wwPDB X-ray Structure Validation Summary Report (i)

Oct 4, 2023 – 11:26 AM EDT

PDB ID	:	6UNZ
Title	:	Crystal structure of cytosolic fumarate hydratase from Leishmania major
Authors	:	Feliciano, P.R.; Drennan, C.L.
Deposited on	:	2019-10-14
Resolution	:	3.19 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i) 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 (i)) were used in the production of this report:

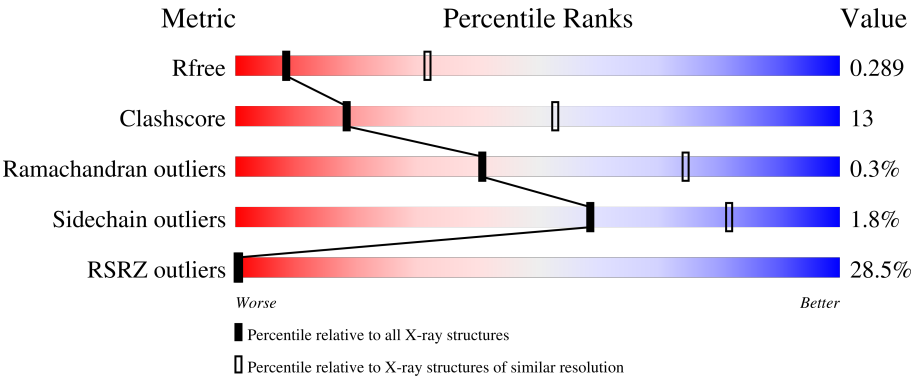
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.19 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}	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	604	22% 68% 20% 11%
1	B	604	20% 67% 21% · 12%
1	C	604	29% 62% 25% · 12%
1	D	604	28% 66% 21% · 12%
1	E	604	29% 66% 21% · 12%

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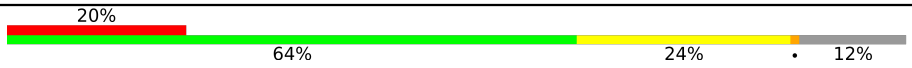
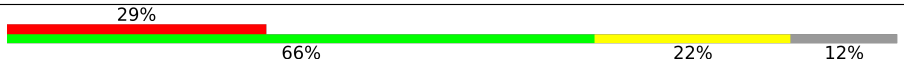
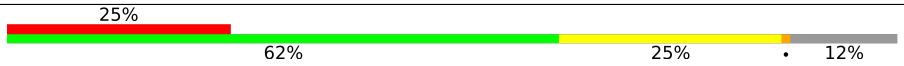
Mol	Chain	Length	Quality of chain
1	F	604	
1	G	604	
1	H	604	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SF4	B	601	-	-	X	-
2	SF4	C	601	-	-	X	-
2	SF4	F	601	-	-	X	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 31246 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 fumarate hydratase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	539	Total	C	N	O	S	0	0	0
			3933	2469	688	758	18			
1	B	534	Total	C	N	O	S	0	0	0
			3933	2480	681	755	17			
1	C	532	Total	C	N	O	S	0	0	0
			3822	2387	678	737	20			
1	D	530	Total	C	N	O	S	0	0	0
			3874	2440	677	738	19			
1	E	531	Total	C	N	O	S	0	0	0
			3863	2429	677	736	21			
1	F	531	Total	C	N	O	S	0	1	0
			3981	2512	690	759	20			
1	G	532	Total	C	N	O	S	0	0	0
			3873	2430	684	742	17			
1	H	531	Total	C	N	O	S	0	0	0
			3888	2448	673	749	18			

There are 288 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-35	MET	-	expression tag	UNP E9AE57
A	-34	GLY	-	expression tag	UNP E9AE57
A	-33	SER	-	expression tag	UNP E9AE57
A	-32	SER	-	expression tag	UNP E9AE57
A	-31	HIS	-	expression tag	UNP E9AE57
A	-30	HIS	-	expression tag	UNP E9AE57
A	-29	HIS	-	expression tag	UNP E9AE57
A	-28	HIS	-	expression tag	UNP E9AE57
A	-27	HIS	-	expression tag	UNP E9AE57
A	-26	HIS	-	expression tag	UNP E9AE57
A	-25	SER	-	expression tag	UNP E9AE57
A	-24	SER	-	expression tag	UNP E9AE57
A	-23	GLY	-	expression tag	UNP E9AE57

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-22	LEU	-	expression tag	UNP E9AE57
A	-21	VAL	-	expression tag	UNP E9AE57
A	-20	PRO	-	expression tag	UNP E9AE57
A	-19	ARG	-	expression tag	UNP E9AE57
A	-18	GLY	-	expression tag	UNP E9AE57
A	-17	SER	-	expression tag	UNP E9AE57
A	-16	HIS	-	expression tag	UNP E9AE57
A	-15	MET	-	expression tag	UNP E9AE57
A	-14	ALA	-	expression tag	UNP E9AE57
A	-13	SER	-	expression tag	UNP E9AE57
A	-12	MET	-	expression tag	UNP E9AE57
A	-11	THR	-	expression tag	UNP E9AE57
A	-10	GLY	-	expression tag	UNP E9AE57
A	-9	GLY	-	expression tag	UNP E9AE57
A	-8	GLN	-	expression tag	UNP E9AE57
A	-7	GLN	-	expression tag	UNP E9AE57
A	-6	MET	-	expression tag	UNP E9AE57
A	-5	GLY	-	expression tag	UNP E9AE57
A	-4	ARG	-	expression tag	UNP E9AE57
A	-3	GLY	-	expression tag	UNP E9AE57
A	-2	SER	-	expression tag	UNP E9AE57
A	-1	GLU	-	expression tag	UNP E9AE57
A	0	PHE	-	expression tag	UNP E9AE57
B	-35	MET	-	expression tag	UNP E9AE57
B	-34	GLY	-	expression tag	UNP E9AE57
B	-33	SER	-	expression tag	UNP E9AE57
B	-32	SER	-	expression tag	UNP E9AE57
B	-31	HIS	-	expression tag	UNP E9AE57
B	-30	HIS	-	expression tag	UNP E9AE57
B	-29	HIS	-	expression tag	UNP E9AE57
B	-28	HIS	-	expression tag	UNP E9AE57
B	-27	HIS	-	expression tag	UNP E9AE57
B	-26	HIS	-	expression tag	UNP E9AE57
B	-25	SER	-	expression tag	UNP E9AE57
B	-24	SER	-	expression tag	UNP E9AE57
B	-23	GLY	-	expression tag	UNP E9AE57
B	-22	LEU	-	expression tag	UNP E9AE57
B	-21	VAL	-	expression tag	UNP E9AE57
B	-20	PRO	-	expression tag	UNP E9AE57
B	-19	ARG	-	expression tag	UNP E9AE57
B	-18	GLY	-	expression tag	UNP E9AE57
B	-17	SER	-	expression tag	UNP E9AE57

