



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2025 – 01:49 pm BST

PDB ID : 9GBU / pdb_00009gbu
Title : Desulfovibrio desulfuricans [FeFe]-hydrogenase variant with both subunits linked by a 13 amino acid linker peptide derived from a group A1 type [FeFe]-hydrogenase of Solobacterium moorei
Authors : Bikbaev, K.; Jaenecke, J.; Winkler, M.; Span, I.
Deposited on : 2024-07-31
Resolution : 1.78 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 Phenix2.0rc1
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.45.1

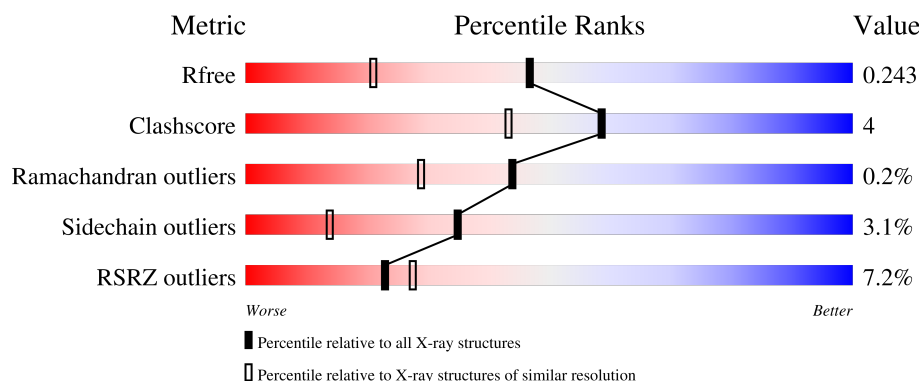
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.78 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}	164625	1191 (1.78-1.78)
Clashscore	180529	1282 (1.78-1.78)
Ramachandran outliers	177936	1270 (1.78-1.78)
Sidechain outliers	177891	1270 (1.78-1.78)
RSRZ outliers	164620	1191 (1.78-1.78)

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	490	<div> <div>8%</div> <div>87%</div> <div>9%</div> <div>..</div> </div>
1	B	490	<div> <div>6%</div> <div>85%</div> <div>11%</div> <div>...</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	SF4	B	503	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 15309 atoms, of which 7514 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 Periplasmic [Fe] hydrogenase large subunit, Periplasmic [Fe] hydrogenase small subunit.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	478	Total	C	H	N	O	S	118	5	0
			7402	2355	3695	629	690	33			
1	B	480	Total	C	H	N	O	S	119	8	0
			7458	2370	3721	637	695	35			

There are 46 discrepancies between the modelled and reference sequences:

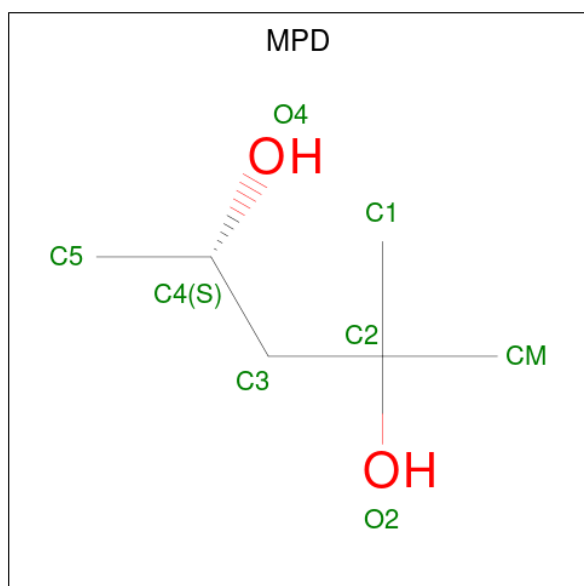
Chain	Residue	Modelled	Actual	Comment	Reference
A	390	ARG	-	linker	UNP P07598
A	391	HIS	-	linker	UNP P07598
A	392	LYS	-	linker	UNP P07598
A	393	LEU	-	linker	UNP P07598
A	394	PRO	-	linker	UNP P07598
A	395	GLN	-	linker	UNP P07598
A	396	VAL	-	linker	UNP P07598
A	397	LYS	-	linker	UNP P07598
A	398	ALA	-	linker	UNP P07598
A	399	ALA	-	linker	UNP P07598
A	400	LYS	-	linker	UNP P07598
A	401	GLU	-	linker	UNP P07598
A	402	SER	-	linker	UNP P07598
A	481	SER	-	expression tag	UNP P07603
A	482	ALA	-	expression tag	UNP P07603
A	483	TRP	-	expression tag	UNP P07603
A	484	SER	-	expression tag	UNP P07603
A	485	HIS	-	expression tag	UNP P07603
A	486	PRO	-	expression tag	UNP P07603
A	487	GLN	-	expression tag	UNP P07603
A	488	PHE	-	expression tag	UNP P07603
A	489	GLU	-	expression tag	UNP P07603
A	490	LYS	-	expression tag	UNP P07603
B	390	ARG	-	linker	UNP P07598

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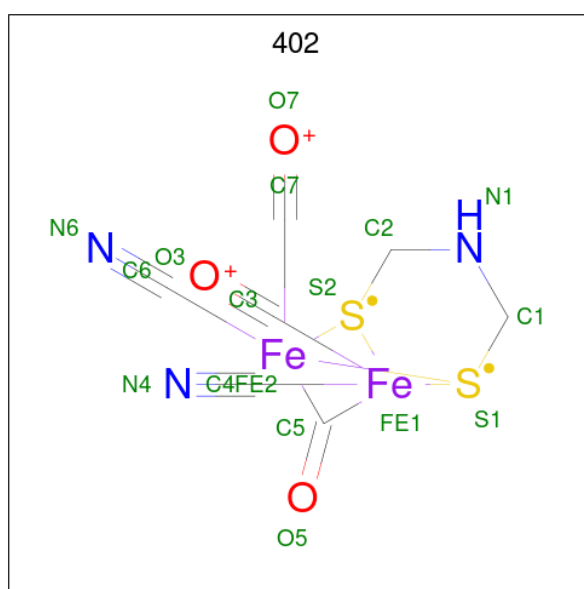
Chain	Residue	Modelled	Actual	Comment	Reference
B	391	HIS	-	linker	UNP P07598
B	392	LYS	-	linker	UNP P07598
B	393	LEU	-	linker	UNP P07598
B	394	PRO	-	linker	UNP P07598
B	395	GLN	-	linker	UNP P07598
B	396	VAL	-	linker	UNP P07598
B	397	LYS	-	linker	UNP P07598
B	398	ALA	-	linker	UNP P07598
B	399	ALA	-	linker	UNP P07598
B	400	LYS	-	linker	UNP P07598
B	401	GLU	-	linker	UNP P07598
B	402	SER	-	linker	UNP P07598
B	481	SER	-	expression tag	UNP P07603
B	482	ALA	-	expression tag	UNP P07603
B	483	TRP	-	expression tag	UNP P07603
B	484	SER	-	expression tag	UNP P07603
B	485	HIS	-	expression tag	UNP P07603
B	486	PRO	-	expression tag	UNP P07603
B	487	GLN	-	expression tag	UNP P07603
B	488	PHE	-	expression tag	UNP P07603
B	489	GLU	-	expression tag	UNP P07603
B	490	LYS	-	expression tag	UNP P07603

- Molecule 2 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	2	0
			22	6	14	2		
2	A	1	Total	C	H	O	2	0
			22	6	14	2		
2	A	1	Total	C	H	O	2	0
			22	6	14	2		
2	A	1	Total	C	H	O	2	0
			22	6	14	2		
2	B	1	Total	C	H	O	2	0
			22	6	14	2		
2	B	1	Total	C	H	O	2	0
			22	6	14	2		

- Molecule 3 is dicarbonyl[bis(cyanide-kappaC)]-mu-(iminodimethanethiolato-1kappaS:2kappaS)-mu-(oxomethylidene)diiron(2+) (CCD ID: 402) (formula: $C_7H_5Fe_2N_3O_3S_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
3	A	1	Total	C	Fe	H	N	O	S	1	0
			24	7	2	7	3	3	2		
3	B	1	Total	C	Fe	H	N	O	S	1	0
			24	7	2	7	3	3	2		

- Molecule 4 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	Fe	S	0	0
			8	4	4		
4	A	1	Total	Fe	S	0	0
			8	4	4		
4	A	1	Total	Fe	S	0	0
			8	4	4		
4	B	1	Total	Fe	S	0	0
			8	4	4		
4	B	1	Total	Fe	S	0	0
			8	4	4		
4	B	1	Total	Fe	S	0	0
			8	4	4		

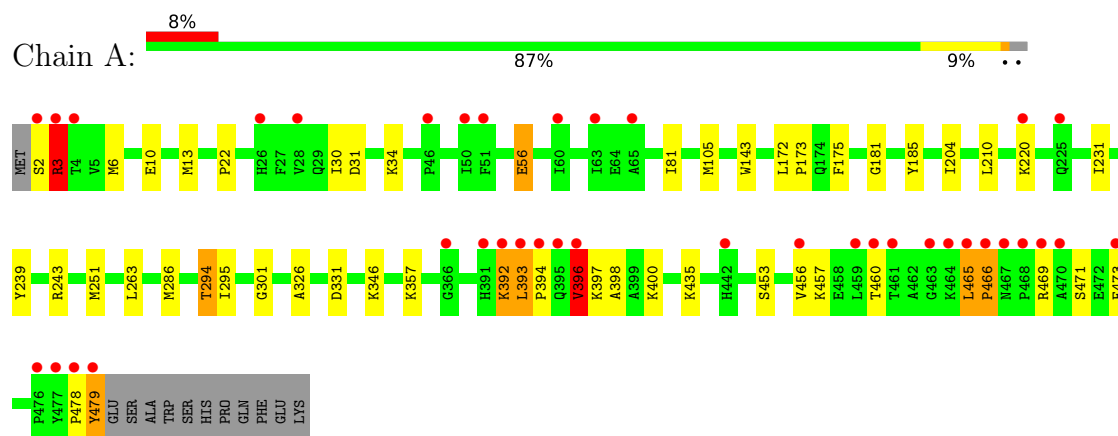
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	130	Total	O	0	0
			130	130		
5	B	91	Total	O	0	0
			91	91		

