this chain.

- Molecule 2: GLU-THR-GLU-VAL

Chain X: 100%

There are no outlier residues recorded for this chain.

- Molecule 2: GLU-THR-GLU-VAL

Chain Y: 75% 25%



- Molecule 2: GLU-THR-GLU-VAL

Chain N: 100%

There are no outlier residues recorded for this chain.

- Molecule 2: GLU-THR-GLU-VAL

Chain O: 75% 25%



- Molecule 2: GLU-THR-GLU-VAL

Chain P: 100%

There are no outlier residues recorded for this chain.

- Molecule 2: GLU-THR-GLU-VAL

Chain Q:  75% 25%



- Molecule 2: GLU-THR-GLU-VAL

Chain R:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: GLU-THR-GLU-VAL

Chain T:  100%

There are no outlier residues recorded for this chain.

- Molecule 2: GLU-THR-GLU-VAL

Chain Z:  75% 25%



- Molecule 2: GLU-THR-GLU-VAL

Chain U:  75% 25%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	53.54Å 82.91Å 87.78Å 64.10° 90.14° 89.87°	Depositor
Resolution (Å)	45.25 – 2.09 45.25 – 2.09	Depositor EDS
% Data completeness (in resolution range)	61.6 (45.25-2.09) 61.8 (45.25-2.09)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 2.08Å)	Xtriage
Refinement program	BUSTER	Depositor
R, R_{free}	0.199 , 0.246 0.207 , 0.253	Depositor DCC
R_{free} test set	2601 reflections (3.22%)	wwPDB-VP
Wilson B-factor (Å ²)	21.9	Xtriage
Anisotropy	0.032	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 44.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.023 for h,-k,-l 0.069 for -h,k,k-l 0.000 for -h,-k,-k+l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9661	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.70% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.36	0/680	0.51	0/916
1	B	0.38	0/721	0.58	0/970
1	C	0.35	0/686	0.52	0/923
1	D	0.35	0/717	0.55	0/966
1	E	0.37	0/708	0.56	0/954
1	F	0.36	0/682	0.49	0/916
1	G	0.33	0/758	0.54	0/1023
1	H	0.33	0/758	0.50	0/1026
1	I	0.32	0/741	0.54	0/999
1	J	0.32	0/740	0.57	0/999
1	K	0.33	0/743	0.56	0/1001
1	L	0.31	0/734	0.50	0/991
2	N	0.42	0/32	0.41	0/41
2	O	0.33	0/32	0.39	0/41
2	P	0.30	0/32	0.50	0/41
2	Q	0.38	0/32	0.38	0/41
2	R	0.43	0/32	0.42	0/41
2	T	0.33	0/32	0.41	0/41
2	U	0.46	0/32	0.39	0/41
2	V	0.28	0/41	0.33	0/53
2	W	0.38	0/32	0.34	0/41
2	X	0.36	0/28	0.40	0/36
2	Y	0.47	0/32	0.56	0/41
2	Z	0.38	0/32	0.44	0/41
All	All	0.34	0/9057	0.53	0/12183

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	676	0	651	4	0
1	B	714	0	712	11	0
1	C	681	0	673	5	0
1	D	710	0	701	10	0
1	E	701	0	695	8	0
1	F	677	0	678	6	0
1	G	750	0	743	20	0
1	H	750	0	725	9	0
1	I	735	0	720	19	0
1	J	733	0	716	12	0
1	K	736	0	727	13	0
1	L	727	0	707	19	0
2	N	33	0	27	0	0
2	O	33	0	27	1	0
2	P	33	0	27	0	0
2	Q	33	0	27	1	0
2	R	33	0	27	0	0
2	T	33	0	27	0	0
2	U	33	0	27	1	0
2	V	39	0	33	2	0
2	W	33	0	27	0	0
2	X	29	0	23	0	0
2	Y	33	0	27	2	0
2	Z	33	0	27	1	0
3	A	5	0	0	0	0
3	B	10	0	0	0	0
3	C	5	0	0	1	0
3	D	10	0	0	0	0
3	F	10	0	0	0	0
3	K	5	0	0	0	0
4	A	53	0	0	2	0
4	B	66	0	0	2	0
4	C	55	0	0	2	0
4	D	54	0	0	2	0
4	E	58	0	0	3	0
4	F	41	0	0	2	1
4	G	59	0	0	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	51	0	0	2	2
4	I	47	0	0	6	0
4	J	40	0	0	4	1
4	K	35	0	0	3	0
4	L	34	0	0	8	0
4	N	1	0	0	0	0
4	O	2	0	0	0	0
4	P	2	0	0	0	0
4	R	4	0	0	0	0
4	T	1	0	0	0	0
4	U	2	0	0	0	0
4	V	6	0	0	0	0
4	W	4	0	0	0	0
4	X	2	0	0	0	0
4	Y	8	0	0	1	0
4	Z	3	0	0	1	0
All	All	9661	0	8774	127	2

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 (127) 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:H:235:GLY:O	4:H:401:HOH:O	1.86	0.92
1:I:217:ASP:OD2	4:I:401:HOH:O	1.87	0.90
1:E:232:SER:OG	4:E:401:HOH:O	1.93	0.79
1:K:284:VAL:O	4:K:501:HOH:O	2.01	0.78
1:L:304:ARG:NH1	4:L:404:HOH:O	2.16	0.78
1:F:294:GLU:OE2	4:F:501:HOH:O	2.03	0.77
1:L:232:SER:O	4:L:401:HOH:O	2.02	0.77
1:G:258:ILE:HB	1:K:216:THR:HG22	1.67	0.76
1:L:273:ASN:O	4:L:402:HOH:O	2.03	0.76
1:K:311:LYS:NZ	4:K:502:HOH:O	2.18	0.75
1:B:47:ASP:HB2	1:I:285:ARG:HH11	1.52	0.74
1:I:288:THR:HG22	1:I:291:LYS:HB2	1.69	0.74
1:A:250:ASP:O	4:A:501:HOH:O	2.04	0.74
1:F:251:SER:O	4:F:502:HOH:O	2.04	0.73
1:B:42:ASN:OD1	4:B:301:HOH:O	2.07	0.72
1:E:235:GLY:O	4:E:402:HOH:O	2.08	0.71
1:G:233:GLY:O	4:G:401:HOH:O	2.10	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:291:LYS:NZ	1:L:228:GLU:OE1	2.26	0.69
1:G:232:SER:O	4:G:402:HOH:O	2.11	0.67
1:E:299:ALA:O	4:E:403:HOH:O	2.12	0.66
1:A:249:ASP:O	4:A:502:HOH:O	2.13	0.66
1:I:221:GLU:OE1	4:I:403:HOH:O	2.14	0.66
1:L:298:GLU:OE2	4:L:403:HOH:O	2.15	0.64
1:C:250:ASP:OD2	4:C:501:HOH:O	2.14	0.63
1:A:257:LYS:HD2	1:I:217:ASP:HB3	1.81	0.63
1:B:47:ASP:HB2	1:I:285:ARG:NH1	2.13	0.63
1:G:247:ILE:HG13	1:G:250:ASP:HB3	1.82	0.61
1:G:274:ASP:OD2	1:G:309:ARG:NH2	2.34	0.60
1:I:219:ASP:O	1:I:311:LYS:HG2	2.02	0.60
1:D:304:ARG:NH1	4:D:503:HOH:O	2.34	0.60
1:L:224:GLU:OE1	4:L:405:HOH:O	2.17	0.59
1:J:266:GLN:OE1	4:J:401:HOH:O	2.15	0.59
1:E:242:THR:HA	1:E:251:SER:HB2	1.84	0.59
1:B:55:LYS:HE2	1:L:218:ALA:O	2.01	0.58
1:G:247:ILE:HA	4:G:410:HOH:O	2.02	0.58
1:G:226:THR:OG1	1:G:304:ARG:HG2	2.06	0.56
1:I:231:ASN:N	4:I:402:HOH:O	2.37	0.56
1:L:296:LEU:HB3	2:Q:37:VAL:HG21	1.89	0.55
1:B:76:ARG:NH2	4:B:304:HOH:O	2.38	0.55
1:D:310:ARG:NH2	4:D:506:HOH:O	2.39	0.55
1:H:222:TYR:O	4:H:402:HOH:O	2.18	0.54
1:K:298:GLU:OE2	4:K:503:HOH:O	2.18	0.54
1:J:216:THR:O	4:J:402:HOH:O	2.18	0.54
1:I:237:SER:HB2	1:I:257:LYS:HB3	1.90	0.54
1:D:224:GLU:OE1	1:D:304:ARG:NH2	2.40	0.54
1:B:17:ASP:O	1:B:109:LYS:N	2.40	0.54
1:L:309:ARG:NH1	4:L:410:HOH:O	2.34	0.53
1:B:92:GLU:OE1	1:H:301:SER:OG	2.23	0.53
1:K:224:GLU:OE2	1:K:304:ARG:HD2	2.08	0.53
1:G:297:LYS:HB3	1:G:297:LYS:NZ	2.23	0.53
1:E:309:ARG:O	1:E:310:ARG:HB2	2.08	0.52
1:L:228:GLU:OE2	4:L:406:HOH:O	2.19	0.52
1:I:310:ARG:HG3	4:I:417:HOH:O	2.09	0.52
1:J:234:LEU:HD21	1:J:303:VAL:HG21	1.92	0.52
1:F:242:THR:HA	1:F:251:SER:HB2	1.92	0.51
1:J:243:ASP:OD2	1:J:243:ASP:N	2.34	0.51
1:L:309:ARG:NH1	4:L:412:HOH:O	2.44	0.50
1:D:277:LEU:HD21	1:D:308:LYS:HG2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:287:VAL:HG12	1:K:291:LYS:HD3	1.93	0.50
1:C:296:LEU:HD13	2:Y:57:VAL:HG21	1.94	0.50
1:J:213:VAL:C	1:J:215:GLY:H	2.20	0.50
1:K:294:GLU:O	1:K:298:GLU:HG3	2.12	0.49
1:C:231:ASN:ND2	4:C:507:HOH:O	2.44	0.49
1:J:274:ASP:OD1	1:J:309:ARG:HD3	2.13	0.48
1:E:248:GLY:O	1:G:285:ARG:NH1	2.46	0.48
1:I:246:HIS:N	4:I:409:HOH:O	2.42	0.48
1:J:274:ASP:OD2	1:J:309:ARG:NH1	2.47	0.48
1:L:287:VAL:HG22	1:L:288:THR:O	2.14	0.48
1:G:248:GLY:N	4:G:410:HOH:O	2.45	0.48
1:G:257:LYS:HE3	1:K:215:GLY:CA	2.44	0.47
1:A:223:GLU:HG2	1:A:225:ILE:HG13	1.96	0.47
1:H:249:ASP:OD1	1:H:249:ASP:N	2.40	0.46
1:C:250:ASP:N	1:C:250:ASP:OD1	2.47	0.46
1:D:277:LEU:HD11	1:D:308:LYS:HG2	1.97	0.46
1:C:301:SER:OG	3:C:401:SO4:O2	2.19	0.46
1:H:257:LYS:HG2	1:H:259:ILE:HD13	1.98	0.46
1:K:243:ASP:OD1	1:K:243:ASP:N	2.42	0.46
1:I:253:ILE:HD12	1:I:253:ILE:N	2.31	0.46
1:D:278:ARG:HG3	1:D:282:VAL:O	2.16	0.46
1:L:287:VAL:CG2	1:L:291:LYS:HB3	2.46	0.46
1:I:310:ARG:NH2	4:I:405:HOH:O	2.30	0.45
1:G:255:ILE:HD11	1:G:276:ILE:HD11	1.97	0.45
1:I:275:CYS:O	1:I:307:VAL:HA	2.16	0.45
1:E:274:ASP:OD2	1:E:309:ARG:NH2	2.35	0.45
1:F:294:GLU:OE2	1:L:301:SER:OG	2.35	0.44
1:I:288:THR:HG23	1:I:291:LYS:H	1.82	0.44
1:K:278:ARG:HH21	1:K:281:GLU:HG2	1.81	0.44
2:Y:57:VAL:HG23	4:Y:102:HOH:O	2.17	0.44
1:G:255:ILE:HG13	1:G:274:ASP:HB2	2.00	0.44
1:G:297:LYS:HB3	1:G:297:LYS:HZ1	1.82	0.44
1:G:280:ASN:ND2	1:G:299:ALA:HB1	2.32	0.44
1:H:229:ARG:HG2	1:H:230:GLY:O	2.18	0.43
1:L:230:GLY:O	1:L:233:GLY:N	2.52	0.43
1:D:278:ARG:HG2	1:D:280:ASN:O	2.19	0.43
1:J:285:ARG:HE	1:J:285:ARG:HB2	1.36	0.43
1:F:221:GLU:HG2	1:F:309:ARG:HG3	2.01	0.42
1:B:17:ASP:OD1	1:B:17:ASP:N	2.52	0.42
1:G:219:ASP:O	1:G:311:LYS:HG2	2.19	0.42
1:G:257:LYS:HE2	4:G:455:HOH:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:287:VAL:HG23	1:L:291:LYS:HB3	2.01	0.42
1:I:225:ILE:HG23	1:I:269:ARG:NH2	2.34	0.42
1:I:245:PRO:HB3	1:I:250:ASP:O	2.18	0.42
2:V:150[A]:GLU:H	2:V:150[A]:GLU:CD	2.28	0.42
1:I:240:GLY:O	1:I:289:HIS:ND1	2.47	0.42
1:I:255:ILE:HD11	1:I:276:ILE:HD11	2.01	0.42
1:E:304:ARG:HH11	1:E:304:ARG:HG2	1.84	0.42
1:H:220:TYR:CD1	1:H:308:LYS:HD2	2.55	0.42
1:H:289:HIS:O	1:H:293:VAL:HG23	2.19	0.42
1:L:247:ILE:HD12	1:L:247:ILE:HA	1.93	0.42
2:Z:120:GLU:OE2	4:Z:201:HOH:O	2.22	0.42
1:D:224:GLU:CD	1:D:304:ARG:HH21	2.28	0.42
1:G:297:LYS:HA	4:G:420:HOH:O	2.20	0.41
1:K:219:ASP:O	1:K:311:LYS:N	2.53	0.41
1:D:220:TYR:CD2	1:D:308:LYS:HD3	2.55	0.41
1:G:258:ILE:HB	1:K:216:THR:CG2	2.45	0.41
1:J:238:ILE:O	2:O:195:GLU:HA	2.20	0.41
1:J:250:ASP:O	4:J:403:HOH:O	2.21	0.41
1:L:252:SER:HB3	1:L:275:CYS:SG	2.61	0.41
1:G:257:LYS:HE3	1:K:215:GLY:HA3	2.03	0.41
1:B:75:LEU:HD11	1:B:106:LYS:HG2	2.02	0.41
1:J:304:ARG:NH2	4:J:406:HOH:O	2.35	0.41
1:D:234:LEU:H	2:U:123:VAL:C	2.27	0.41
1:B:45:ILE:HD13	1:B:45:ILE:HA	1.73	0.40
1:B:42:ASN:HA	2:V:148:GLU:O	2.22	0.40
1:H:281:GLU:H	1:H:281:GLU:CD	2.29	0.40
1:J:274:ASP:CG	1:J:309:ARG:HH11	2.30	0.40
1:L:224:GLU:OE2	1:L:304:ARG:HG2	2.22	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:537:HOH:O	4:H:438:HOH:O[1_556]	1.91	0.29
4:H:441:HOH:O	4:J:431:HOH:O[1_554]	1.95	0.25