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-16	HIS	-	expression tag	UNP E9AE57
B	-15	MET	-	expression tag	UNP E9AE57
B	-14	ALA	-	expression tag	UNP E9AE57
B	-13	SER	-	expression tag	UNP E9AE57
B	-12	MET	-	expression tag	UNP E9AE57
B	-11	THR	-	expression tag	UNP E9AE57
B	-10	GLY	-	expression tag	UNP E9AE57
B	-9	GLY	-	expression tag	UNP E9AE57
B	-8	GLN	-	expression tag	UNP E9AE57
B	-7	GLN	-	expression tag	UNP E9AE57
B	-6	MET	-	expression tag	UNP E9AE57
B	-5	GLY	-	expression tag	UNP E9AE57
B	-4	ARG	-	expression tag	UNP E9AE57
B	-3	GLY	-	expression tag	UNP E9AE57
B	-2	SER	-	expression tag	UNP E9AE57
B	-1	GLU	-	expression tag	UNP E9AE57
B	0	PHE	-	expression tag	UNP E9AE57
C	-35	MET	-	expression tag	UNP E9AE57
C	-34	GLY	-	expression tag	UNP E9AE57
C	-33	SER	-	expression tag	UNP E9AE57
C	-32	SER	-	expression tag	UNP E9AE57
C	-31	HIS	-	expression tag	UNP E9AE57
C	-30	HIS	-	expression tag	UNP E9AE57
C	-29	HIS	-	expression tag	UNP E9AE57
C	-28	HIS	-	expression tag	UNP E9AE57
C	-27	HIS	-	expression tag	UNP E9AE57
C	-26	HIS	-	expression tag	UNP E9AE57
C	-25	SER	-	expression tag	UNP E9AE57
C	-24	SER	-	expression tag	UNP E9AE57
C	-23	GLY	-	expression tag	UNP E9AE57
C	-22	LEU	-	expression tag	UNP E9AE57
C	-21	VAL	-	expression tag	UNP E9AE57
C	-20	PRO	-	expression tag	UNP E9AE57
C	-19	ARG	-	expression tag	UNP E9AE57
C	-18	GLY	-	expression tag	UNP E9AE57
C	-17	SER	-	expression tag	UNP E9AE57
C	-16	HIS	-	expression tag	UNP E9AE57
C	-15	MET	-	expression tag	UNP E9AE57
C	-14	ALA	-	expression tag	UNP E9AE57
C	-13	SER	-	expression tag	UNP E9AE57
C	-12	MET	-	expression tag	UNP E9AE57
C	-11	THR	-	expression tag	UNP E9AE57

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-10	GLY	-	expression tag	UNP E9AE57
C	-9	GLY	-	expression tag	UNP E9AE57
C	-8	GLN	-	expression tag	UNP E9AE57
C	-7	GLN	-	expression tag	UNP E9AE57
C	-6	MET	-	expression tag	UNP E9AE57
C	-5	GLY	-	expression tag	UNP E9AE57
C	-4	ARG	-	expression tag	UNP E9AE57
C	-3	GLY	-	expression tag	UNP E9AE57
C	-2	SER	-	expression tag	UNP E9AE57
C	-1	GLU	-	expression tag	UNP E9AE57
C	0	PHE	-	expression tag	UNP E9AE57
D	-35	MET	-	expression tag	UNP E9AE57
D	-34	GLY	-	expression tag	UNP E9AE57
D	-33	SER	-	expression tag	UNP E9AE57
D	-32	SER	-	expression tag	UNP E9AE57
D	-31	HIS	-	expression tag	UNP E9AE57
D	-30	HIS	-	expression tag	UNP E9AE57
D	-29	HIS	-	expression tag	UNP E9AE57
D	-28	HIS	-	expression tag	UNP E9AE57
D	-27	HIS	-	expression tag	UNP E9AE57
D	-26	HIS	-	expression tag	UNP E9AE57
D	-25	SER	-	expression tag	UNP E9AE57
D	-24	SER	-	expression tag	UNP E9AE57
D	-23	GLY	-	expression tag	UNP E9AE57
D	-22	LEU	-	expression tag	UNP E9AE57
D	-21	VAL	-	expression tag	UNP E9AE57
D	-20	PRO	-	expression tag	UNP E9AE57
D	-19	ARG	-	expression tag	UNP E9AE57
D	-18	GLY	-	expression tag	UNP E9AE57
D	-17	SER	-	expression tag	UNP E9AE57
D	-16	HIS	-	expression tag	UNP E9AE57
D	-15	MET	-	expression tag	UNP E9AE57
D	-14	ALA	-	expression tag	UNP E9AE57
D	-13	SER	-	expression tag	UNP E9AE57
D	-12	MET	-	expression tag	UNP E9AE57
D	-11	THR	-	expression tag	UNP E9AE57
D	-10	GLY	-	expression tag	UNP E9AE57
D	-9	GLY	-	expression tag	UNP E9AE57
D	-8	GLN	-	expression tag	UNP E9AE57
D	-7	GLN	-	expression tag	UNP E9AE57
D	-6	MET	-	expression tag	UNP E9AE57
D	-5	GLY	-	expression tag	UNP E9AE57