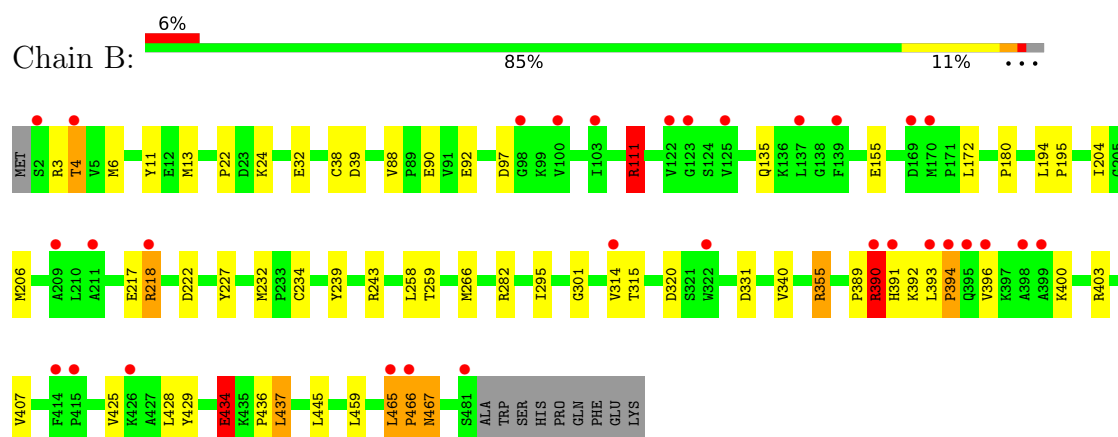
3 Residue-property plots

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: Periplasmic [Fe] hydrogenase large subunit, Periplasmic [Fe] hydrogenase small subunit



- Molecule 1: Periplasmic [Fe] hydrogenase large subunit, Periplasmic [Fe] hydrogenase small subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	93.02Å 98.81Å 112.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.84 – 1.78 48.84 – 1.78	Depositor EDS
% Data completeness (in resolution range)	99.5 (48.84-1.78) 99.5 (48.84-1.78)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 1.78Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, R_{free}	0.201 , 0.242 0.203 , 0.243	Depositor DCC
R_{free} test set	4729 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	29.6	Xtriage
Anisotropy	0.373	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 32.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	15309	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.85% 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: MPD, SF4, 402

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	0.63	1/3823 (0.0%)	1.13	16/5166 (0.3%)
1	B	0.60	1/3859 (0.0%)	1.19	12/5214 (0.2%)
All	All	0.62	2/7682 (0.0%)	1.16	28/10380 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	10
All	All	0	12

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	434	GLU	C-O	5.45	1.30	1.24
1	A	466	PRO	N-CD	5.13	1.54	1.47

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	4	THR	CA-CB-OG1	-21.54	77.29	109.60
1	B	4	THR	OG1-CB-CG2	-18.01	73.28	109.30
1	B	434	GLU	CB-CA-C	-11.94	86.66	110.42
1	A	3	ARG	N-CA-C	10.64	128.93	111.37
1	B	466	PRO	N-CA-C	-9.86	92.16	112.47
1	A	479	TYR	N-CA-CB	8.83	125.51	110.50
1	A	3	ARG	CB-CA-C	-8.27	97.02	110.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	466	PRO	CB-CA-C	7.87	124.54	111.56
1	B	111	ARG	CB-CA-C	-7.83	96.15	110.63
1	A	398	ALA	N-CA-C	-7.52	103.57	112.89
1	A	466	PRO	N-CA-C	-7.41	98.87	110.50
1	A	478	PRO	N-CA-C	-7.28	99.15	110.95
1	B	4	THR	CA-CB-CG2	6.48	121.52	110.50
1	A	397	LYS	N-CA-C	-5.81	98.43	110.80
1	A	175	PHE	CA-CB-CG	5.77	119.57	113.80
1	A	3	ARG	CA-C-O	-5.63	114.62	120.92
1	A	56	GLU	N-CA-CB	5.58	116.21	109.74
1	B	467	ASN	CA-CB-CG	5.35	117.95	112.60
1	B	222	ASP	CA-CB-CG	5.21	117.81	112.60
1	A	435	LYS	N-CA-C	5.17	112.87	108.22
1	B	391	HIS	CB-CA-C	5.16	119.94	110.24
1	A	181	GLY	CA-C-N	5.14	127.17	120.28
1	A	181	GLY	C-N-CA	5.14	127.17	120.28
1	A	294	THR	CA-CB-OG1	-5.11	101.93	109.60
1	B	331	ASP	CA-CB-CG	5.11	117.71	112.60
1	B	320	ASP	CA-CB-CG	5.02	117.62	112.60
1	A	331	ASP	CA-C-N	5.01	125.55	119.98
1	A	331	ASP	C-N-CA	5.01	125.55	119.98

There are no chirality outliers.

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	243	ARG	Sidechain
1	A	3	ARG	Sidechain
1	B	111	ARG	Sidechain
1	B	172	LEU	Peptide,Mainchain
1	B	218[A]	ARG	Sidechain
1	B	243	ARG	Sidechain
1	B	355	ARG	Sidechain
1	B	389	PRO	Mainchain
1	B	390	ARG	Sidechain
1	B	434	GLU	Peptide,Mainchain

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	3707	3695	3658	22	1
1	B	3737	3721	3668	40	1
2	A	32	56	56	3	0
2	B	16	28	28	0	0
3	A	17	7	5	0	0
3	B	17	7	5	0	0
4	A	24	0	0	0	0
4	B	24	0	0	2	0
5	A	130	0	0	2	0
5	B	91	0	0	1	0
All	All	7795	7514	7420	64	1

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

All (64) 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:B:434:GLU:O	1:B:434:GLU:HG2	1.72	0.86
1:B:434:GLU:O	1:B:434:GLU:CG	2.25	0.82
1:B:465:LEU:O	1:B:466:PRO:C	2.23	0.81
2:A:502:MPD:O2	5:A:601:HOH:O	2.04	0.75
1:B:4:THR:HB	1:B:13:MET:HE3	1.67	0.74
1:A:6:MET:HE2	1:A:13:MET:HE1	1.71	0.71
1:B:6:MET:HE3	1:B:13:MET:HE1	1.80	0.64
1:A:465:LEU:HD23	1:A:465:LEU:O	2.00	0.61
1:B:6:MET:HE3	1:B:13:MET:CE	2.30	0.61
1:B:217:GLU:OE2	1:B:218[B]:ARG:NH1	2.39	0.55
1:B:459:LEU:HB3	1:B:465:LEU:HB2	1.88	0.55
1:B:390:ARG:N	1:B:390:ARG:CD	2.72	0.53
1:B:436:PRO:O	1:B:437:LEU:HB2	2.09	0.52
1:B:38:CYS:O	1:B:39:ASP:HB2	2.10	0.52
1:B:88:VAL:O	1:B:92:GLU:HG3	2.09	0.52
1:B:465:LEU:O	1:B:467:ASN:N	2.43	0.52
1:A:460:THR:HA	1:A:466:PRO:HD3	1.92	0.52
1:A:6:MET:CE	1:A:13:MET:HE1	2.40	0.51
1:B:155:GLU:OE2	1:B:429:TYR:OH	2.19	0.50
1:B:11:TYR:HB2	1:B:13:MET:HE2	1.92	0.50
1:A:469:ARG:O	1:A:473:PHE:CE2	2.64	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:295:ILE:O	1:B:301:GLY:HA3	2.11	0.50
1:A:185:TYR:OH	5:A:602:HOH:O	2.20	0.50
1:A:295:ILE:O	1:A:301:GLY:HA3	2.11	0.49
1:A:172:LEU:HA	1:A:173:PRO:C	2.39	0.48
1:A:393:LEU:HD22	1:A:396:VAL:HG13	1.94	0.48
1:A:105:MET:HE3	1:A:204:ILE:HD11	1.94	0.48
1:B:194:LEU:N	1:B:195:PRO:CD	2.77	0.47
1:B:390:ARG:H	1:B:390:ARG:HD2	1.80	0.46
1:B:204:ILE:HD13	1:B:232:MET:HE3	1.98	0.46
1:B:314:VAL:HG23	1:B:315:THR:HG23	1.97	0.46
1:B:465:LEU:C	1:B:466:PRO:O	2.55	0.46
1:A:143:TRP:CD2	1:A:286:MET:HE3	2.50	0.45
1:B:234:CYS:HB2	4:B:503:SF4:S3	2.56	0.45
1:A:30:ILE:HD12	1:A:81:ILE:HG12	1.97	0.45
1:B:22:PRO:HB2	1:B:239:TYR:CD2	2.52	0.45
1:A:465:LEU:O	1:A:465:LEU:CD2	2.64	0.45
1:A:453:SER:O	1:A:457:LYS:HG3	2.17	0.45
1:B:390:ARG:CD	1:B:390:ARG:H	2.29	0.44
1:A:2:SER:HA	1:A:10:GLU:HB3	1.98	0.44
1:B:459:LEU:CB	1:B:465:LEU:HB2	2.47	0.44
1:B:314:VAL:HG21	1:B:340:VAL:HG11	2.00	0.43
1:A:31:ASP:OD2	1:A:34:LYS:HE2	2.18	0.43
1:B:88:VAL:HG22	1:B:266:MET:HE3	2.00	0.43
1:B:11:TYR:CB	1:B:13:MET:HE2	2.48	0.43
1:A:396:VAL:O	1:A:400:LYS:HG3	2.19	0.43
1:B:180:PRO:HD2	4:B:503:SF4:S2	2.59	0.42
1:A:326:ALA:HB2	2:A:504:MPD:H53	2.01	0.42
1:A:392:LYS:C	1:A:394:PRO:HD3	2.45	0.42
1:A:479:TYR:CD1	1:A:479:TYR:C	2.97	0.42
1:B:206[A]:MET:HB3	1:B:445:LEU:HD22	2.02	0.42
1:B:425:VAL:O	1:B:428:LEU:HB3	2.20	0.42
1:A:22:PRO:HB2	1:A:239:TYR:CD2	2.55	0.42
2:A:502:MPD:O4	2:A:502:MPD:HM1	2.20	0.42
1:B:88:VAL:HG13	1:B:266:MET:HE3	2.01	0.42
1:B:90:GLU:OE2	1:B:227:TYR:OH	2.18	0.42
1:B:393:LEU:N	1:B:394:PRO:CD	2.83	0.41
1:B:390:ARG:N	1:B:390:ARG:HD2	2.35	0.41
1:A:231:ILE:HG21	1:A:263:LEU:HD22	2.03	0.41
1:B:403:ARG:O	1:B:407:VAL:HG23	2.20	0.41
1:B:97:ASP:OD1	1:B:97:ASP:C	2.64	0.41
1:B:282[A]:ARG:NH1	5:B:609:HOH:O	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:232:MET:O	1:B:259:THR:HA	2.21	0.40
1:B:3:ARG:HG3	1:B:11:TYR:C	2.46	0.40

All (1) 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)
1:A:220[B]:LYS:HZ1	1:B:24:LYS:O[3_544]	1.58	0.02

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	481/490 (98%)	462 (96%)	17 (4%)	2 (0%)	30	16
1	B	486/490 (99%)	472 (97%)	14 (3%)	0	100	100
All	All	967/980 (99%)	934 (97%)	31 (3%)	2 (0%)	44	29

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	396	VAL
1	A	393	LEU

5.3.2 Protein sidechains [i](#)

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	396/402 (98%)	384 (97%)	12 (3%)	36	15
1	B	401/402 (100%)	389 (97%)	12 (3%)	36	15
All	All	797/804 (99%)	773 (97%)	24 (3%)	35	15