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	87/116 (75%)	81 (93%)	6 (7%)	0	100	100
1	B	91/116 (78%)	87 (96%)	4 (4%)	0	100	100
1	C	86/116 (74%)	83 (96%)	3 (4%)	0	100	100
1	D	91/116 (78%)	89 (98%)	2 (2%)	0	100	100
1	E	90/116 (78%)	86 (96%)	4 (4%)	0	100	100
1	F	85/116 (73%)	81 (95%)	4 (5%)	0	100	100
1	G	98/116 (84%)	92 (94%)	6 (6%)	0	100	100
1	H	99/116 (85%)	95 (96%)	4 (4%)	0	100	100
1	I	94/116 (81%)	91 (97%)	3 (3%)	0	100	100
1	J	97/116 (84%)	90 (93%)	6 (6%)	1 (1%)	12	9
1	K	96/116 (83%)	88 (92%)	8 (8%)	0	100	100
1	L	96/116 (83%)	85 (88%)	11 (12%)	0	100	100
2	N	2/4 (50%)	2 (100%)	0	0	100	100
2	O	2/4 (50%)	2 (100%)	0	0	100	100
2	P	2/4 (50%)	2 (100%)	0	0	100	100
2	Q	2/4 (50%)	2 (100%)	0	0	100	100
2	R	2/4 (50%)	2 (100%)	0	0	100	100
2	T	2/4 (50%)	2 (100%)	0	0	100	100
2	U	2/4 (50%)	2 (100%)	0	0	100	100
2	V	3/4 (75%)	3 (100%)	0	0	100	100
2	W	2/4 (50%)	2 (100%)	0	0	100	100
2	X	2/4 (50%)	2 (100%)	0	0	100	100
2	Y	2/4 (50%)	2 (100%)	0	0	100	100
2	Z	2/4 (50%)	2 (100%)	0	0	100	100
All	All	1135/1440 (79%)	1073 (94%)	61 (5%)	1 (0%)	48	50

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	J	248	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	69/95 (73%)	68 (99%)	1 (1%)	59	67
1	B	76/95 (80%)	73 (96%)	3 (4%)	28	31
1	C	71/95 (75%)	67 (94%)	4 (6%)	19	18
1	D	75/95 (79%)	75 (100%)	0	100	100
1	E	74/95 (78%)	72 (97%)	2 (3%)	39	45
1	F	71/95 (75%)	71 (100%)	0	100	100
1	G	78/95 (82%)	74 (95%)	4 (5%)	21	21
1	H	79/95 (83%)	78 (99%)	1 (1%)	61	69
1	I	76/95 (80%)	74 (97%)	2 (3%)	40	46
1	J	74/95 (78%)	71 (96%)	3 (4%)	27	29
1	K	76/95 (80%)	73 (96%)	3 (4%)	28	31
1	L	75/95 (79%)	72 (96%)	3 (4%)	28	29
2	N	4/4 (100%)	4 (100%)	0	100	100
2	O	4/4 (100%)	4 (100%)	0	100	100
2	P	4/4 (100%)	4 (100%)	0	100	100
2	Q	4/4 (100%)	4 (100%)	0	100	100
2	R	4/4 (100%)	4 (100%)	0	100	100
2	T	4/4 (100%)	4 (100%)	0	100	100
2	U	4/4 (100%)	4 (100%)	0	100	100
2	V	5/4 (125%)	5 (100%)	0	100	100
2	W	4/4 (100%)	4 (100%)	0	100	100
2	X	3/4 (75%)	3 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	Y	4/4 (100%)	4 (100%)	0	100	100
2	Z	4/4 (100%)	4 (100%)	0	100	100
All	All	942/1188 (79%)	916 (97%)	26 (3%)	38	43

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	45	ILE
1	B	55	LYS
1	B	109	LYS
1	A	249	ASP
1	C	219	ASP
1	C	252	SER
1	C	286	ASP
1	C	307	VAL
1	E	251	SER
1	E	310	ARG
1	G	221	GLU
1	G	255	ILE
1	G	286	ASP
1	G	290	SER
1	H	290	SER
1	I	255	ILE
1	I	294	GLU
1	J	214	ASN
1	J	224	GLU
1	J	258	ILE
1	K	257	LYS
1	K	307	VAL
1	K	308	LYS
1	L	283	ASP
1	L	298	GLU
1	L	307	VAL

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

Mol	Chain	Res	Type
1	C	244	ASN
1	C	266	GLN
1	J	266	GLN

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](#)

9 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	$\# Z > 2$
3	SO4	D	401	-	4,4,4	0.33	0	6,6,6	0.07	0
3	SO4	C	401	-	4,4,4	0.22	0	6,6,6	0.14	0
3	SO4	F	401	-	4,4,4	0.29	0	6,6,6	0.11	0
3	SO4	B	201	-	4,4,4	0.21	0	6,6,6	0.14	0
3	SO4	F	402	-	4,4,4	0.23	0	6,6,6	0.35	0
3	SO4	K	401	-	4,4,4	0.23	0	6,6,6	0.06	0
3	SO4	A	401	-	4,4,4	0.24	0	6,6,6	0.32	0
3	SO4	D	402	-	4,4,4	0.29	0	6,6,6	0.34	0
3	SO4	B	202	-	4,4,4	0.28	0	6,6,6	0.30	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