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-4	ARG	-	expression tag	UNP E9AE57
D	-3	GLY	-	expression tag	UNP E9AE57
D	-2	SER	-	expression tag	UNP E9AE57
D	-1	GLU	-	expression tag	UNP E9AE57
D	0	PHE	-	expression tag	UNP E9AE57
E	-35	MET	-	expression tag	UNP E9AE57
E	-34	GLY	-	expression tag	UNP E9AE57
E	-33	SER	-	expression tag	UNP E9AE57
E	-32	SER	-	expression tag	UNP E9AE57
E	-31	HIS	-	expression tag	UNP E9AE57
E	-30	HIS	-	expression tag	UNP E9AE57
E	-29	HIS	-	expression tag	UNP E9AE57
E	-28	HIS	-	expression tag	UNP E9AE57
E	-27	HIS	-	expression tag	UNP E9AE57
E	-26	HIS	-	expression tag	UNP E9AE57
E	-25	SER	-	expression tag	UNP E9AE57
E	-24	SER	-	expression tag	UNP E9AE57
E	-23	GLY	-	expression tag	UNP E9AE57
E	-22	LEU	-	expression tag	UNP E9AE57
E	-21	VAL	-	expression tag	UNP E9AE57
E	-20	PRO	-	expression tag	UNP E9AE57
E	-19	ARG	-	expression tag	UNP E9AE57
E	-18	GLY	-	expression tag	UNP E9AE57
E	-17	SER	-	expression tag	UNP E9AE57
E	-16	HIS	-	expression tag	UNP E9AE57
E	-15	MET	-	expression tag	UNP E9AE57
E	-14	ALA	-	expression tag	UNP E9AE57
E	-13	SER	-	expression tag	UNP E9AE57
E	-12	MET	-	expression tag	UNP E9AE57
E	-11	THR	-	expression tag	UNP E9AE57
E	-10	GLY	-	expression tag	UNP E9AE57
E	-9	GLY	-	expression tag	UNP E9AE57
E	-8	GLN	-	expression tag	UNP E9AE57
E	-7	GLN	-	expression tag	UNP E9AE57
E	-6	MET	-	expression tag	UNP E9AE57
E	-5	GLY	-	expression tag	UNP E9AE57
E	-4	ARG	-	expression tag	UNP E9AE57
E	-3	GLY	-	expression tag	UNP E9AE57
E	-2	SER	-	expression tag	UNP E9AE57
E	-1	GLU	-	expression tag	UNP E9AE57
E	0	PHE	-	expression tag	UNP E9AE57
F	-35	MET	-	expression tag	UNP E9AE57

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-34	GLY	-	expression tag	UNP E9AE57
F	-33	SER	-	expression tag	UNP E9AE57
F	-32	SER	-	expression tag	UNP E9AE57
F	-31	HIS	-	expression tag	UNP E9AE57
F	-30	HIS	-	expression tag	UNP E9AE57
F	-29	HIS	-	expression tag	UNP E9AE57
F	-28	HIS	-	expression tag	UNP E9AE57
F	-27	HIS	-	expression tag	UNP E9AE57
F	-26	HIS	-	expression tag	UNP E9AE57
F	-25	SER	-	expression tag	UNP E9AE57
F	-24	SER	-	expression tag	UNP E9AE57
F	-23	GLY	-	expression tag	UNP E9AE57
F	-22	LEU	-	expression tag	UNP E9AE57
F	-21	VAL	-	expression tag	UNP E9AE57
F	-20	PRO	-	expression tag	UNP E9AE57
F	-19	ARG	-	expression tag	UNP E9AE57
F	-18	GLY	-	expression tag	UNP E9AE57
F	-17	SER	-	expression tag	UNP E9AE57
F	-16	HIS	-	expression tag	UNP E9AE57
F	-15	MET	-	expression tag	UNP E9AE57
F	-14	ALA	-	expression tag	UNP E9AE57
F	-13	SER	-	expression tag	UNP E9AE57
F	-12	MET	-	expression tag	UNP E9AE57
F	-11	THR	-	expression tag	UNP E9AE57
F	-10	GLY	-	expression tag	UNP E9AE57
F	-9	GLY	-	expression tag	UNP E9AE57
F	-8	GLN	-	expression tag	UNP E9AE57
F	-7	GLN	-	expression tag	UNP E9AE57
F	-6	MET	-	expression tag	UNP E9AE57
F	-5	GLY	-	expression tag	UNP E9AE57
F	-4	ARG	-	expression tag	UNP E9AE57
F	-3	GLY	-	expression tag	UNP E9AE57
F	-2	SER	-	expression tag	UNP E9AE57
F	-1	GLU	-	expression tag	UNP E9AE57
F	0	PHE	-	expression tag	UNP E9AE57
G	-35	MET	-	expression tag	UNP E9AE57
G	-34	GLY	-	expression tag	UNP E9AE57
G	-33	SER	-	expression tag	UNP E9AE57
G	-32	SER	-	expression tag	UNP E9AE57
G	-31	HIS	-	expression tag	UNP E9AE57
G	-30	HIS	-	expression tag	UNP E9AE57
G	-29	HIS	-	expression tag	UNP E9AE57