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ARG
1	A	56	GLU
1	A	210	LEU
1	A	251	MET
1	A	294	THR
1	A	346	LYS
1	A	357	LYS
1	A	392	LYS
1	A	396	VAL
1	A	456	VAL
1	A	465	LEU
1	A	471	SER
1	B	32	GLU
1	B	111	ARG
1	B	135	GLN
1	B	258	LEU
1	B	355	ARG
1	B	390	ARG
1	B	392	LYS
1	B	394	PRO
1	B	396	VAL
1	B	400	LYS
1	B	437	LEU
1	B	465	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	225	GLN
1	B	391	HIS

5.3.3 RNA ⓘ

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](#)

14 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	MPD	B	502	-	7,7,7	0.08	0	9,10,10	0.31	0
4	SF4	A	507	1	0,12,12	-	-	-		
4	SF4	A	506	1	0,12,12	-	-	-		
2	MPD	A	503	-	7,7,7	0.22	0	9,10,10	0.59	0
3	402	B	504	1	13,19,19	5.41	8 (61%)	2,36,36	1.44	0
2	MPD	B	501	-	7,7,7	0.14	0	9,10,10	0.24	0
4	SF4	B	505	1	0,12,12	-	-	-		
4	SF4	B	506	1	0,12,12	-	-	-		
2	MPD	A	504	-	7,7,7	0.12	0	9,10,10	0.42	0
4	SF4	A	508	1	0,12,12	-	-	-		
4	SF4	B	503	1	0,12,12	-	-	-		
2	MPD	A	501	-	7,7,7	0.17	0	9,10,10	0.55	0
2	MPD	A	502	-	7,7,7	0.21	0	9,10,10	0.36	0
3	402	A	505	1	13,19,19	5.29	7 (53%)	2,36,36	1.53	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
2	MPD	B	502	-	-	1/5/5/5	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SF4	A	507	1	-	-	0/6/5/5
4	SF4	A	506	1	-	-	0/6/5/5
2	MPD	A	503	-	-	2/5/5/5	-
3	402	B	504	1	-	-	0/5/3/3
2	MPD	B	501	-	-	0/5/5/5	-
4	SF4	B	505	1	-	-	0/6/5/5
4	SF4	B	506	1	-	-	0/6/5/5
2	MPD	A	504	-	-	0/5/5/5	-
4	SF4	A	508	1	-	-	0/6/5/5
4	SF4	B	503	1	-	-	0/6/5/5
2	MPD	A	501	-	-	1/5/5/5	-
2	MPD	A	502	-	-	1/5/5/5	-
3	402	A	505	1	-	-	0/5/3/3

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	505	402	C2-S2	-10.41	1.66	1.85
3	B	504	402	C1-S1	-10.08	1.67	1.85
3	B	504	402	C2-S2	-9.58	1.68	1.85
3	A	505	402	S1-FE2	-8.62	2.14	2.26
3	A	505	402	C1-S1	-8.58	1.69	1.85
3	B	504	402	S2-FE1	-7.21	2.16	2.26
3	A	505	402	O5-C5	7.20	1.29	1.17
3	B	504	402	S1-FE2	-6.71	2.16	2.26
3	B	504	402	C4-N4	6.17	1.26	1.15
3	B	504	402	O5-C5	6.05	1.28	1.17
3	A	505	402	S1-FE1	-5.57	2.18	2.26
3	A	505	402	S2-FE2	-3.98	2.20	2.26
3	B	504	402	S2-FE2	-2.86	2.22	2.26
3	B	504	402	C6-N6	2.12	1.18	1.15
3	A	505	402	O3-C3	2.01	1.20	1.15

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	MPD	C2-C3-C4-O4
2	A	502	MPD	C2-C3-C4-C5
2	A	503	MPD	C2-C3-C4-O4

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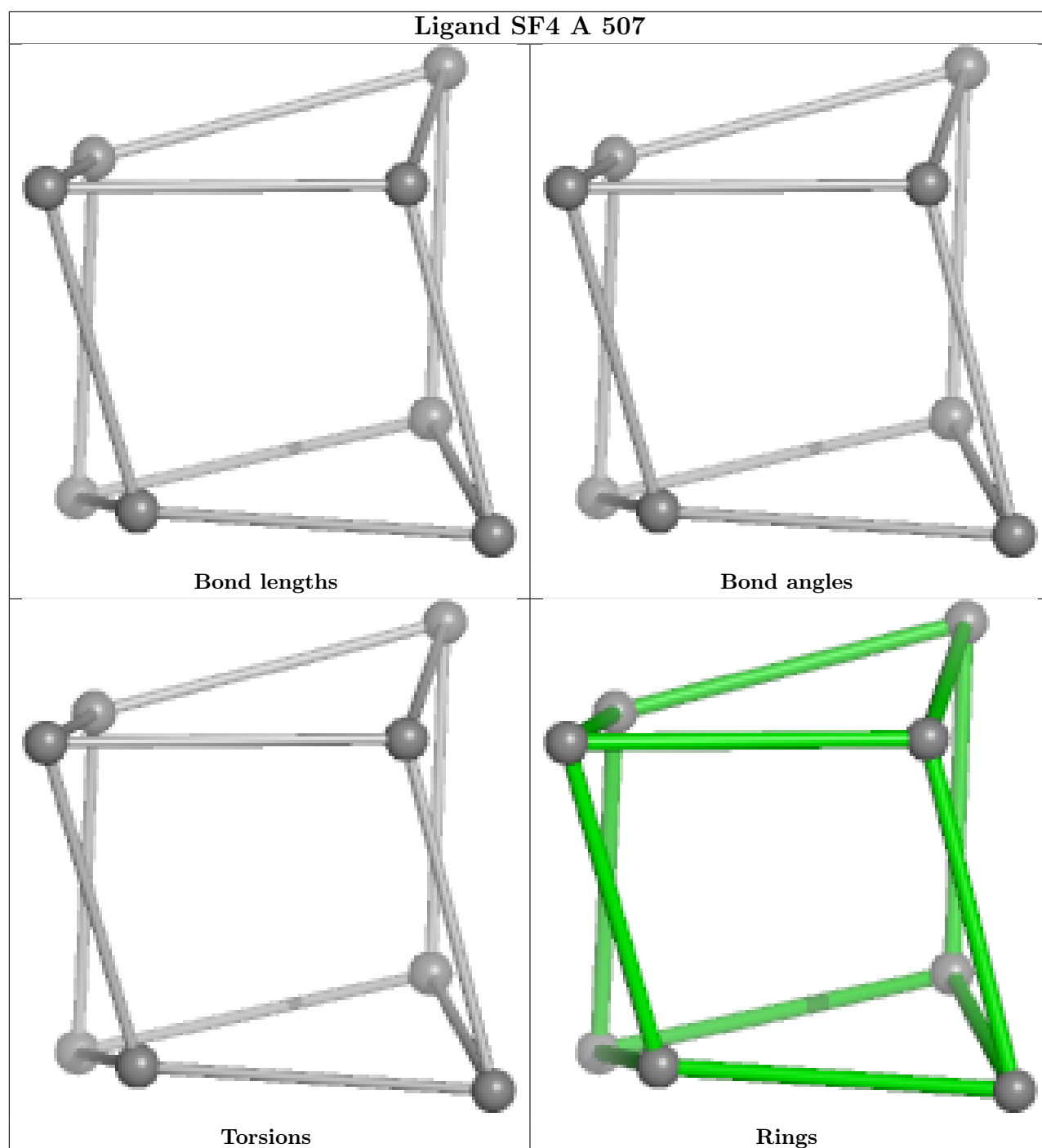
Mol	Chain	Res	Type	Atoms
2	B	502	MPD	O2-C2-C3-C4
2	A	503	MPD	C2-C3-C4-C5

There are no ring outliers.

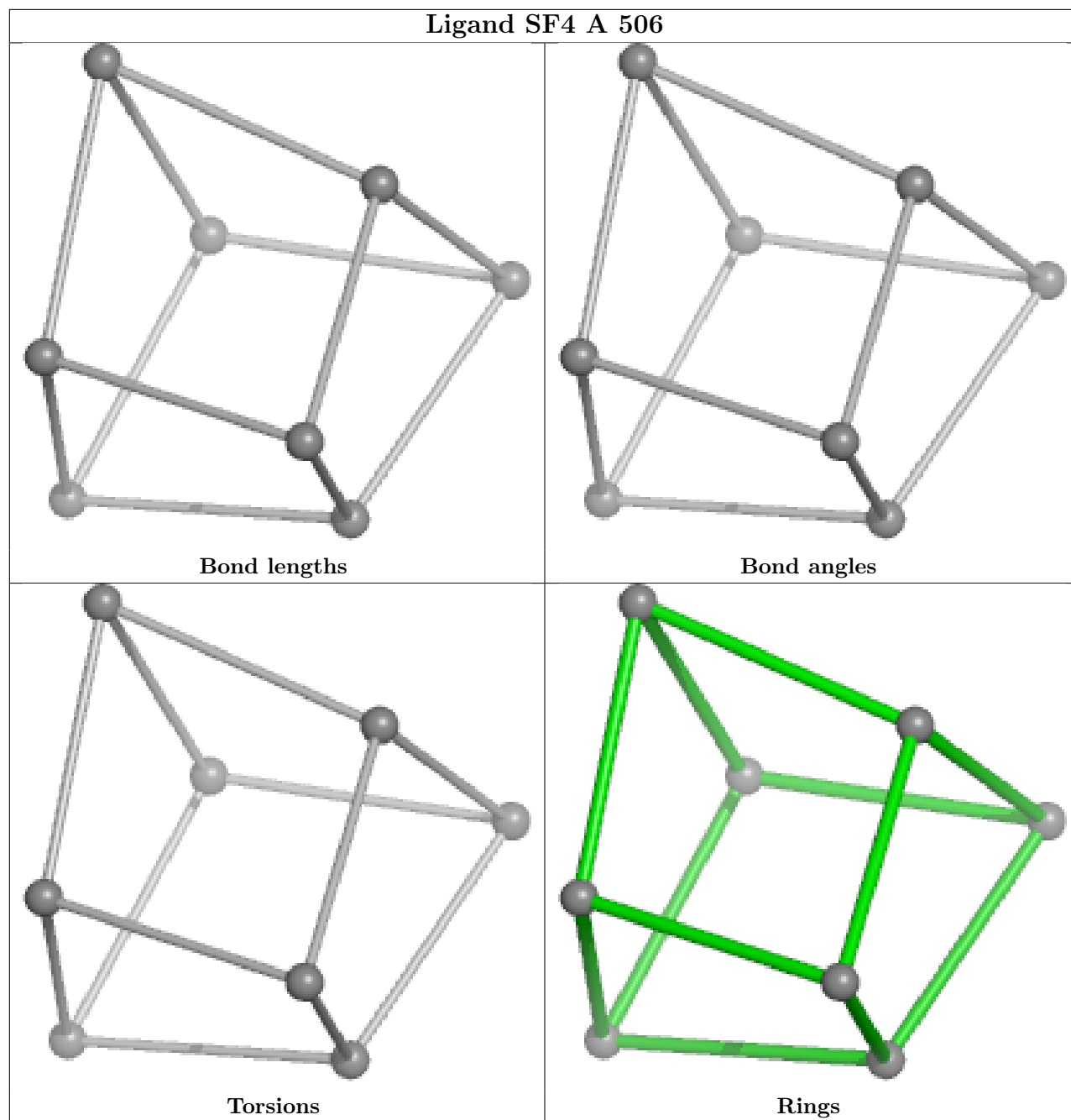
3 monomers are involved in 5 short contacts:

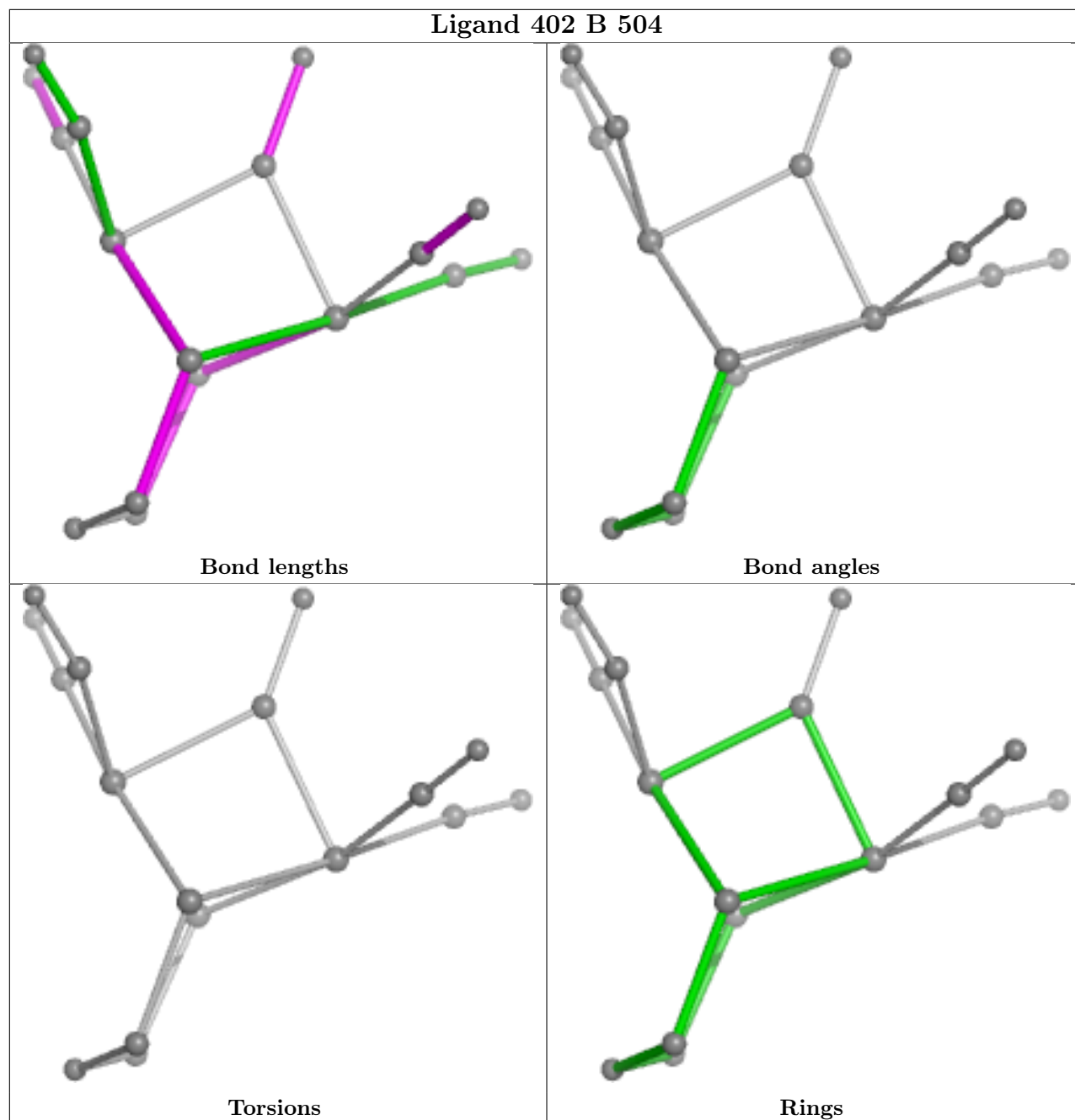
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	504	MPD	1	0
4	B	503	SF4	2	0
2	A	502	MPD	2	0

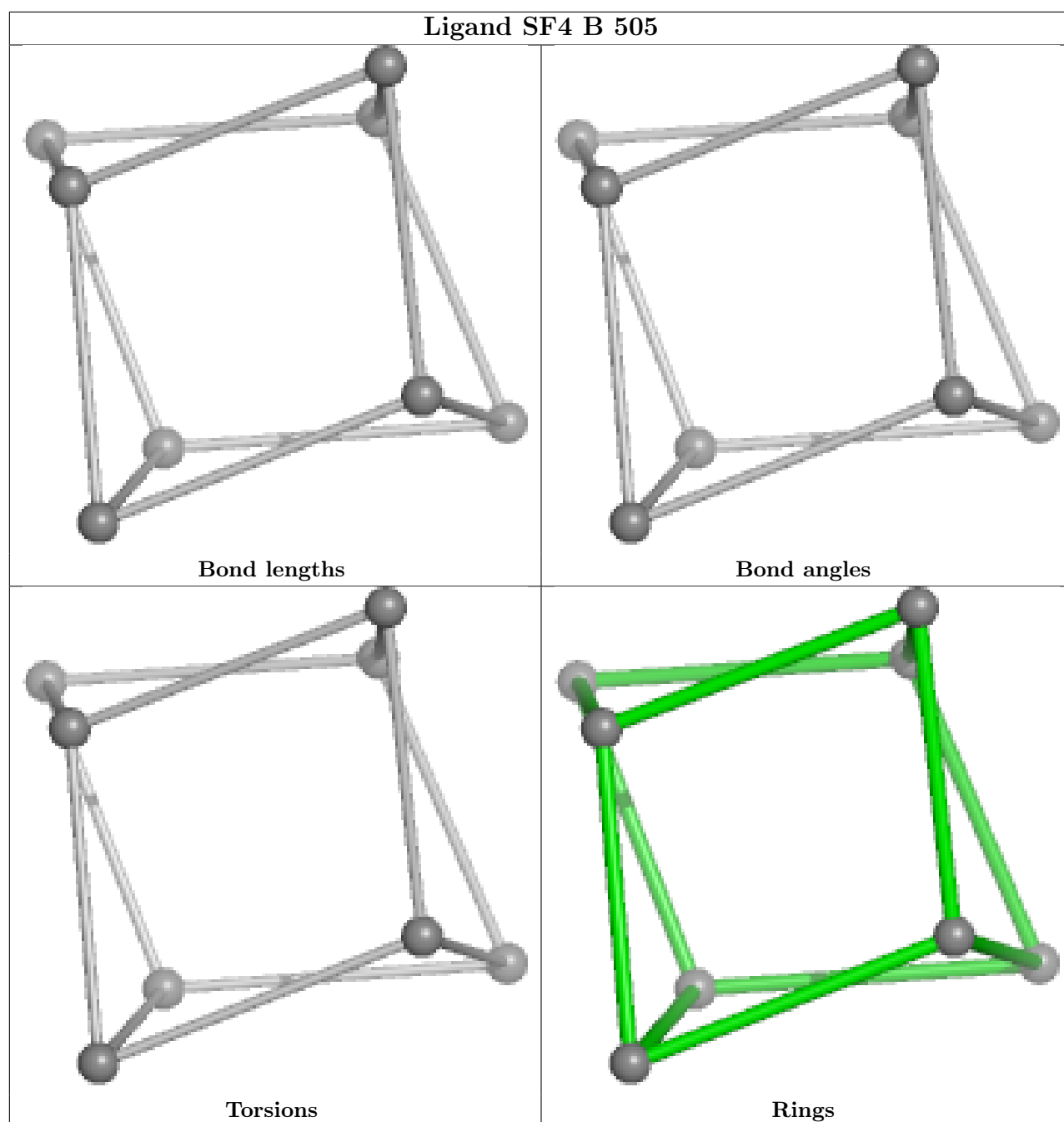
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