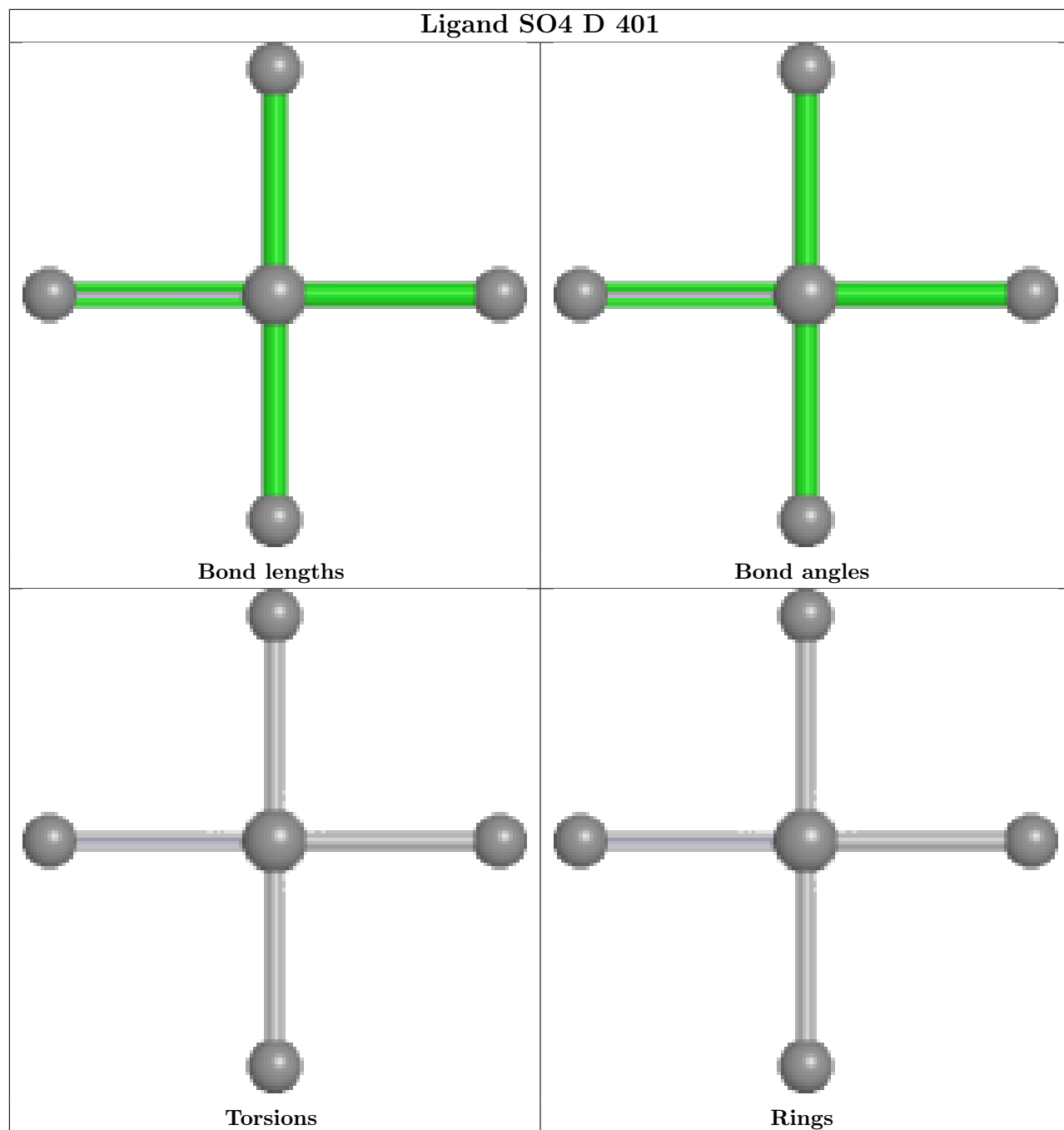
There are no torsion outliers.

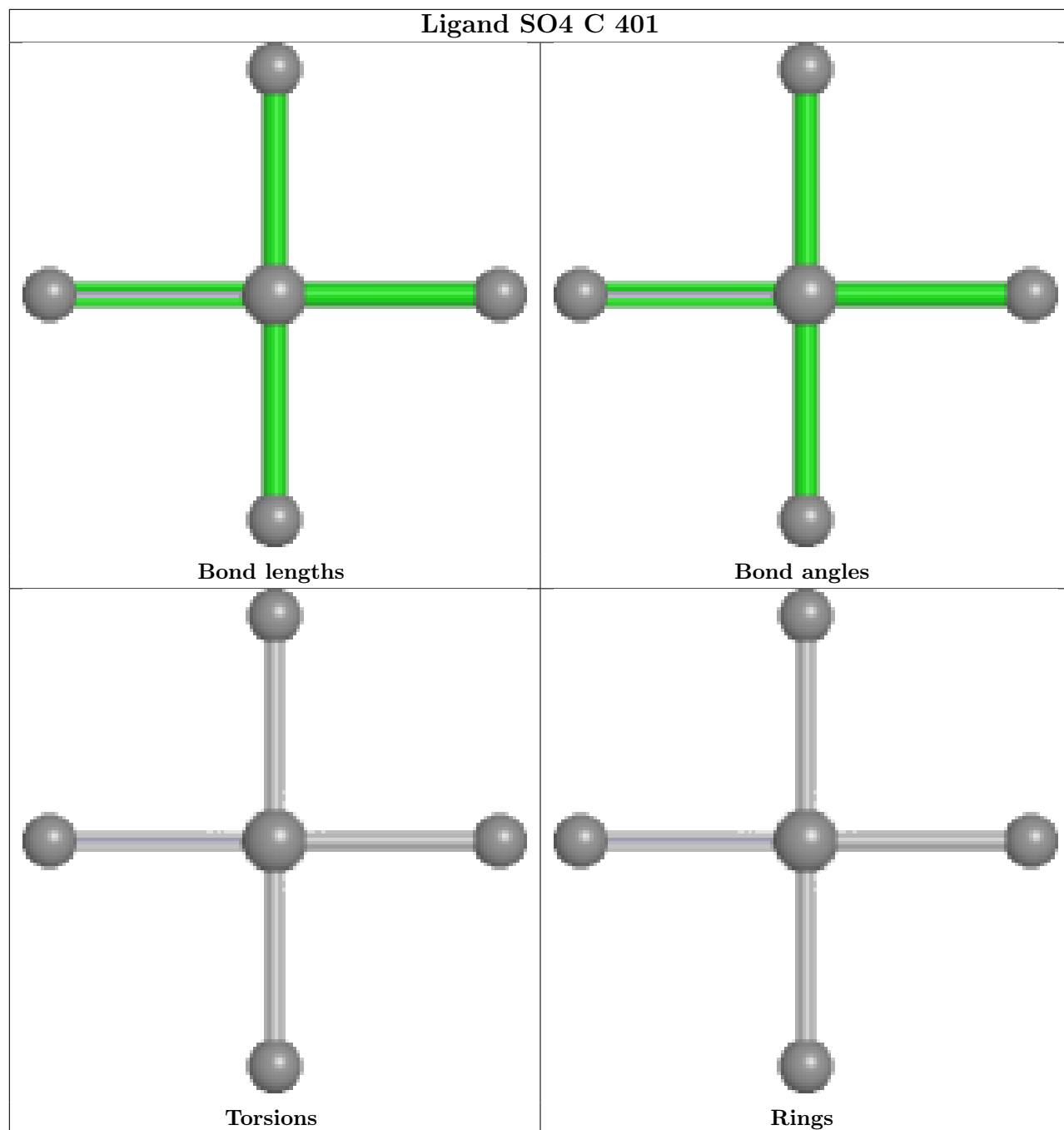
There are no ring outliers.

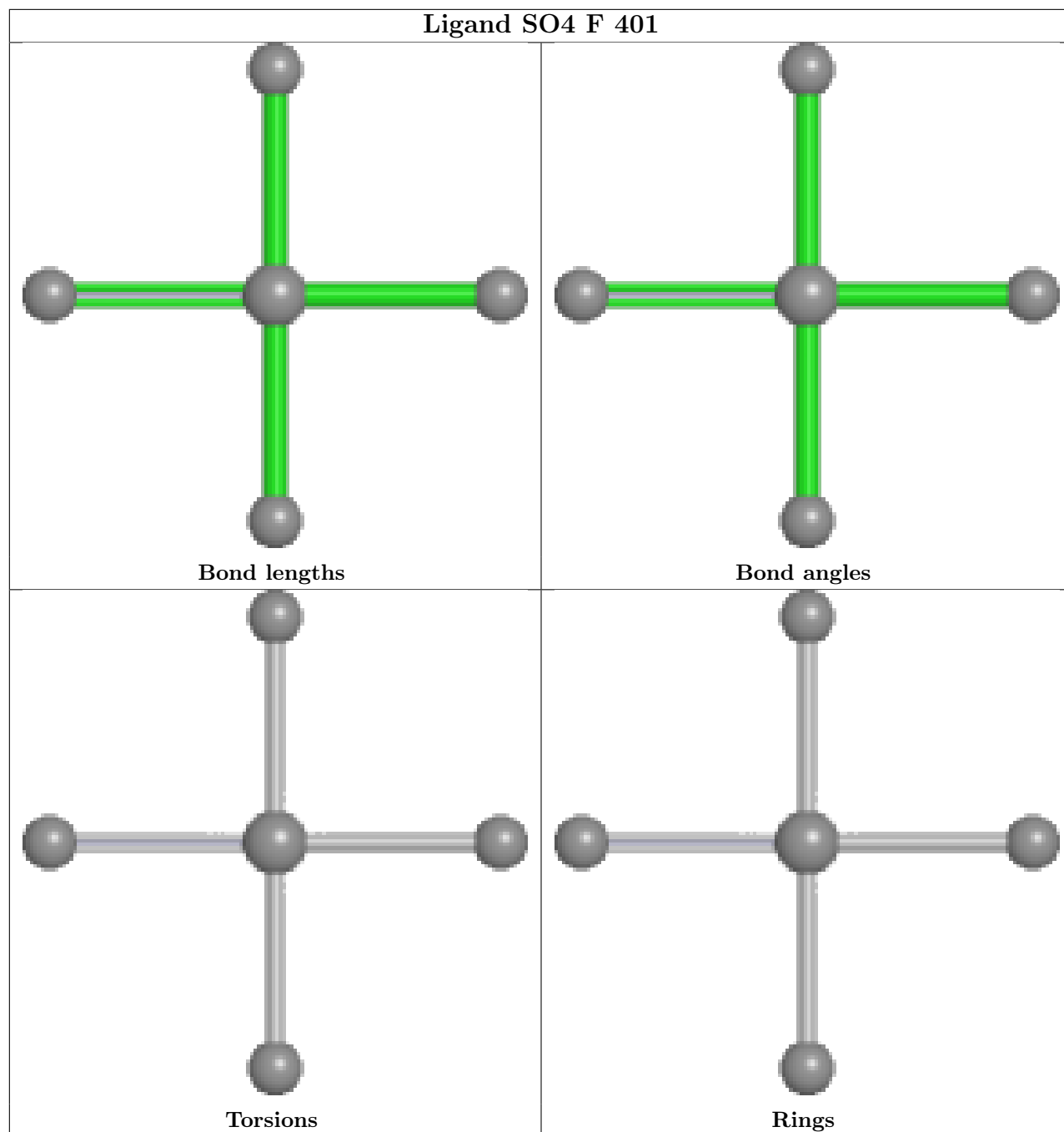
1 monomer is involved in 1 short contact:

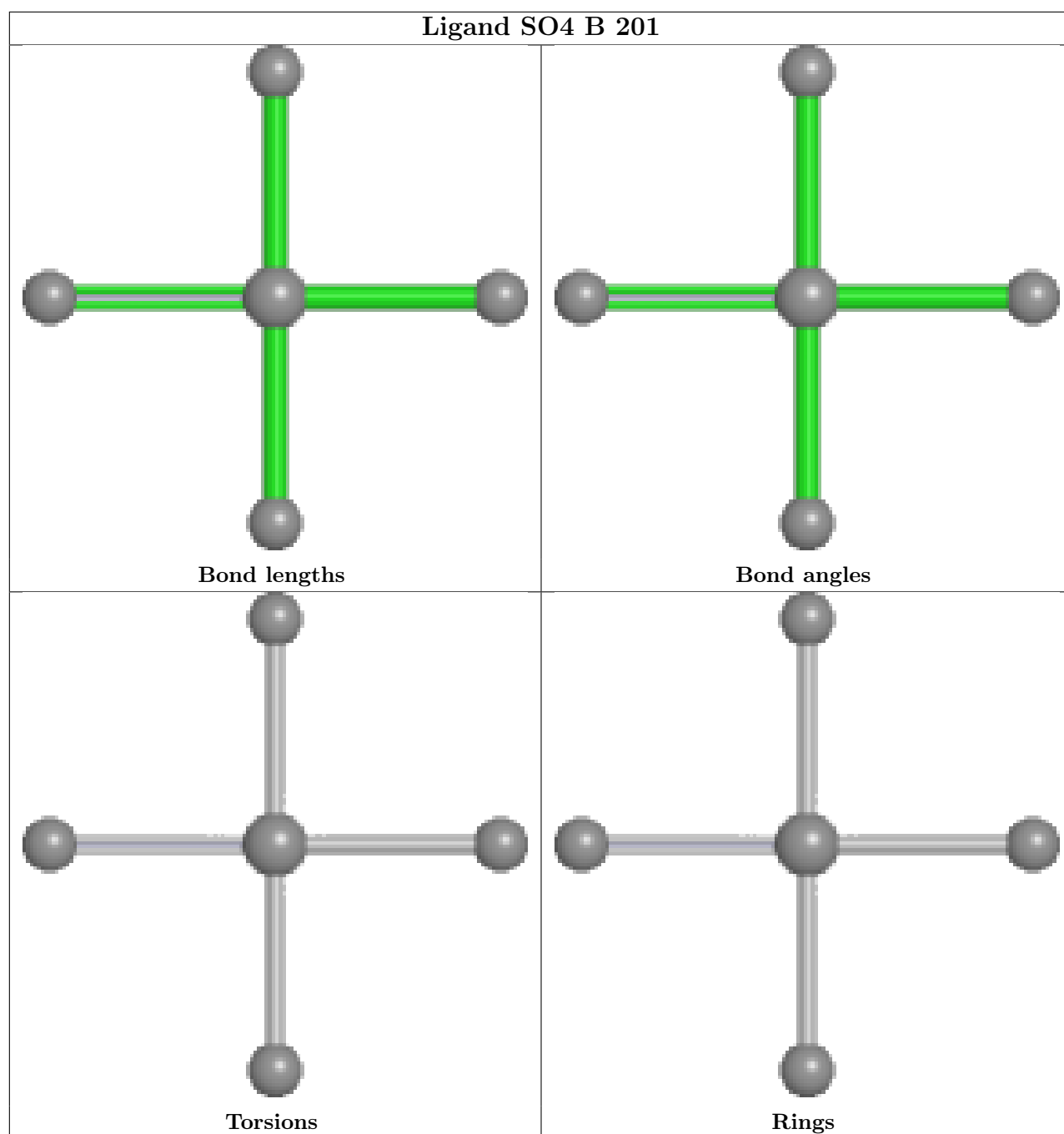
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	401	SO4	1	0

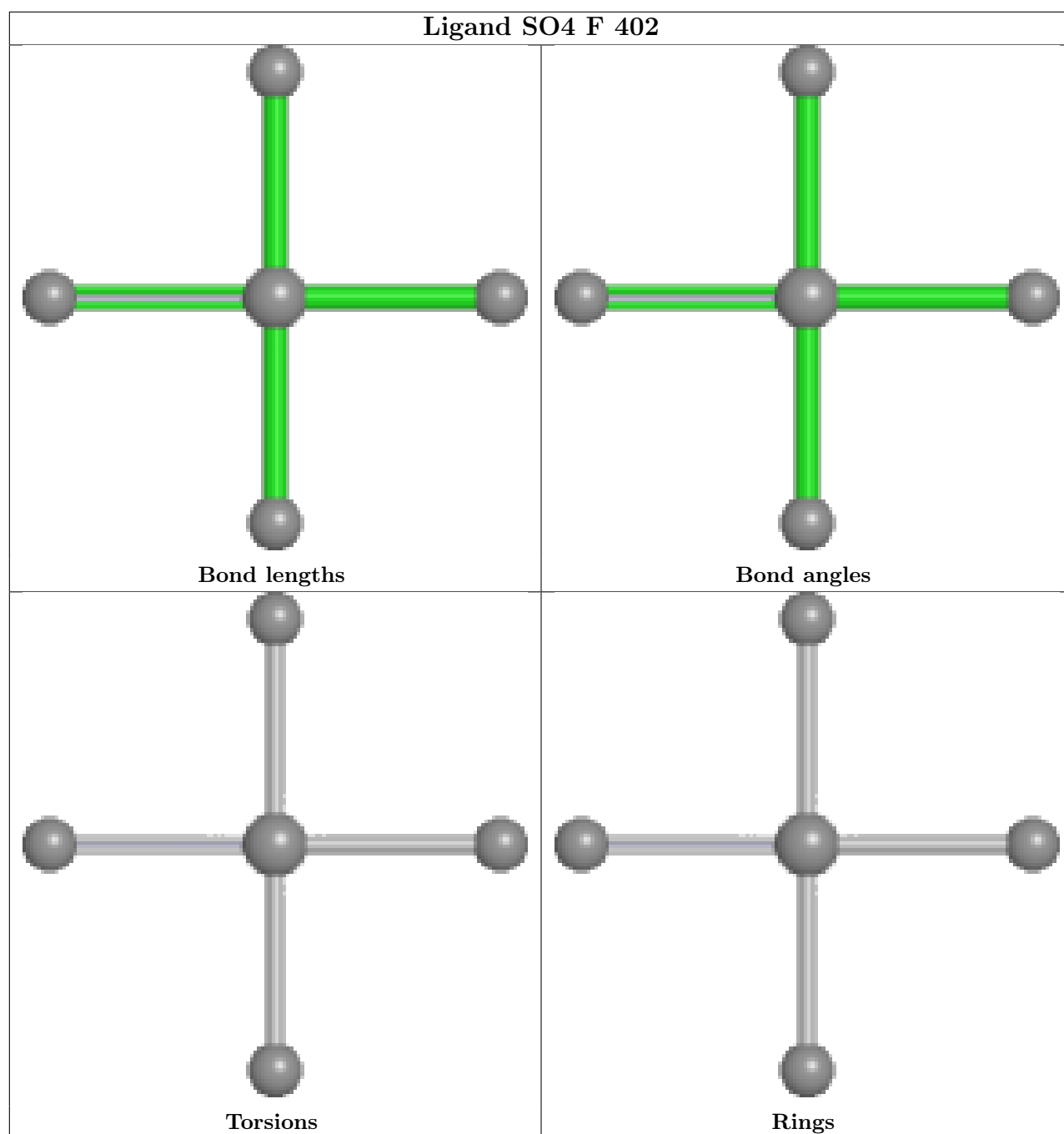
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