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-28	HIS	-	expression tag	UNP E9AE57
G	-27	HIS	-	expression tag	UNP E9AE57
G	-26	HIS	-	expression tag	UNP E9AE57
G	-25	SER	-	expression tag	UNP E9AE57
G	-24	SER	-	expression tag	UNP E9AE57
G	-23	GLY	-	expression tag	UNP E9AE57
G	-22	LEU	-	expression tag	UNP E9AE57
G	-21	VAL	-	expression tag	UNP E9AE57
G	-20	PRO	-	expression tag	UNP E9AE57
G	-19	ARG	-	expression tag	UNP E9AE57
G	-18	GLY	-	expression tag	UNP E9AE57
G	-17	SER	-	expression tag	UNP E9AE57
G	-16	HIS	-	expression tag	UNP E9AE57
G	-15	MET	-	expression tag	UNP E9AE57
G	-14	ALA	-	expression tag	UNP E9AE57
G	-13	SER	-	expression tag	UNP E9AE57
G	-12	MET	-	expression tag	UNP E9AE57
G	-11	THR	-	expression tag	UNP E9AE57
G	-10	GLY	-	expression tag	UNP E9AE57
G	-9	GLY	-	expression tag	UNP E9AE57
G	-8	GLN	-	expression tag	UNP E9AE57
G	-7	GLN	-	expression tag	UNP E9AE57
G	-6	MET	-	expression tag	UNP E9AE57
G	-5	GLY	-	expression tag	UNP E9AE57
G	-4	ARG	-	expression tag	UNP E9AE57
G	-3	GLY	-	expression tag	UNP E9AE57
G	-2	SER	-	expression tag	UNP E9AE57
G	-1	GLU	-	expression tag	UNP E9AE57
G	0	PHE	-	expression tag	UNP E9AE57
H	-35	MET	-	expression tag	UNP E9AE57
H	-34	GLY	-	expression tag	UNP E9AE57
H	-33	SER	-	expression tag	UNP E9AE57
H	-32	SER	-	expression tag	UNP E9AE57
H	-31	HIS	-	expression tag	UNP E9AE57
H	-30	HIS	-	expression tag	UNP E9AE57
H	-29	HIS	-	expression tag	UNP E9AE57
H	-28	HIS	-	expression tag	UNP E9AE57
H	-27	HIS	-	expression tag	UNP E9AE57
H	-26	HIS	-	expression tag	UNP E9AE57
H	-25	SER	-	expression tag	UNP E9AE57
H	-24	SER	-	expression tag	UNP E9AE57
H	-23	GLY	-	expression tag	UNP E9AE57

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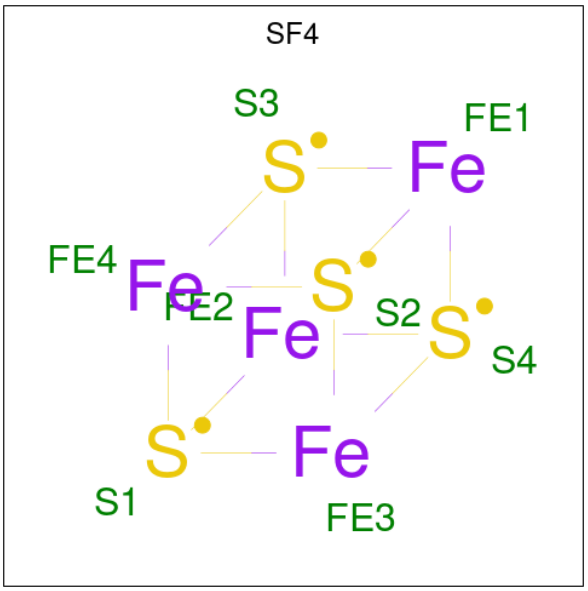
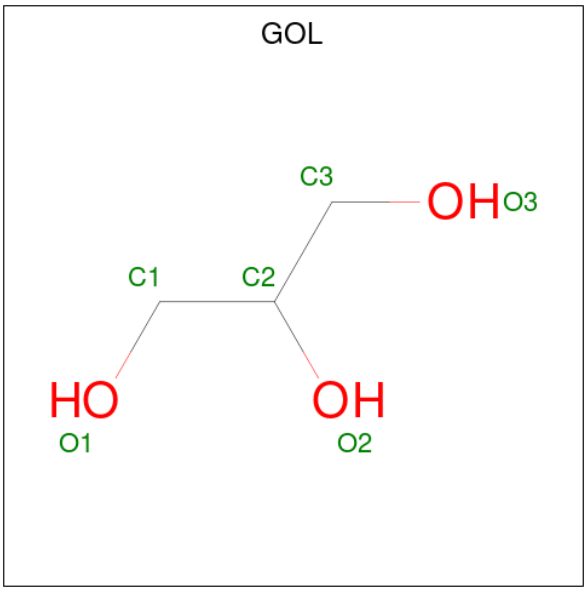
Chain	Residue	Modelled	Actual	Comment	Reference
H	-22	LEU	-	expression tag	UNP E9AE57
H	-21	VAL	-	expression tag	UNP E9AE57
H	-20	PRO	-	expression tag	UNP E9AE57
H	-19	ARG	-	expression tag	UNP E9AE57
H	-18	GLY	-	expression tag	UNP E9AE57
H	-17	SER	-	expression tag	UNP E9AE57
H	-16	HIS	-	expression tag	UNP E9AE57
H	-15	MET	-	expression tag	UNP E9AE57
H	-14	ALA	-	expression tag	UNP E9AE57
H	-13	SER	-	expression tag	UNP E9AE57
H	-12	MET	-	expression tag	UNP E9AE57
H	-11	THR	-	expression tag	UNP E9AE57
H	-10	GLY	-	expression tag	UNP E9AE57
H	-9	GLY	-	expression tag	UNP E9AE57
H	-8	GLN	-	expression tag	UNP E9AE57
H	-7	GLN	-	expression tag	UNP E9AE57
H	-6	MET	-	expression tag	UNP E9AE57
H	-5	GLY	-	expression tag	UNP E9AE57
H	-4	ARG	-	expression tag	UNP E9AE57
H	-3	GLY	-	expression tag	UNP E9AE57
H	-2	SER	-	expression tag	UNP E9AE57
H	-1	GLU	-	expression tag	UNP E9AE57
H	0	PHE	-	expression tag	UNP E9AE57