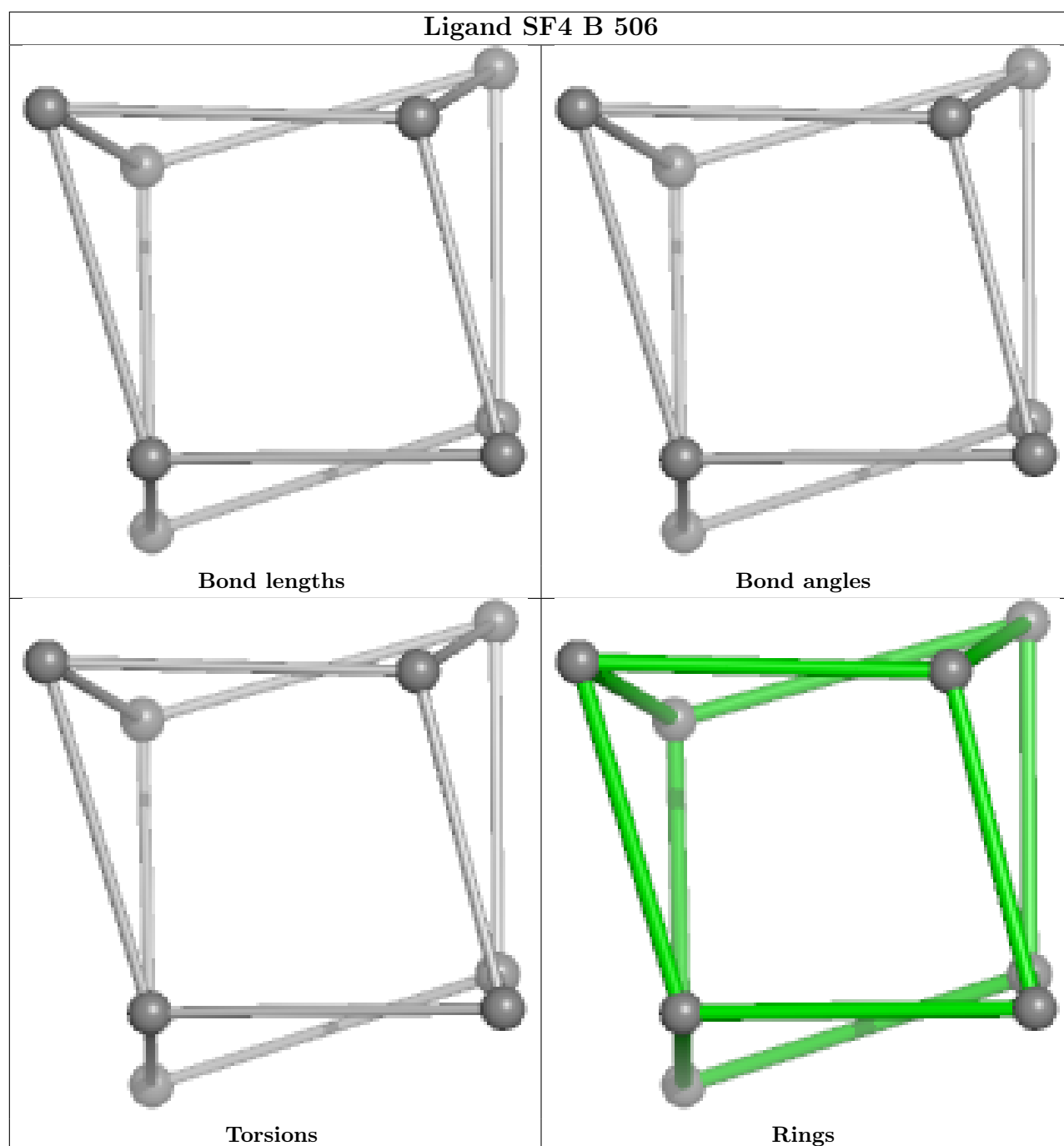


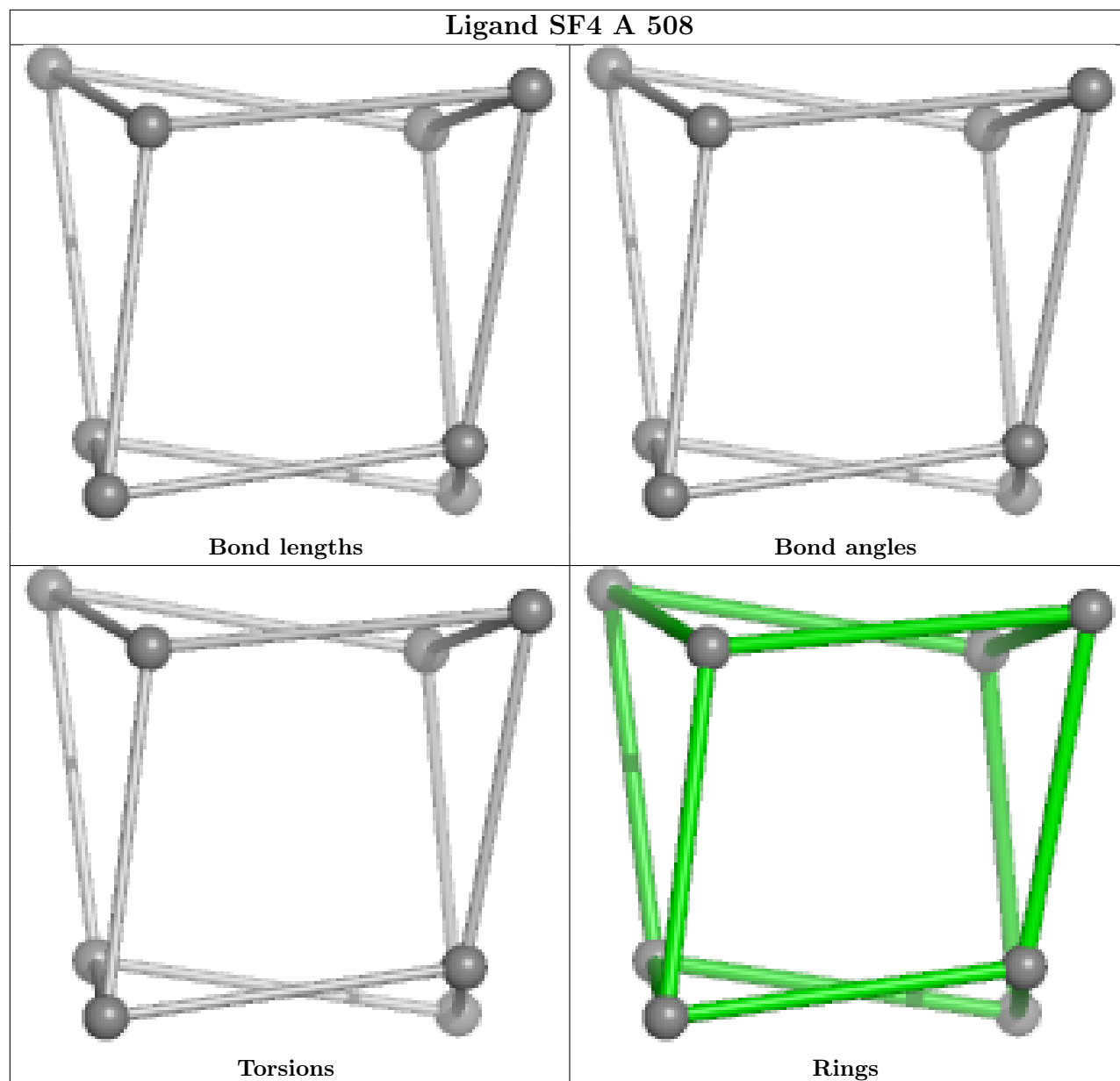
Ligand SF4 A 506



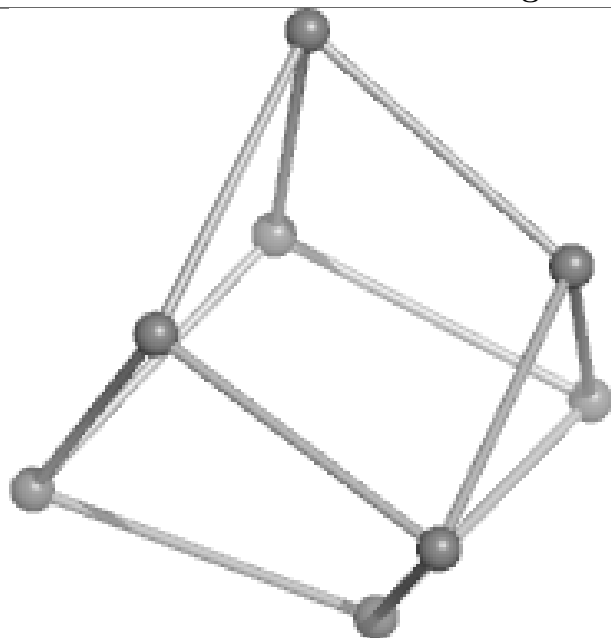




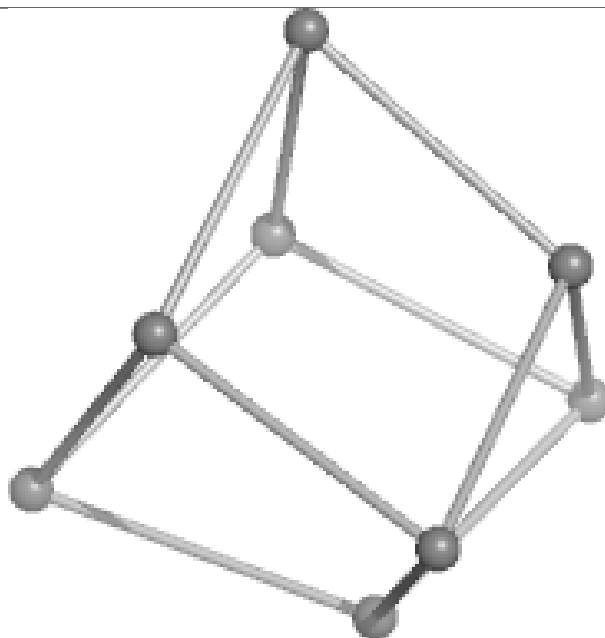




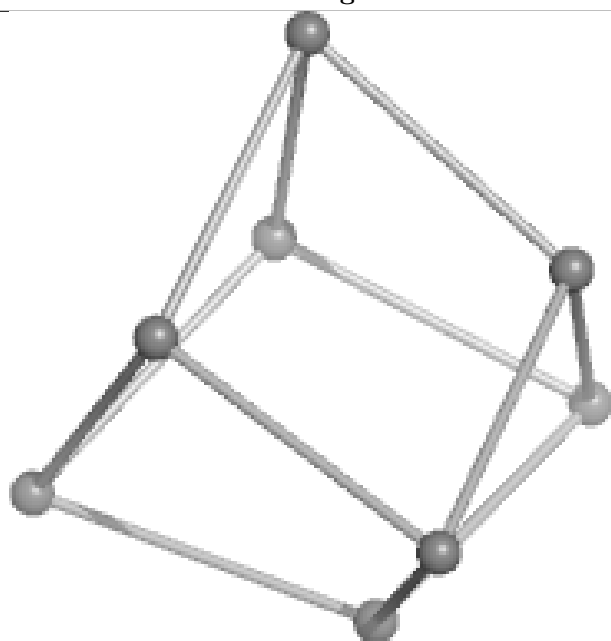
Ligand SF4 B 503



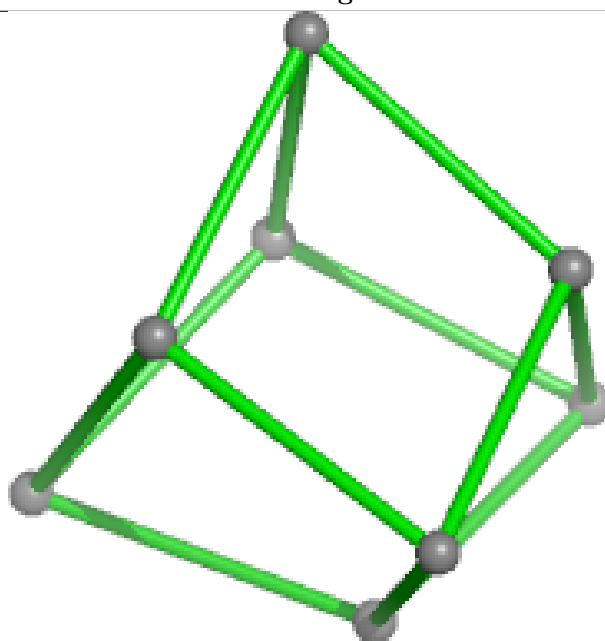
Bond lengths



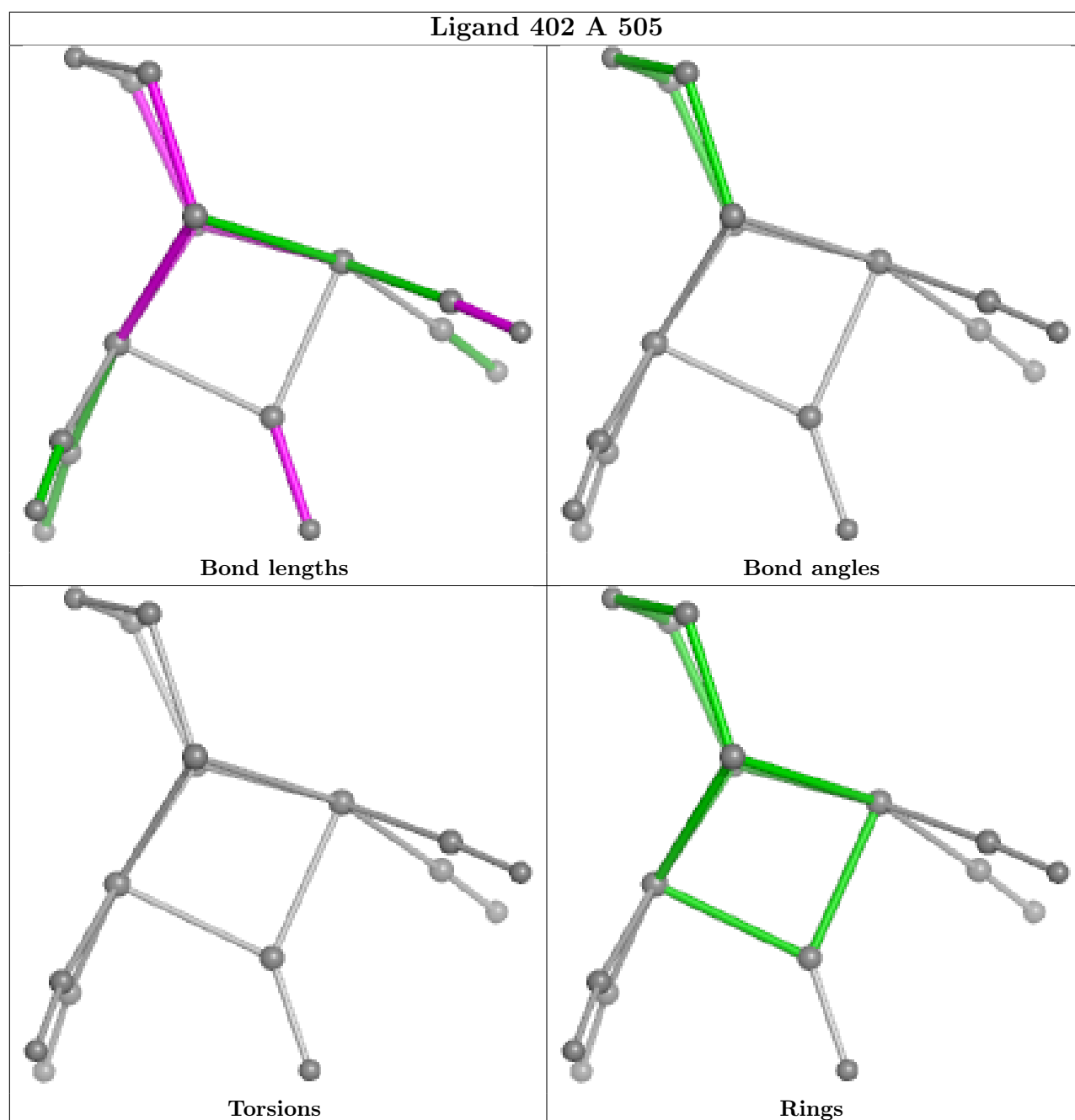
Bond angles



Torsions



Rings



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	478/490 (97%)	0.48	38 (7%)	20 23	17, 35, 69, 134	4 (0%)
1	B	480/490 (97%)	0.71	31 (6%)	26 31	15, 39, 68, 134	5 (1%)
All	All	958/980 (97%)	0.59	69 (7%)	23 27	15, 37, 69, 134	9 (0%)

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	SER	6.5
1	B	393	LEU	6.0
1	B	390	ARG	5.2
1	A	393	LEU	5.0
1	B	396	VAL	4.8
1	A	465	LEU	4.8
1	B	465	LEU	4.8
1	A	473	PHE	4.6
1	A	466	PRO	4.6
1	B	399	ALA	4.5
1	A	396	VAL	4.4
1	A	51	PHE	4.3
1	A	391	HIS	4.0
1	A	3	ARG	3.9
1	A	467	ASN	3.6
1	A	63	ILE	3.6
1	B	466	PRO	3.6
1	A	4	THR	3.5
1	A	459	LEU	3.5
1	A	456	VAL	3.5
1	A	476	PRO	3.4
1	B	122	VAL	3.3
1	A	394	PRO	3.3
1	A	460	THR	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	392	LYS	3.2
1	A	478	PRO	3.2
1	A	46	PRO	3.2
1	B	2	SER	3.1
1	B	391	HIS	3.1
1	B	415	PRO	3.0
1	B	481	SER	3.0
1	B	139	PHE	3.0
1	A	479	TYR	3.0
1	A	28	VAL	2.9
1	B	314	VAL	2.8
1	A	442	HIS	2.8
1	A	60	ILE	2.7
1	B	398	ALA	2.7
1	A	470	ALA	2.7