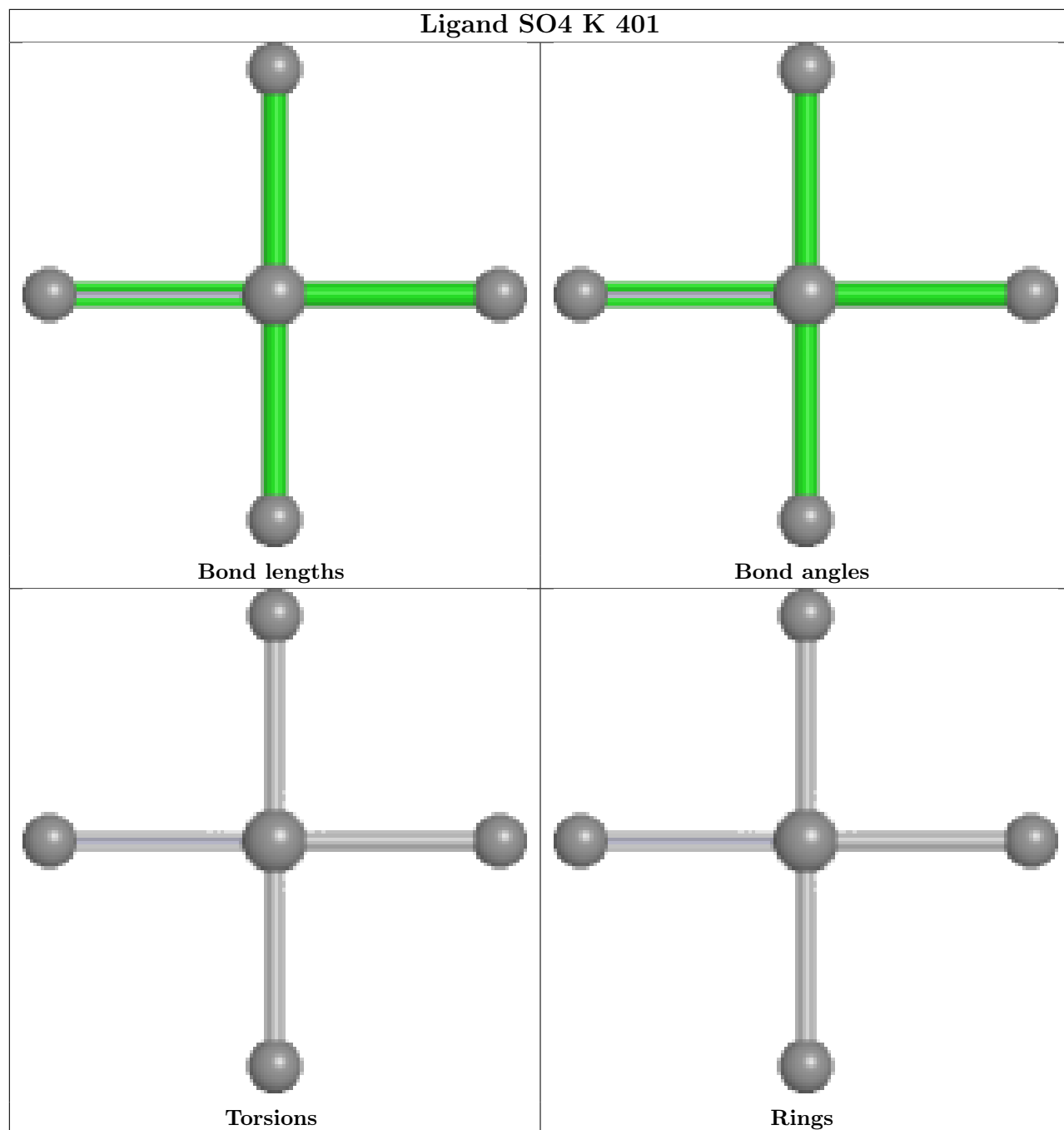


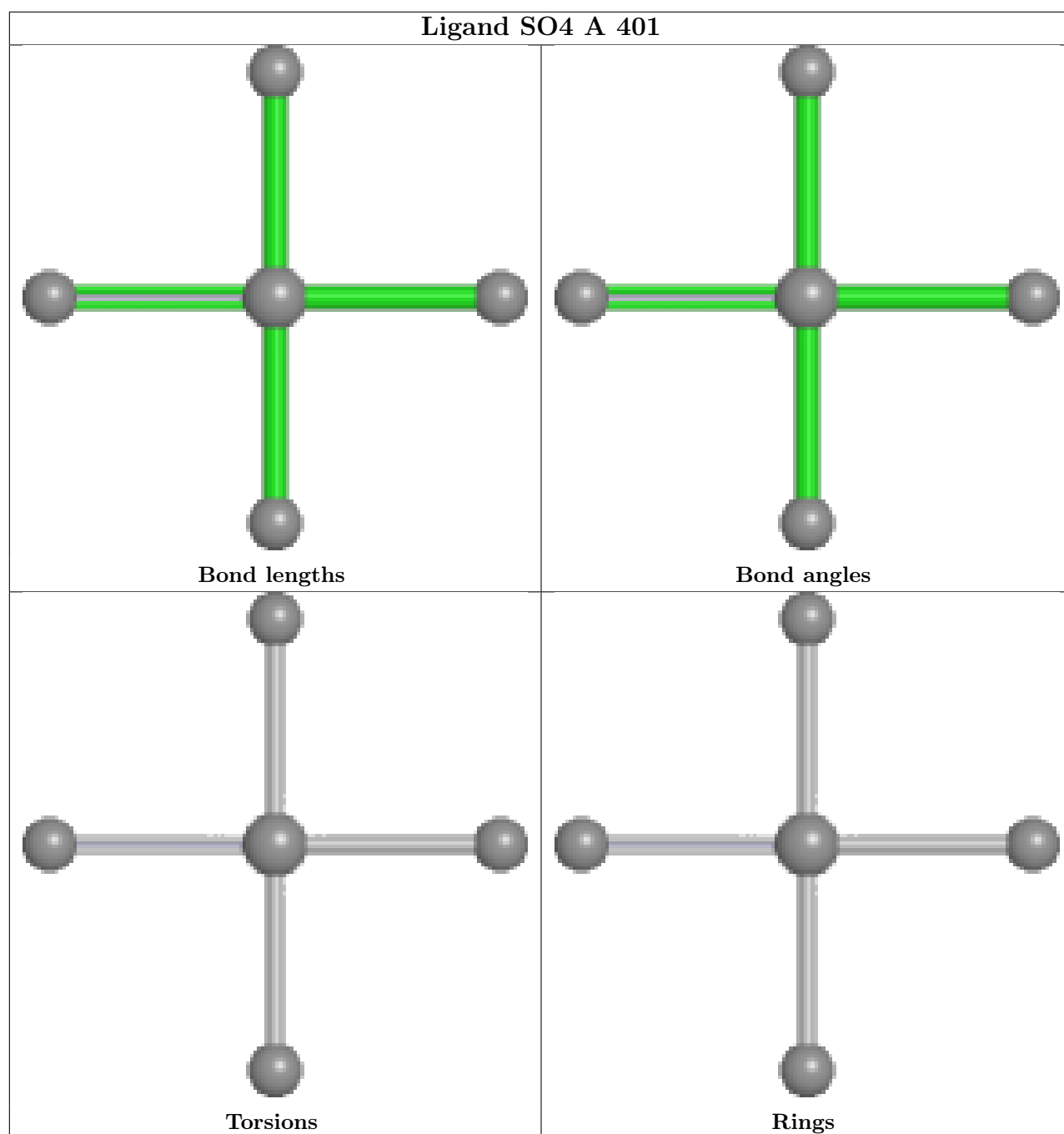


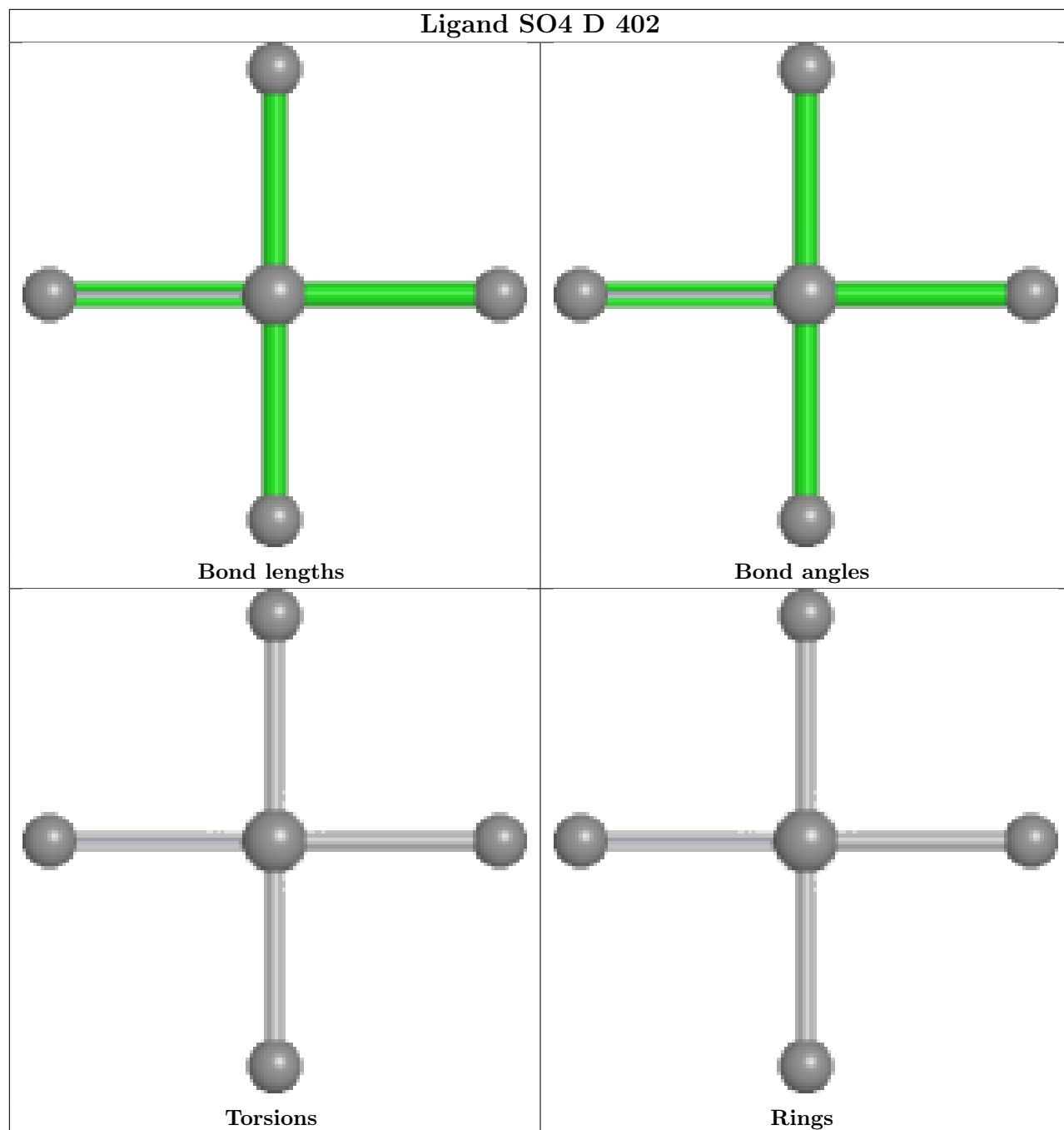


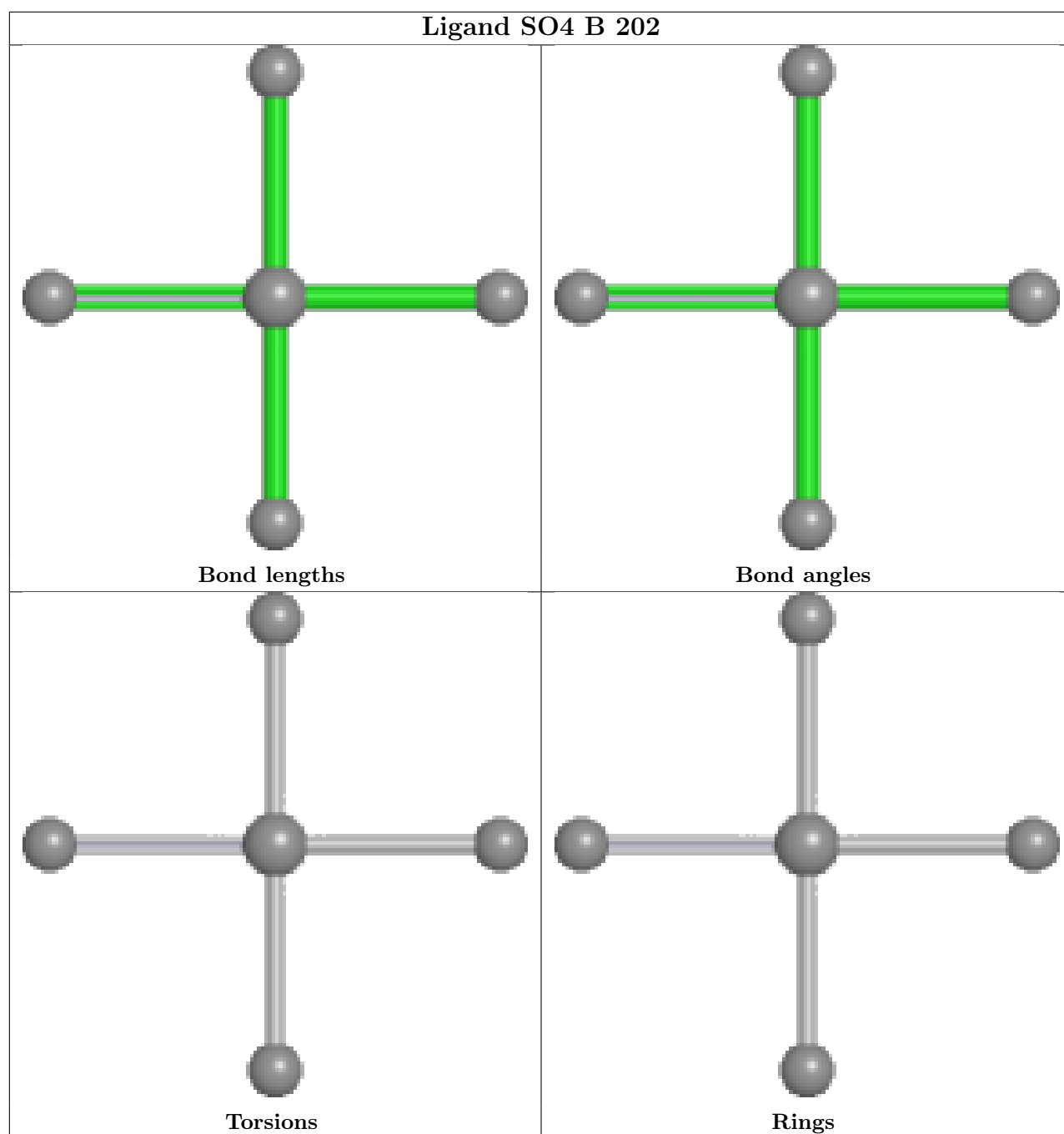












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	91/116 (78%)	-0.04	5 (5%) 30 32	16, 22, 42, 63	0
1	B	93/116 (80%)	-0.12	0 100 100	14, 20, 32, 46	0
1	C	90/116 (77%)	-0.05	2 (2%) 62 65	16, 21, 46, 65	0
1	D	93/116 (80%)	-0.03	1 (1%) 78 80	16, 22, 33, 47	0
1	E	92/116 (79%)	-0.07	0 100 100	16, 21, 32, 45	0
1	F	89/116 (76%)	0.11	6 (6%) 24 25	17, 22, 42, 55	0
1	G	100/116 (86%)	0.16	2 (2%) 65 67	17, 26, 37, 47	0
1	H	101/116 (87%)	0.22	2 (1%) 65 67	18, 26, 40, 53	0
1	I	98/116 (84%)	0.26	3 (3%) 51 54	17, 28, 39, 53	0
1	J	99/116 (85%)	0.33	2 (2%) 65 67	18, 29, 44, 46	0
1	K	98/116 (84%)	0.53	2 (2%) 65 67	20, 32, 48, 56	0
1	L	98/116 (84%)	0.58	6 (6%) 27 29	19, 34, 52, 59	0
2	N	4/4 (100%)	0.27	0 100 100	25, 27, 32, 35	0
2	O	4/4 (100%)	0.02	0 100 100	27, 33, 37, 40	0
2	P	4/4 (100%)	0.02	0 100 100	27, 31, 37, 37	0
2	Q	4/4 (100%)	0.61	0 100 100	34, 36, 36, 41	0
2	R	4/4 (100%)	-0.09	0 100 100	21, 23, 29, 35	0
2	T	4/4 (100%)	-0.04	0 100 100	31, 32, 35, 38	0
2	U	4/4 (100%)	0.23	0 100 100	22, 26, 33, 36	0
2	V	4/4 (100%)	0.16	0 100 100	17, 22, 25, 29	1 (25%)
2	W	4/4 (100%)	0.04	0 100 100	21, 27, 30, 34	0
2	X	4/4 (100%)	-0.28	0 100 100	20, 22, 23, 31	0
2	Y	4/4 (100%)	0.01	0 100 100	21, 24, 29, 31	0