- Molecule 2 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Fe S 8 4 4	0	0
2	B	1	Total Fe S 8 4 4	0	0
2	C	1	Total Fe S 8 4 4	0	0
2	D	1	Total Fe S 8 4 4	0	0
2	E	1	Total Fe S 8 4 4	0	0
2	F	1	Total Fe S 8 4 4	0	0
2	G	1	Total Fe S 8 4 4	0	0
2	H	1	Total Fe S 8 4 4	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 6 3 3	0	0
3	E	1	Total C O 6 3 3	0	0

- Molecule 4 is water.

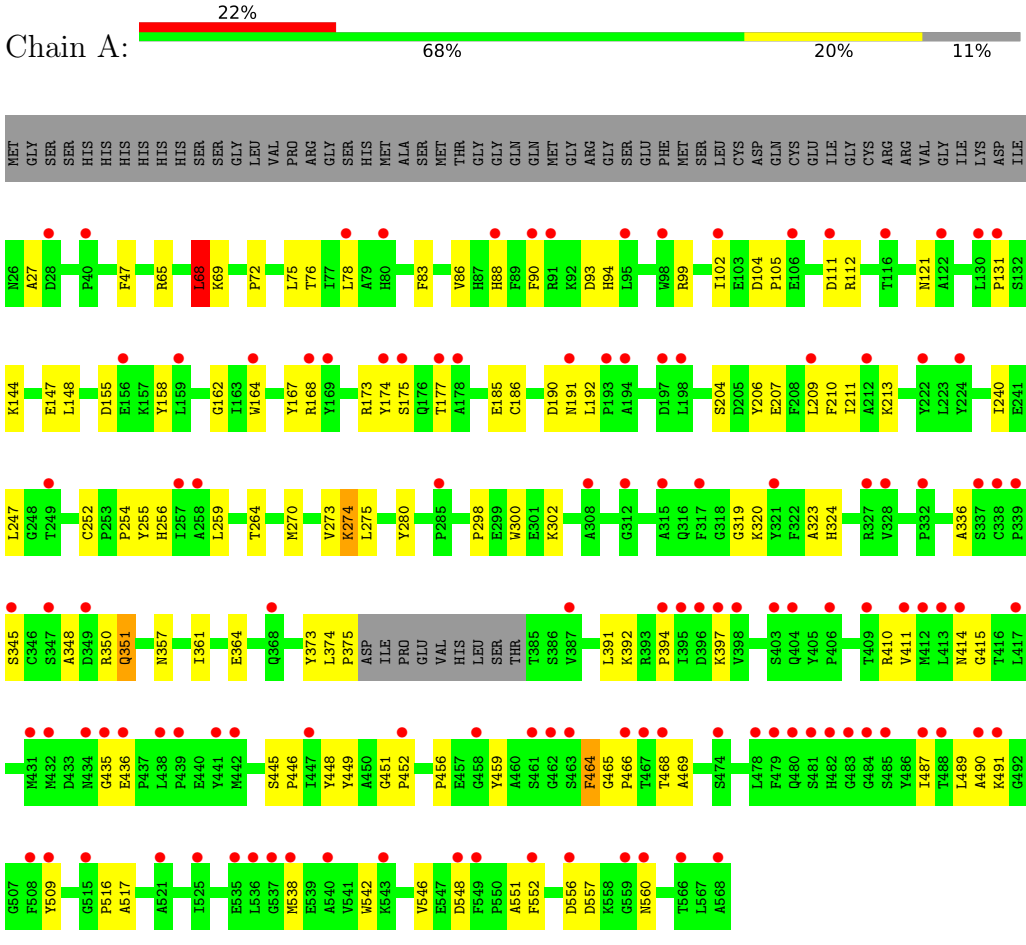
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O 1 1	0	0
4	D	1	Total O 1 1	0	0
4	F	1	Total O 1 1	0	0

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.