1	A	225[A]	GLN	2.7
1	B	394	PRO	2.6
1	B	137	LEU	2.6
1	B	426	LYS	2.5
1	A	395	GLN	2.5
1	B	98	GLY	2.4
1	A	464	LYS	2.3
1	A	468	PRO	2.3
1	A	461	THR	2.3
1	B	4	THR	2.3
1	B	125	VAL	2.3
1	B	395	GLN	2.3
1	B	209	ALA	2.3
1	B	414	PHE	2.2
1	A	366	GLY	2.2
1	B	218[A]	ARG	2.2
1	B	322	TRP	2.2
1	B	100	VAL	2.2
1	A	50	ILE	2.2
1	A	65	ALA	2.2
1	A	469	ARG	2.2
1	A	463	GLY	2.1
1	A	477	TYR	2.1
1	A	26	HIS	2.1
1	B	170[A]	MET	2.1
1	A	220[A]	LYS	2.1
1	B	169	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	211	ALA	2.0
1	B	123	GLY	2.0
1	B	103	ILE	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](#)

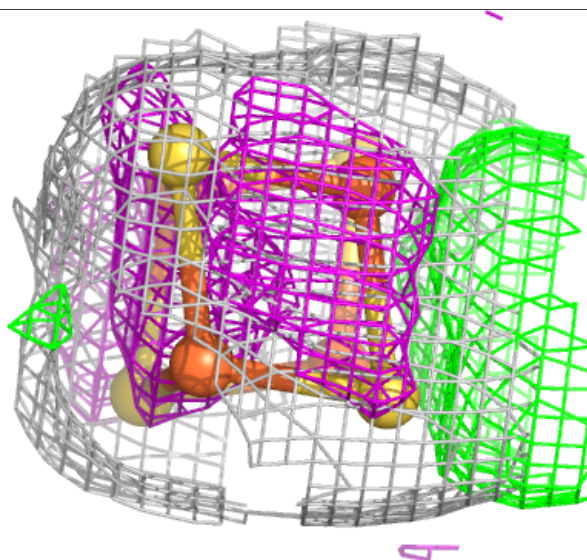
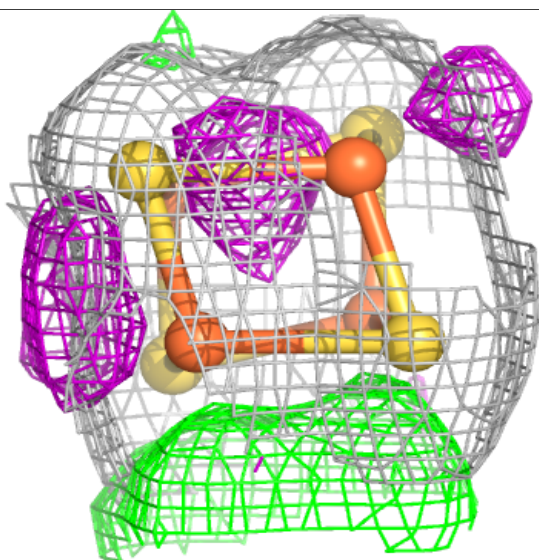
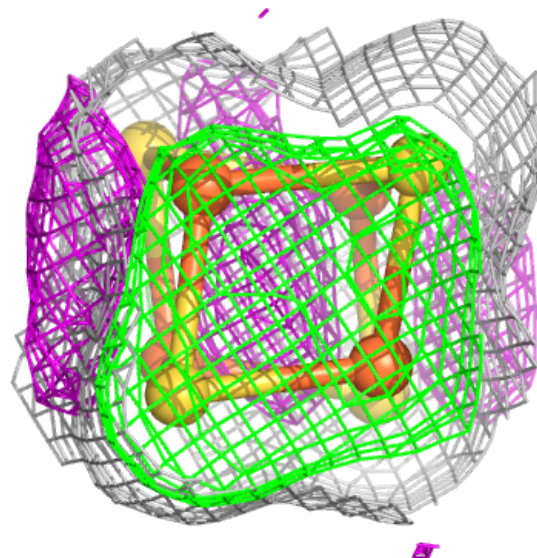
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MPD	A	504	8/8	0.65	0.20	60,70,73,73	2
2	MPD	A	503	8/8	0.66	0.25	68,72,72,77	2
2	MPD	A	502	8/8	0.83	0.19	68,75,78,84	2
2	MPD	B	502	8/8	0.87	0.17	63,68,72,72	2
2	MPD	B	501	8/8	0.89	0.11	49,53,57,58	2
2	MPD	A	501	8/8	0.90	0.13	49,56,61,61	2
4	SF4	A	508	8/8	0.96	0.06	33,40,43,46	0
4	SF4	A	507	8/8	0.97	0.06	33,37,39,41	0
3	402	B	504	17/17	0.98	0.07	22,31,37,37	1
4	SF4	A	506	8/8	0.98	0.04	27,28,29,30	0
4	SF4	B	503	8/8	0.98	0.04	26,27,28,29	0
3	402	A	505	17/17	0.99	0.05	21,26,28,29	1
4	SF4	B	505	8/8	0.99	0.04	29,31,33,33	0
4	SF4	B	506	8/8	0.99	0.04	26,27,28,29	0