2	Z	4/4 (100%)	0.28	0 100 100	32, 34, 41, 42	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	1190/1440 (82%)	0.16	31 (2%) 57 60	14, 25, 44, 65	1 (0%)

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	245	PRO	4.6
1	J	213	VAL	4.4
1	C	246	HIS	4.3
1	A	247	ILE	4.1
1	L	248	GLY	4.1
1	A	248	GLY	3.6
1	F	244	ASN	3.2
1	F	312	PRO	3.1
1	H	312	PRO	3.0
1	J	221	GLU	2.9
1	I	231	ASN	2.9
1	K	281	GLU	2.8
1	A	219	ASP	2.8
1	A	249	ASP	2.7
1	I	247	ILE	2.7
1	I	286	ASP	2.6
1	F	250	ASP	2.4
1	L	249	ASP	2.4
1	F	219	ASP	2.3
1	K	214	ASN	2.3
1	G	249	ASP	2.3
1	L	247	ILE	2.3
1	D	220	TYR	2.2
1	A	244	ASN	2.2
1	L	287	VAL	2.2
1	L	297	LYS	2.2
1	L	281	GLU	2.1
1	F	310	ARG	2.1
1	F	220	TYR	2.1
1	H	247	ILE	2.0
1	G	248	GLY	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

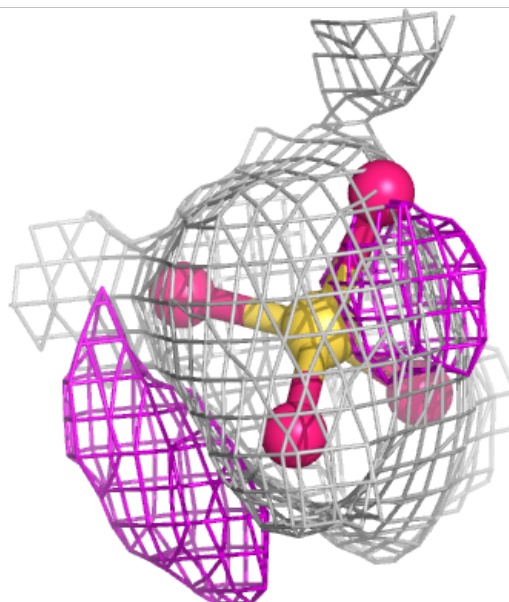
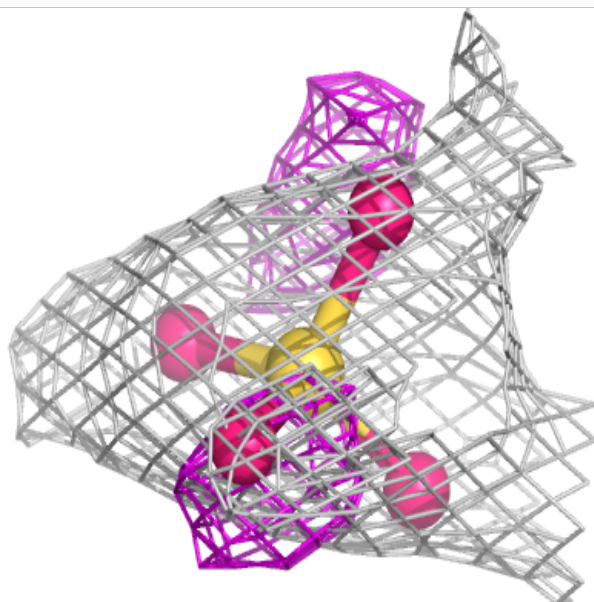
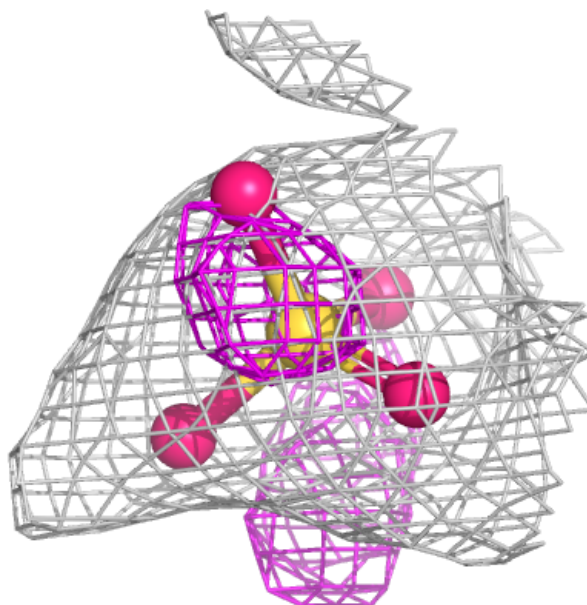
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	D	402	5/5	0.91	0.20	38,39,47,54	0
3	SO4	D	401	5/5	0.95	0.10	33,33,38,49	0
3	SO4	B	202	5/5	0.95	0.10	21,23,26,28	5
3	SO4	F	401	5/5	0.97	0.08	23,26,35,38	0
3	SO4	F	402	5/5	0.97	0.09	26,29,37,40	0
3	SO4	C	401	5/5	0.98	0.05	17,23,25,32	0
3	SO4	K	401	5/5	0.98	0.05	25,27,29,31	0
3	SO4	B	201	5/5	0.99	0.04	21,24,27,27	0
3	SO4	A	401	5/5	0.99	0.05	19,23,26,28	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.

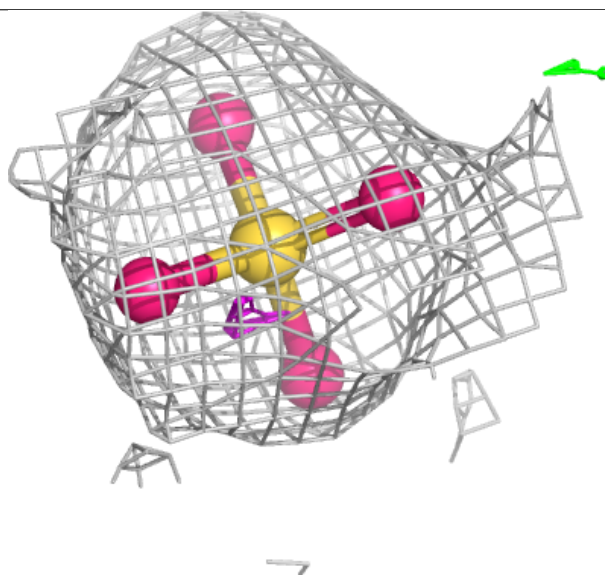
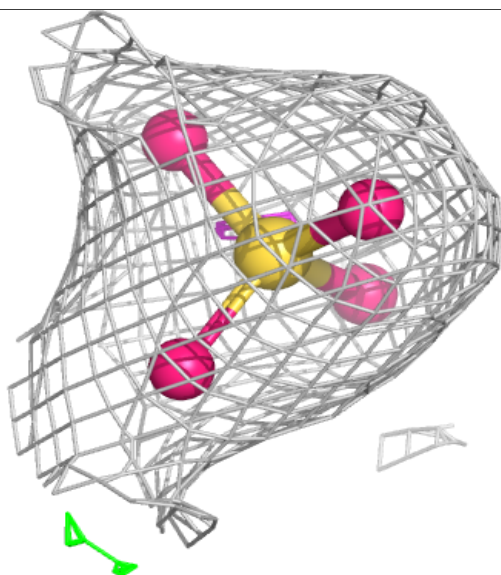
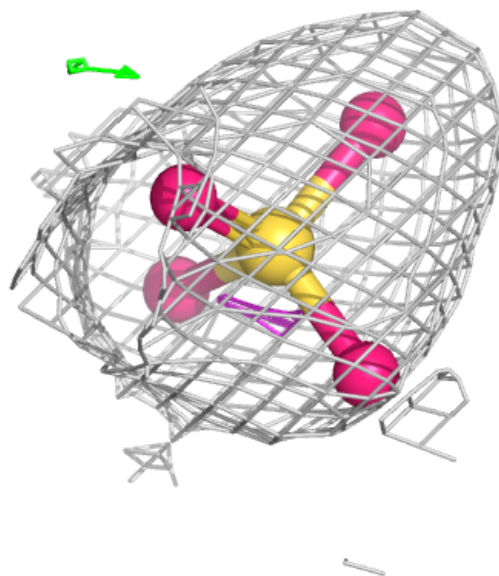
Electron density around SO4 D 402:

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



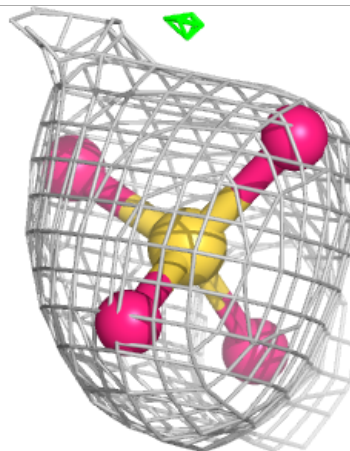
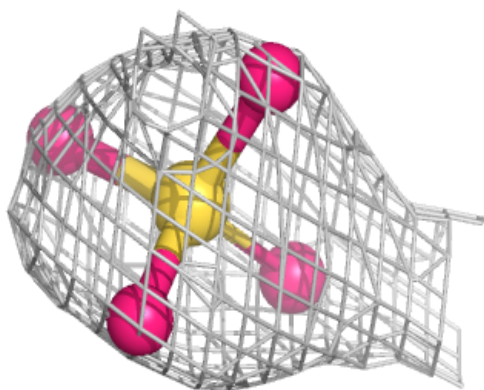
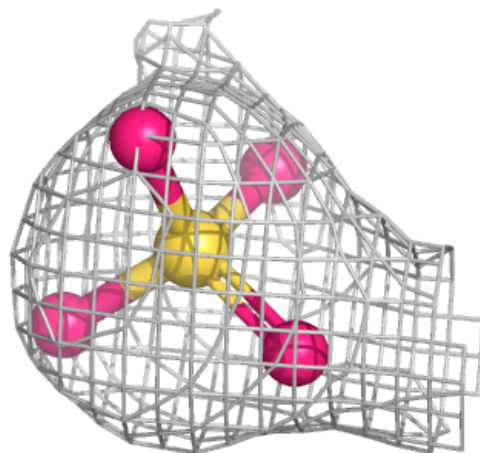
Electron density around SO4 D 401:

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



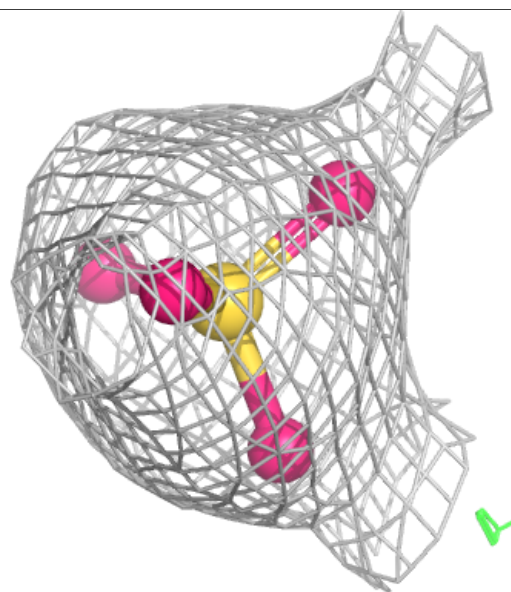
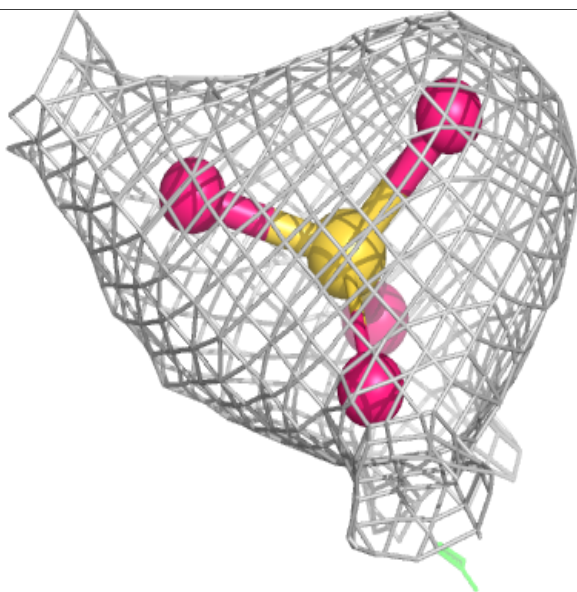
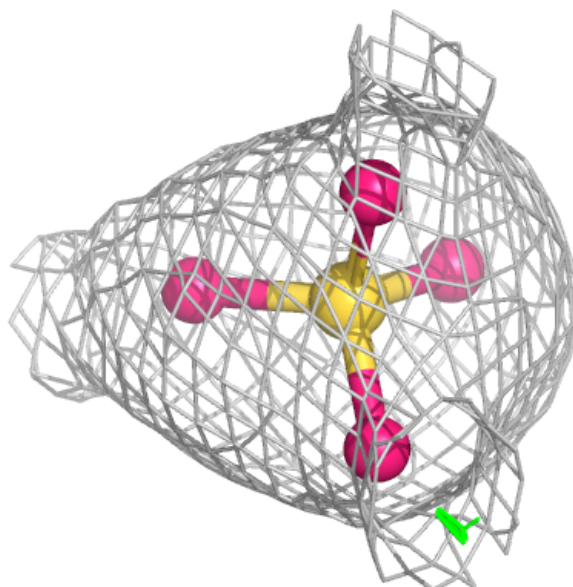
Electron density around SO4 B 202:

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



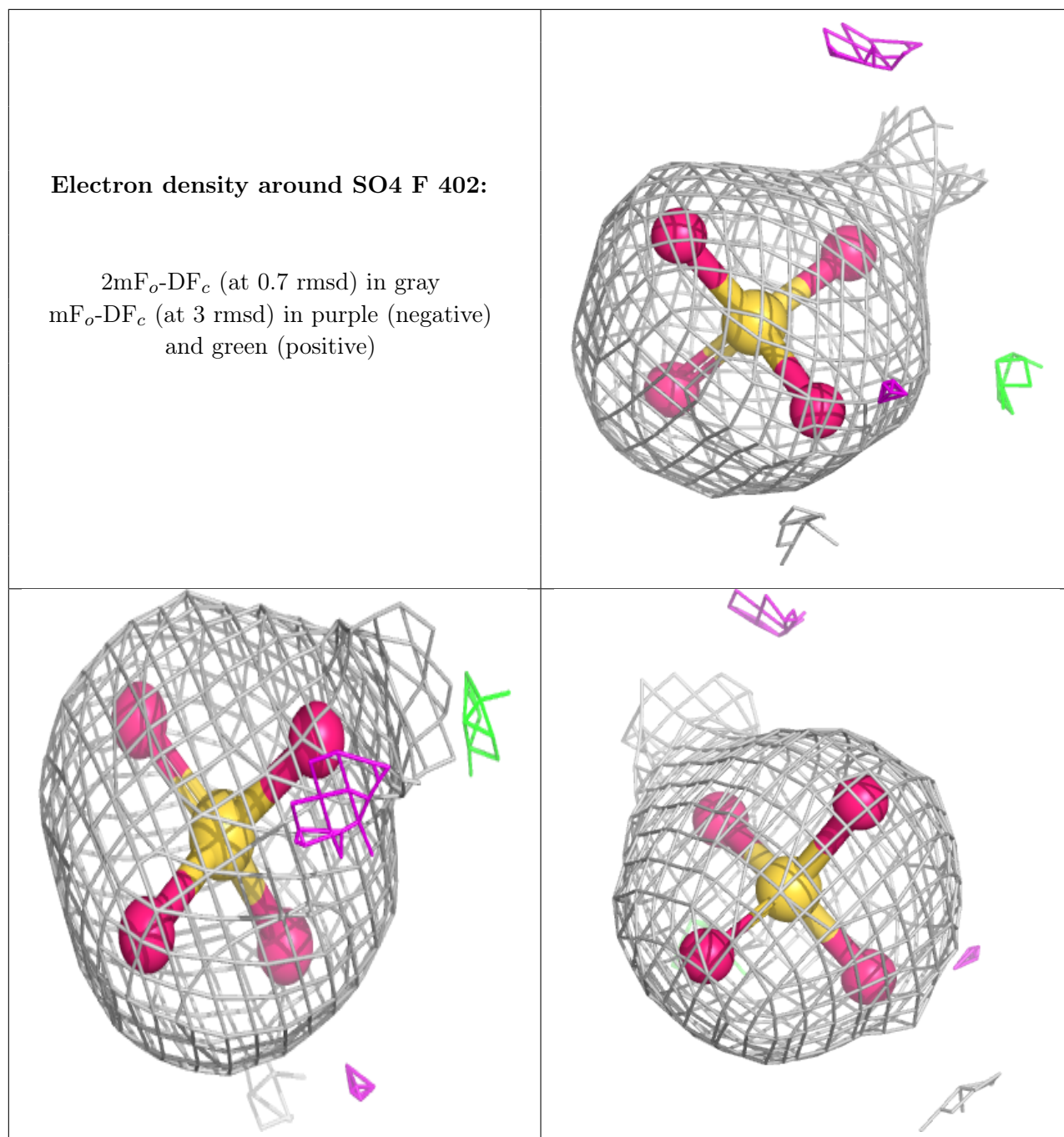
Electron density around SO4 F 401:

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



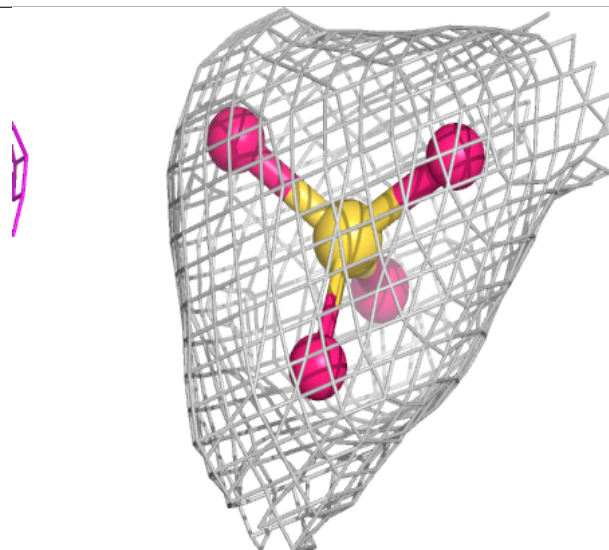
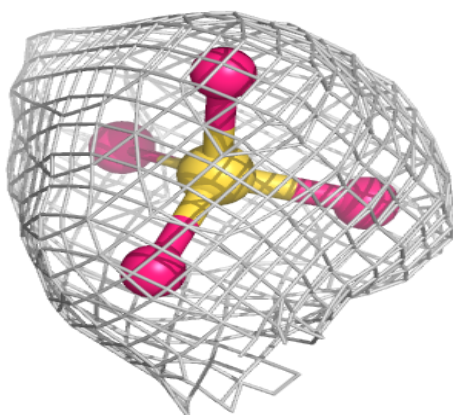
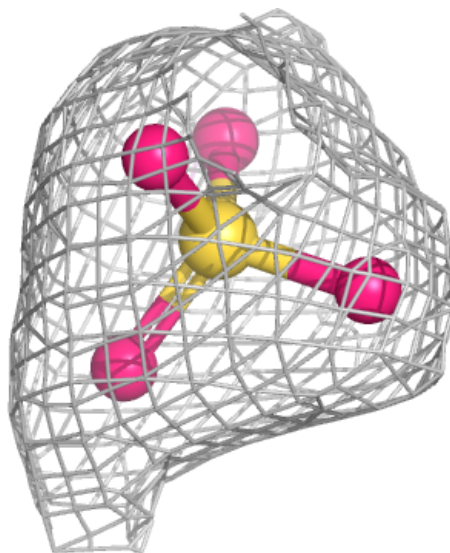
Electron density around SO4 F 402:

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



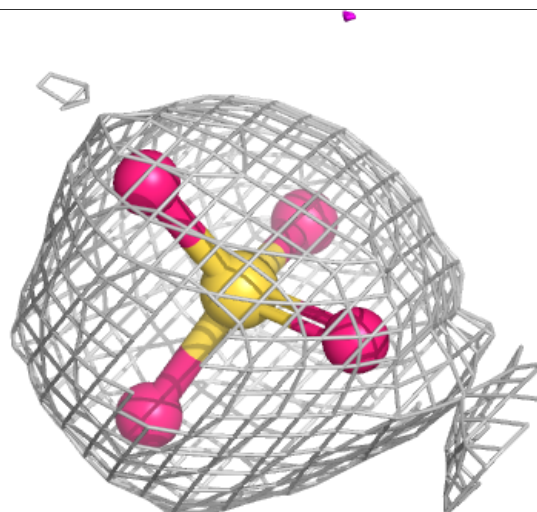
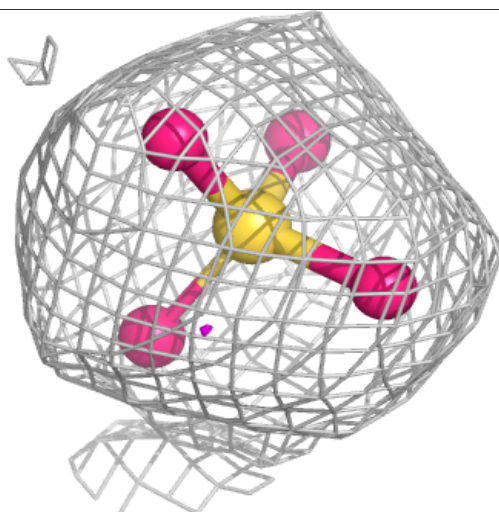
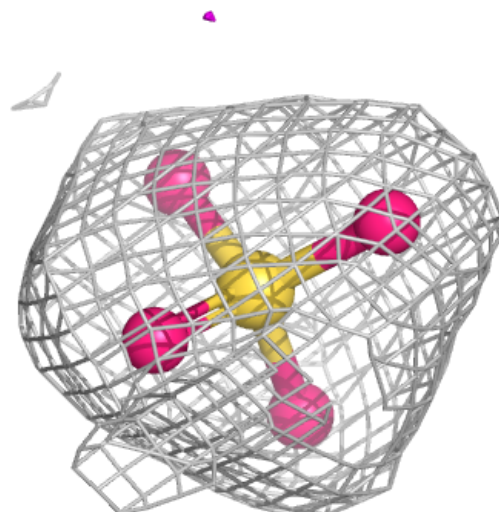
Electron density around SO4 C 401:

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and green (positive)



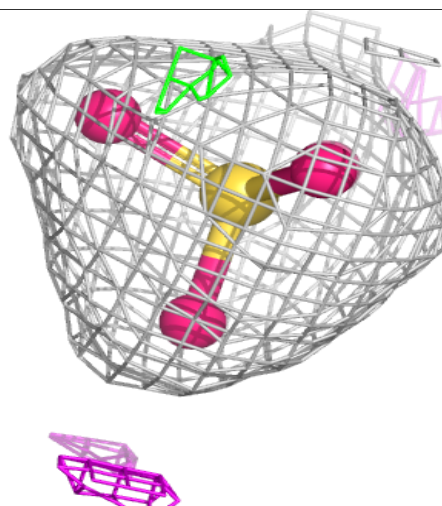
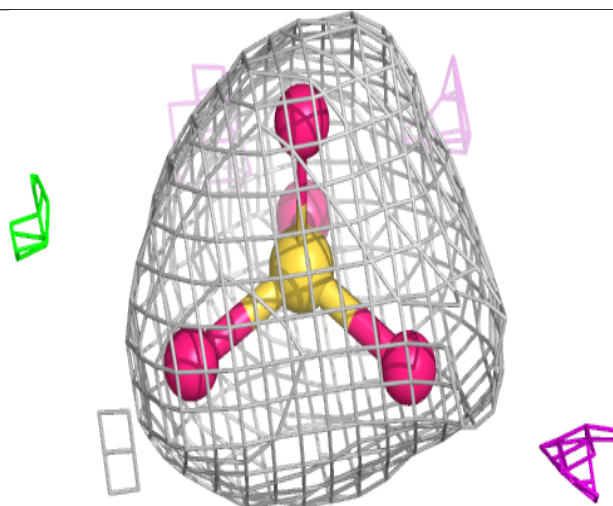
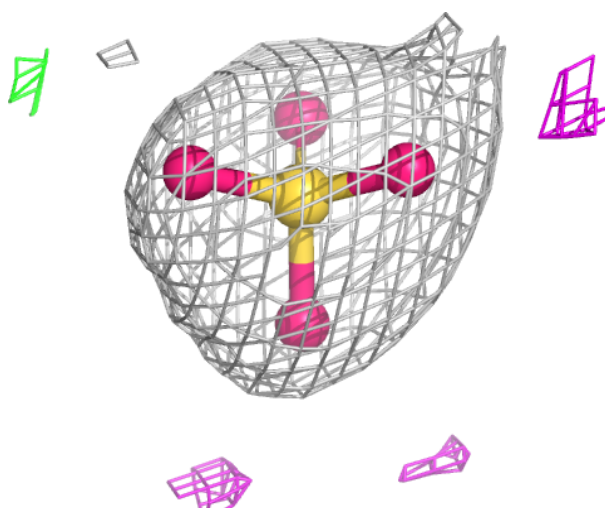
Electron density around SO4 K 401:

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and green (positive)



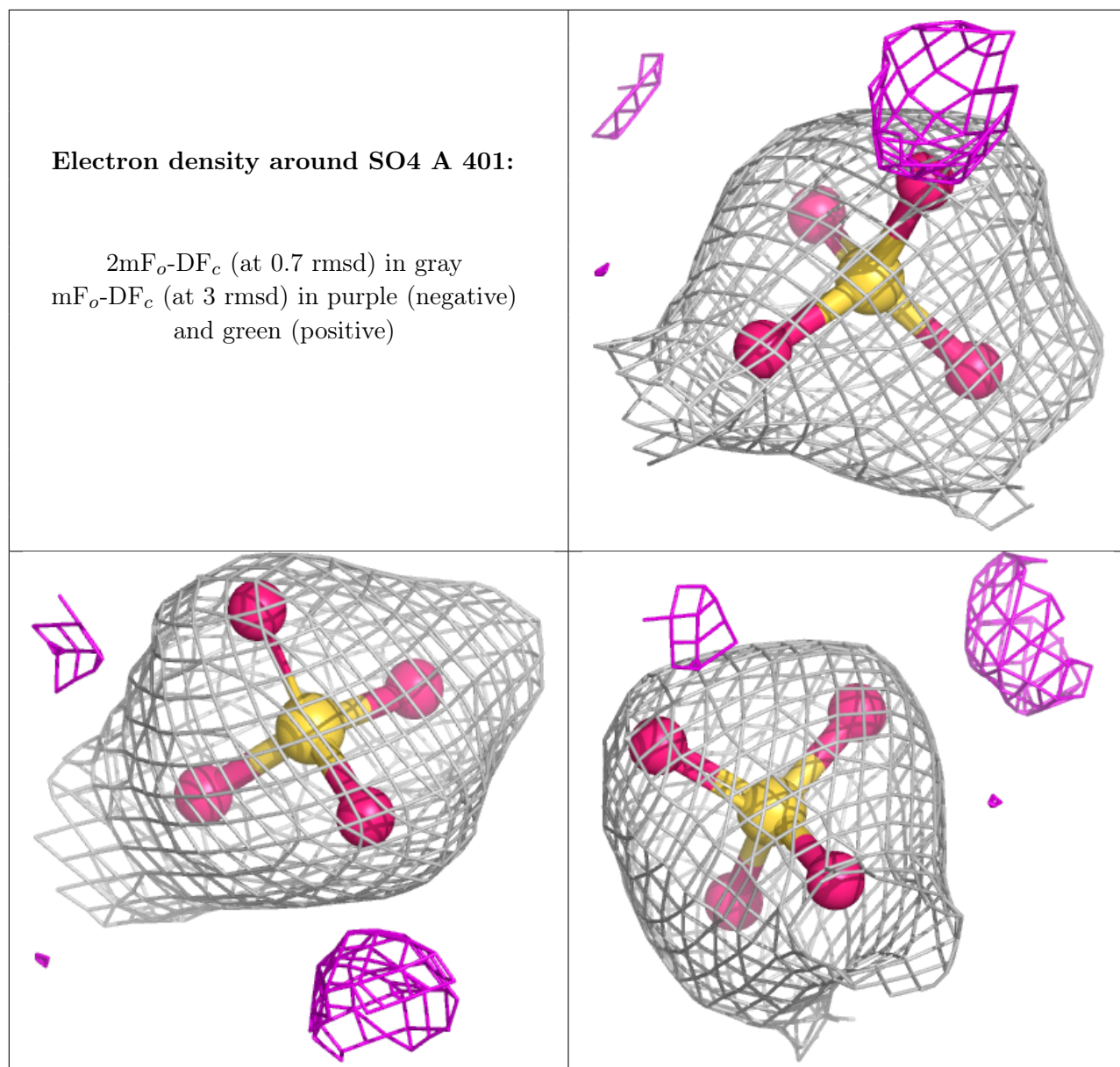
Electron density around SO4 B 201:

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



Electron density around SO4 A 401:

$2mF_o-DF_c$ (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.