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

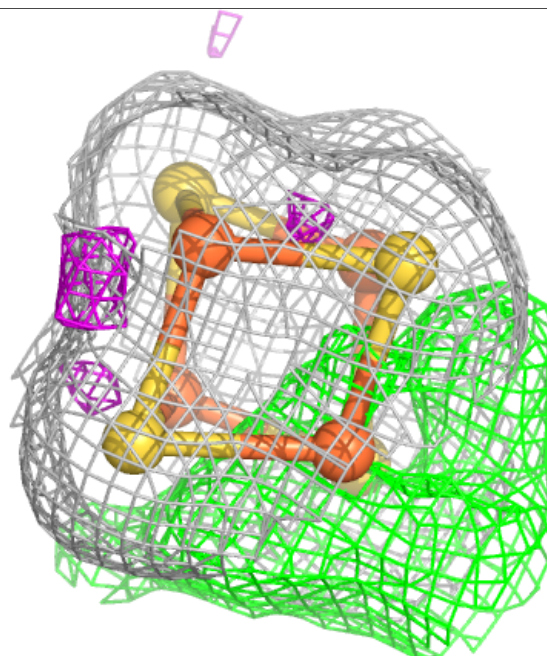
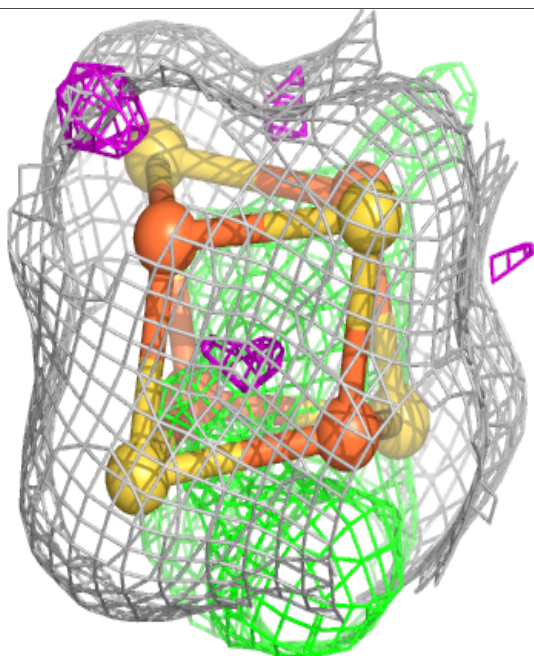
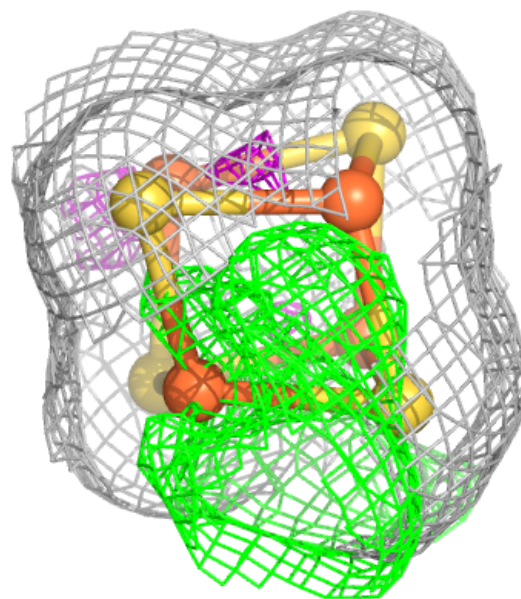
Electron density around SF4 A 508:

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



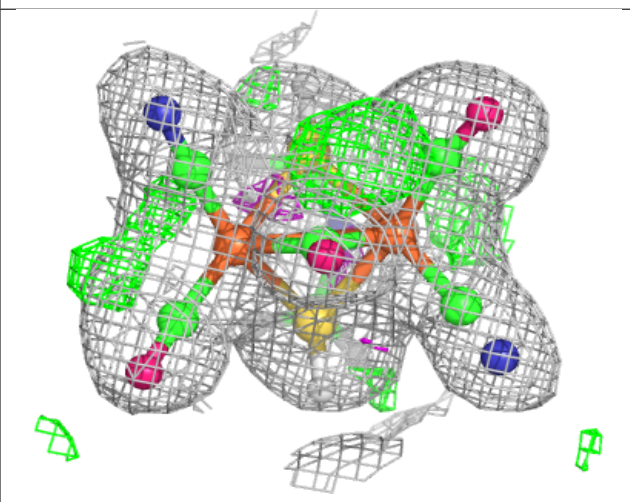
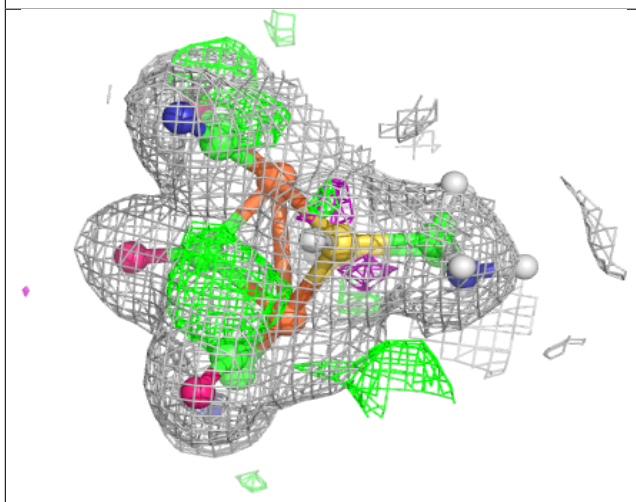
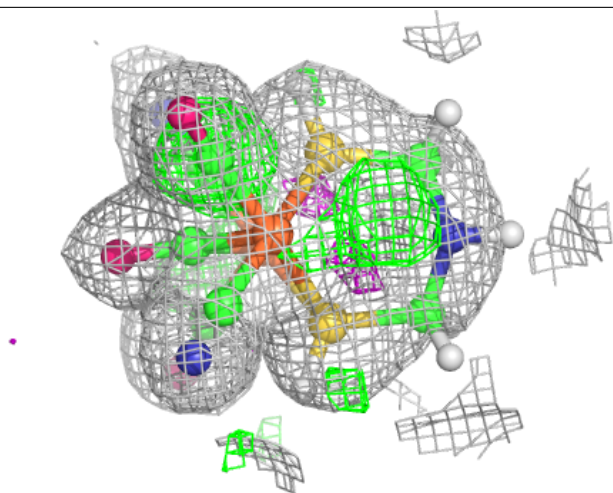
Electron density around SF4 A 507:

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



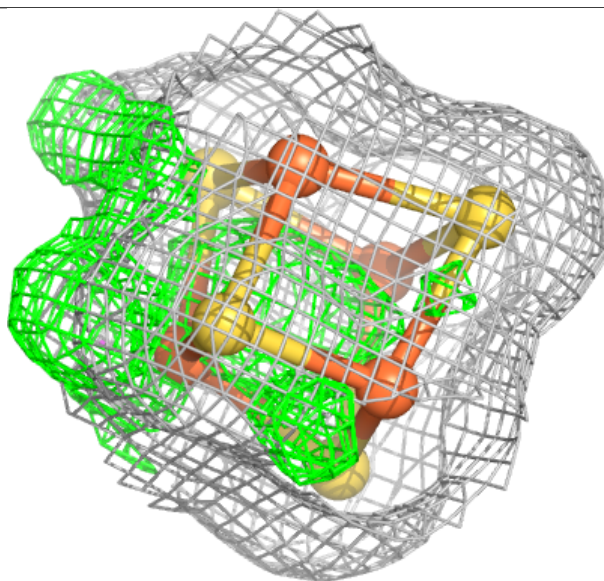
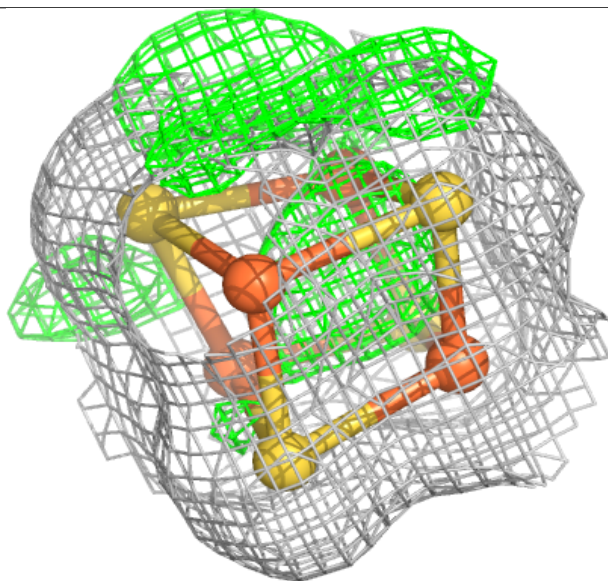
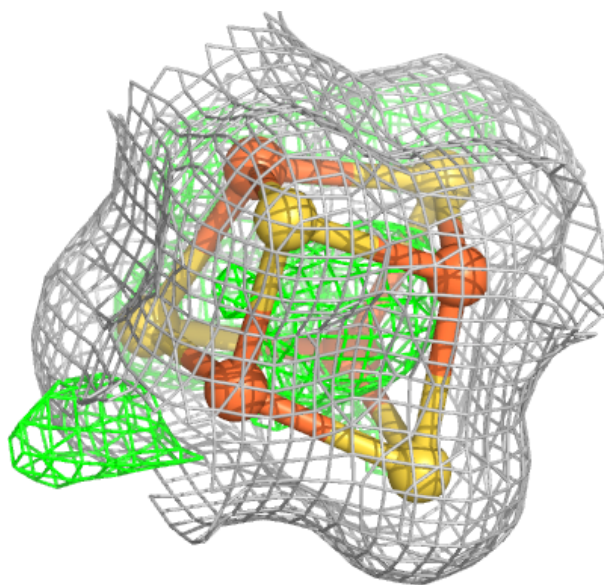
Electron density around 402 B 504:

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



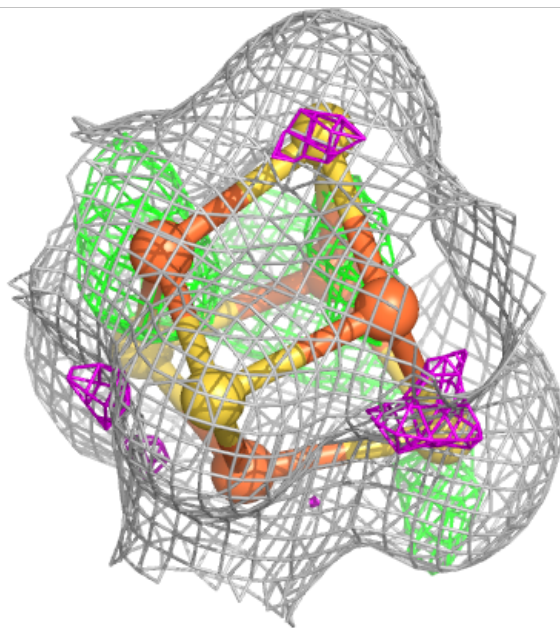
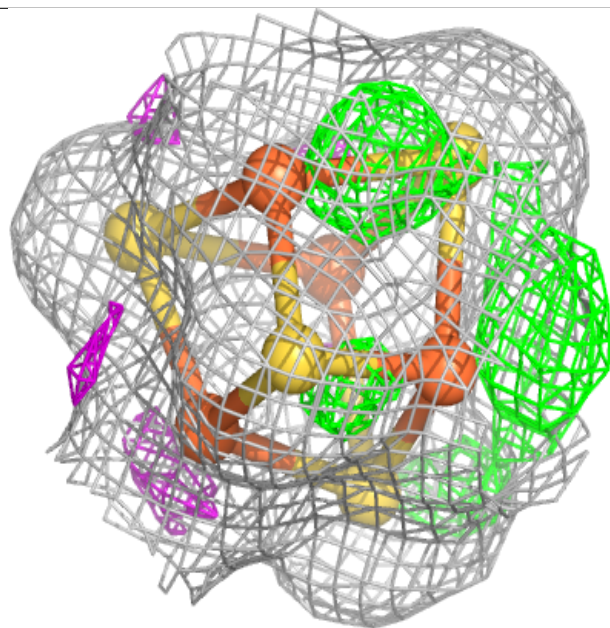
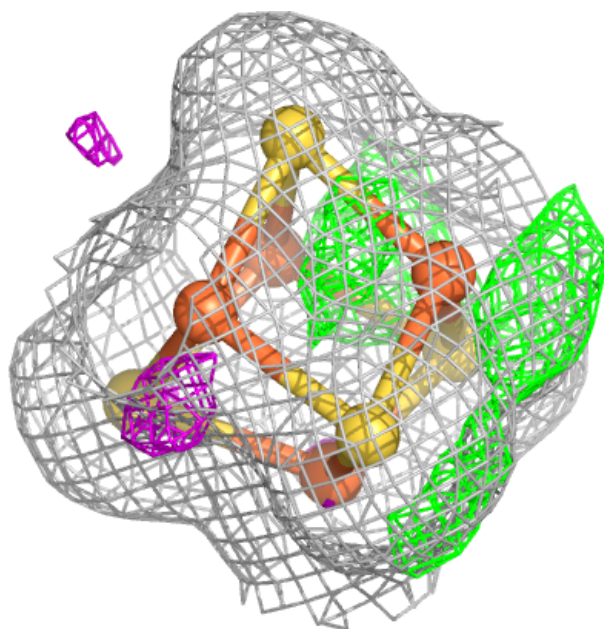
Electron density around SF4 A 506:

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



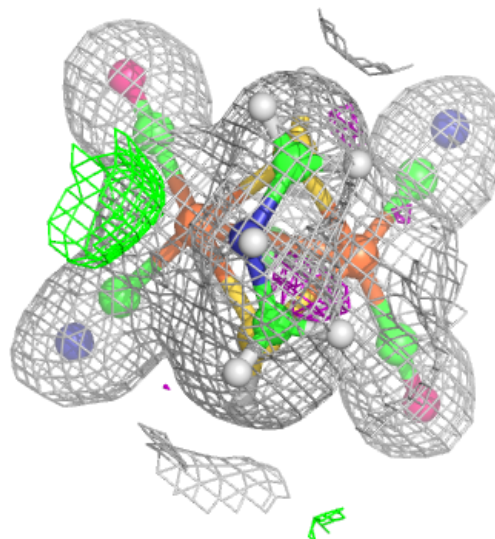
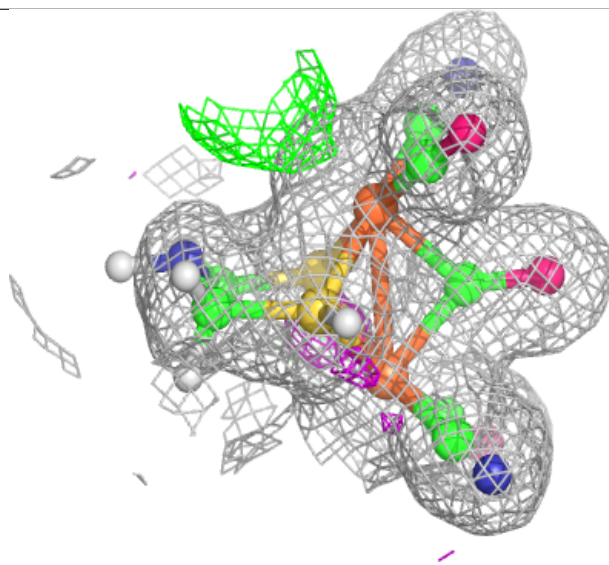
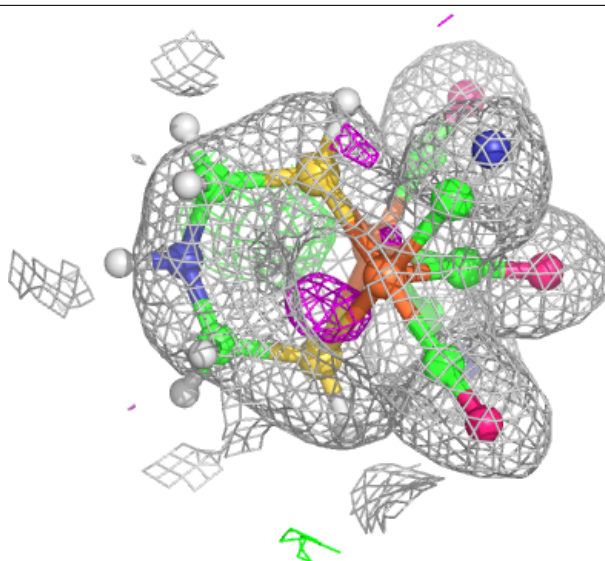
Electron density around SF4 B 503:

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



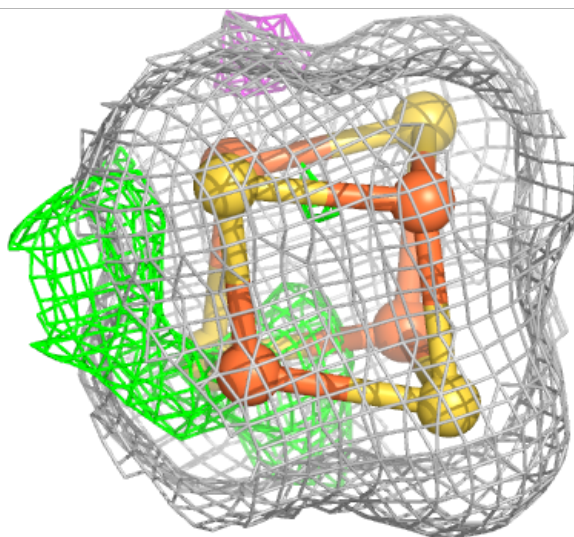
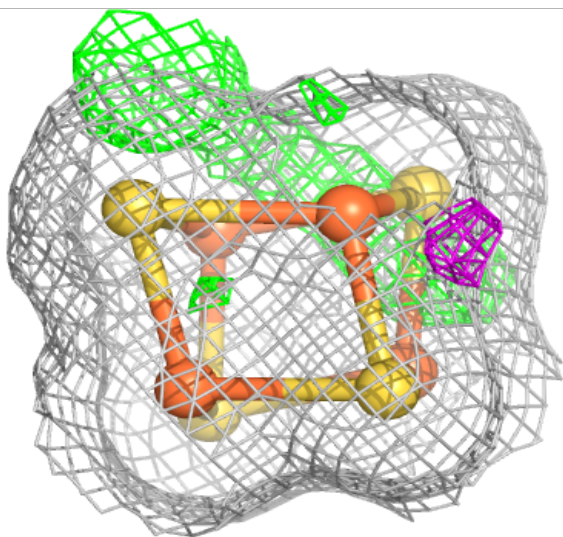
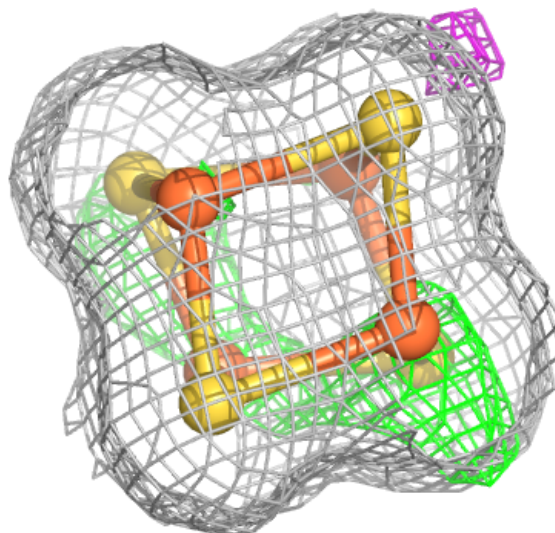
Electron density around 402 A 505:

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



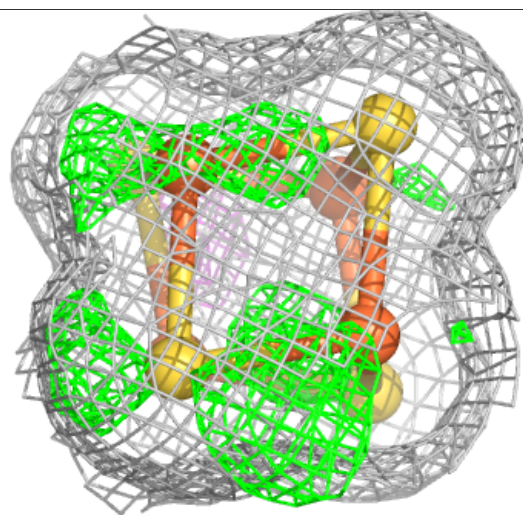
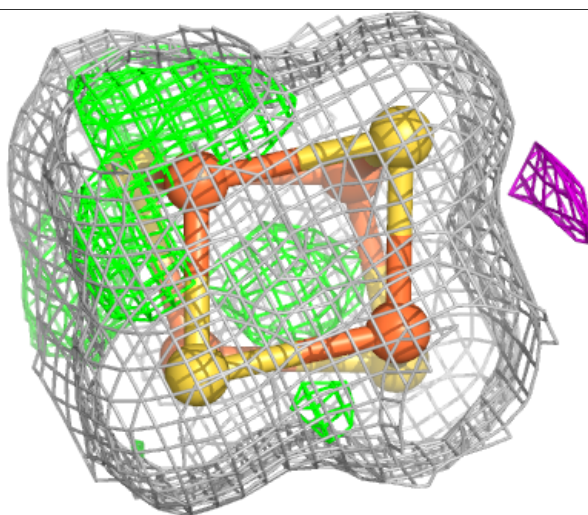
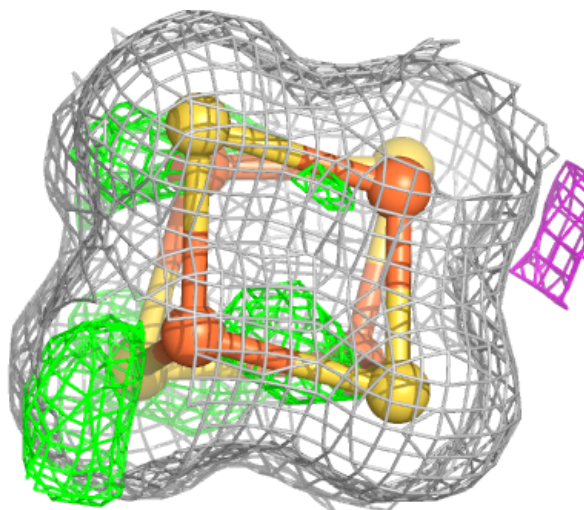
Electron density around SF4 B 505:

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



Electron density around SF4 B 506:

$2mF_o-DF_c$ (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.