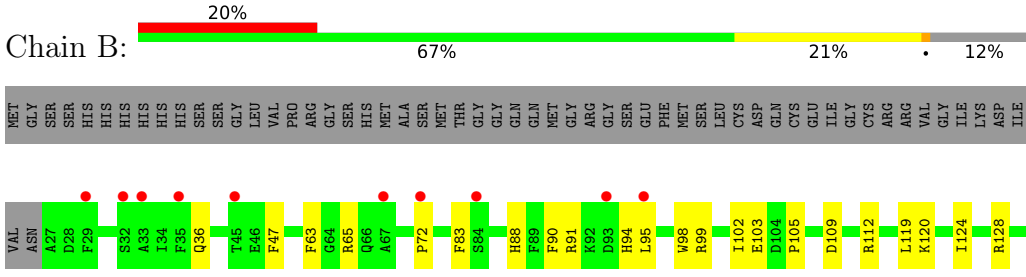
• Molecule 1: fumarate hydratase 2

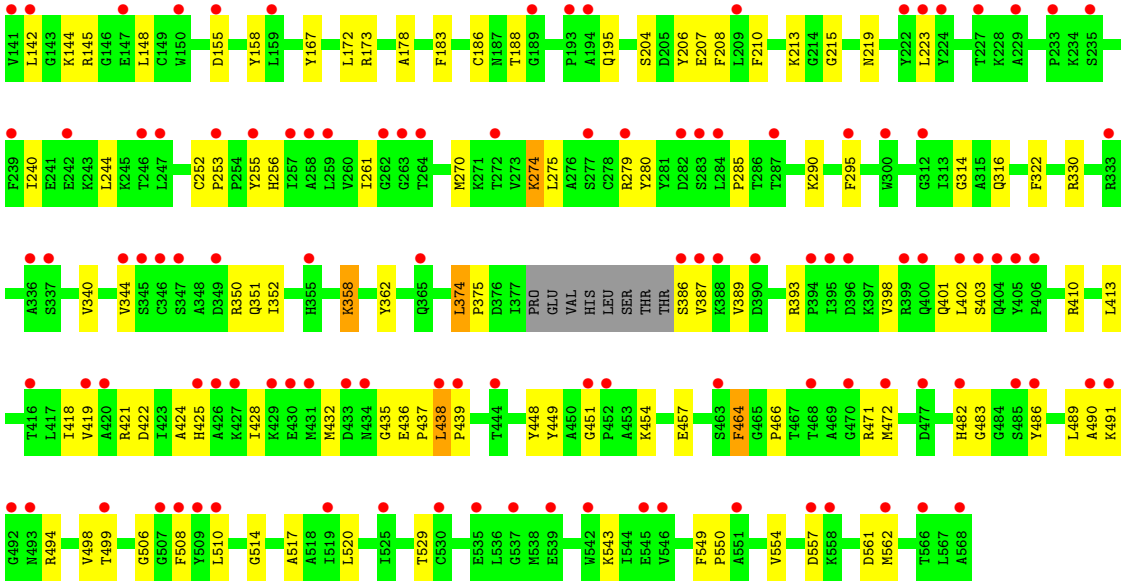
Chain A:



• Molecule 1: fumarate hydratase 2

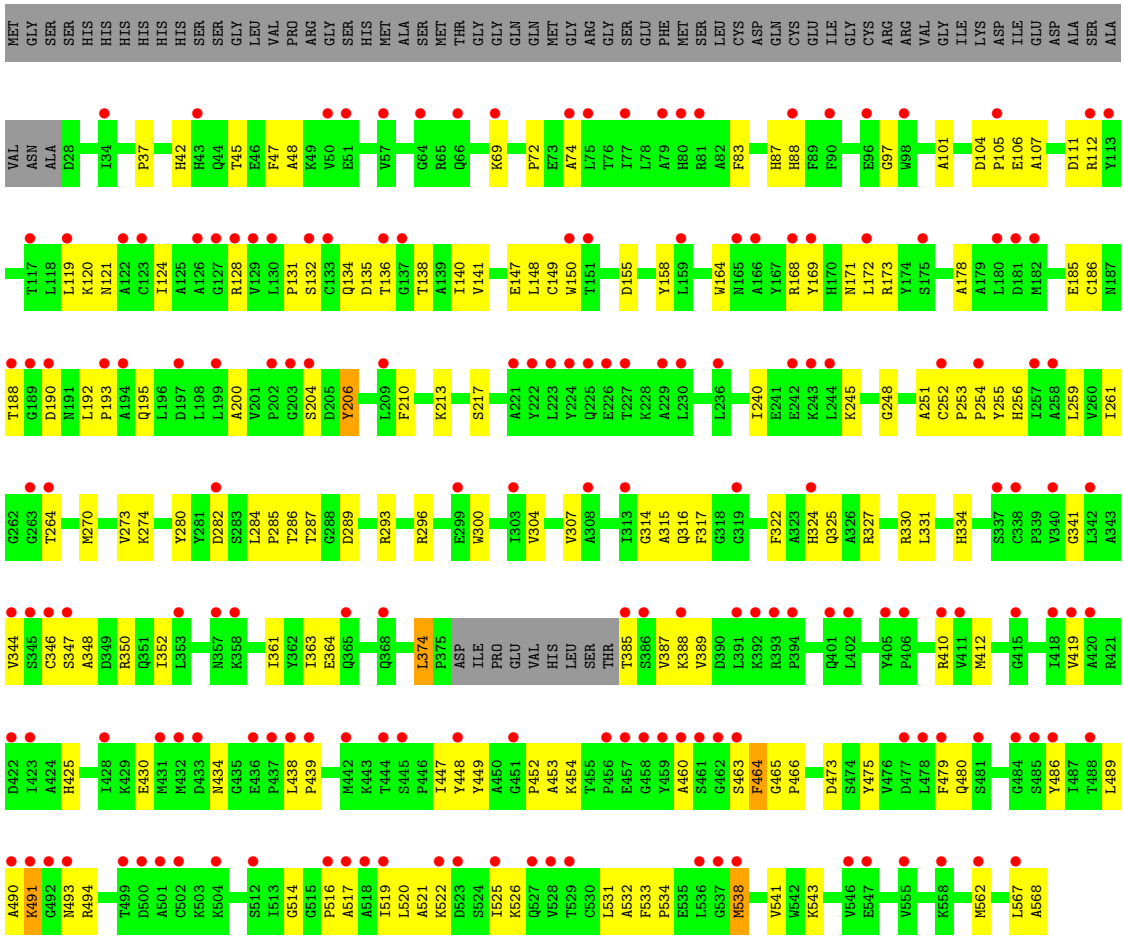
Chain B:





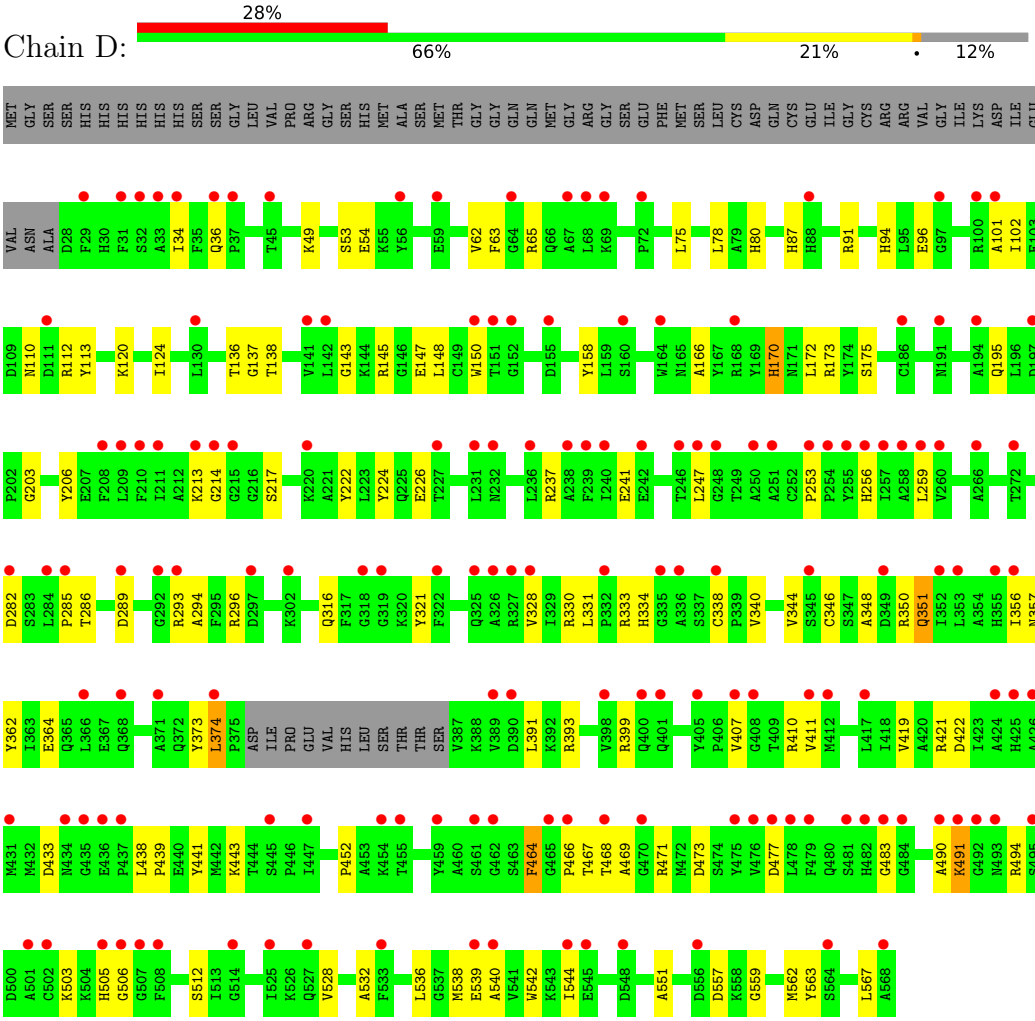
• Molecule 1: fumarate hydratase 2

Chain C:



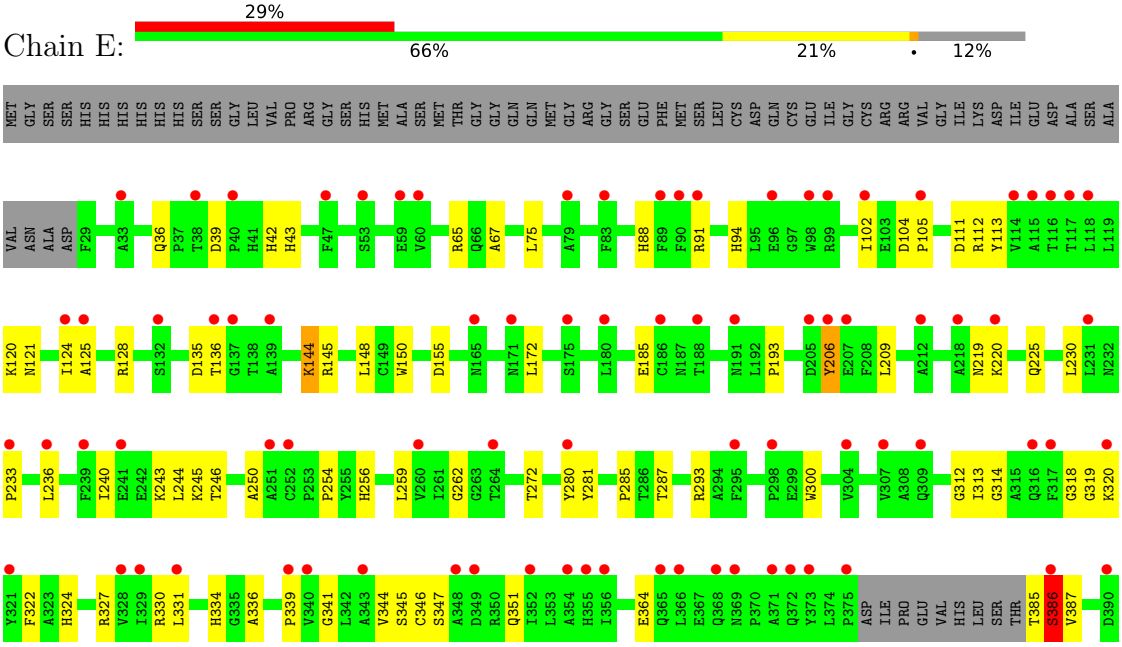
• Molecule 1: fumarate hydratase 2

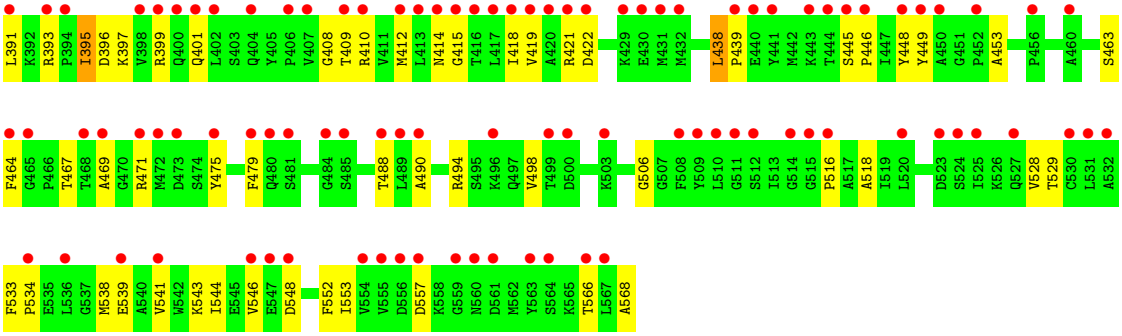
Chain D:



• Molecule 1: fumarate hydratase 2

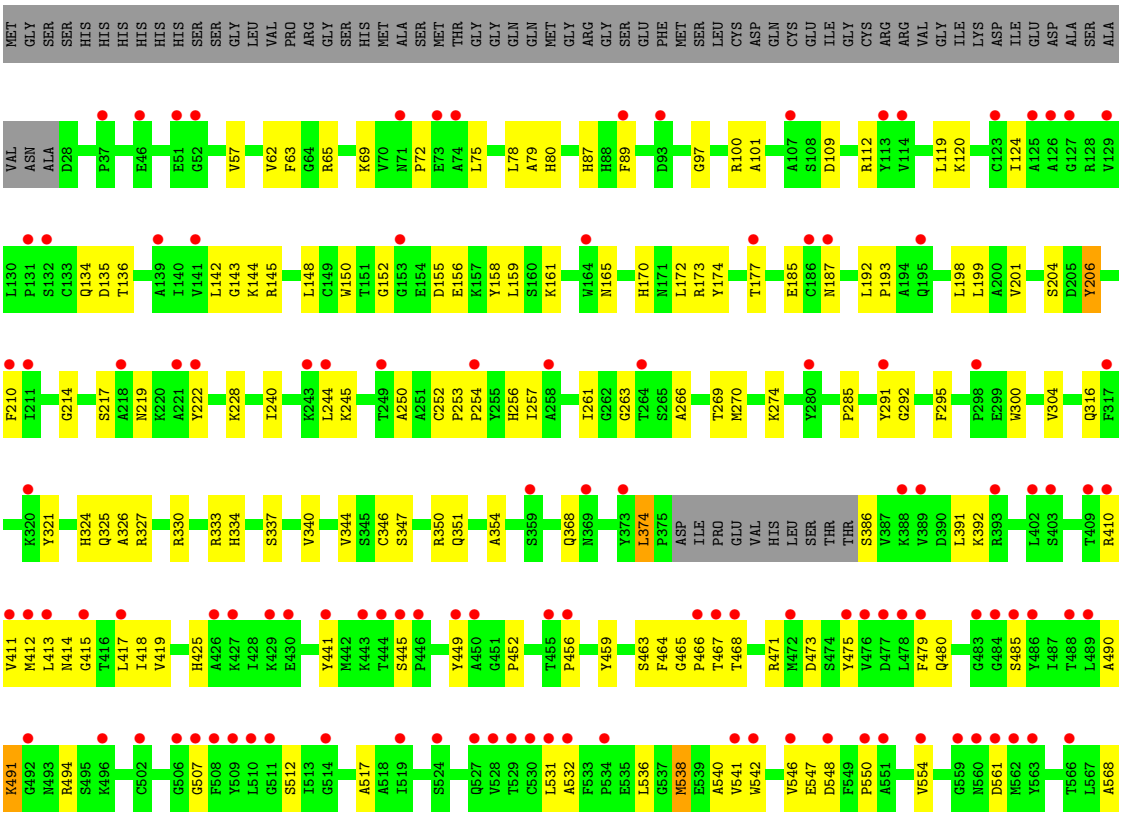
Chain E:





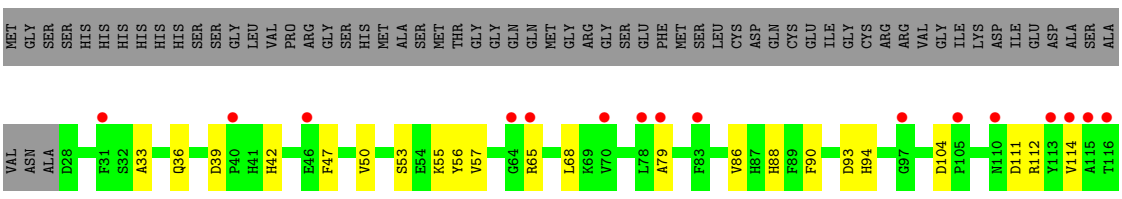
• Molecule 1: fumarate hydratase 2

Chain F:

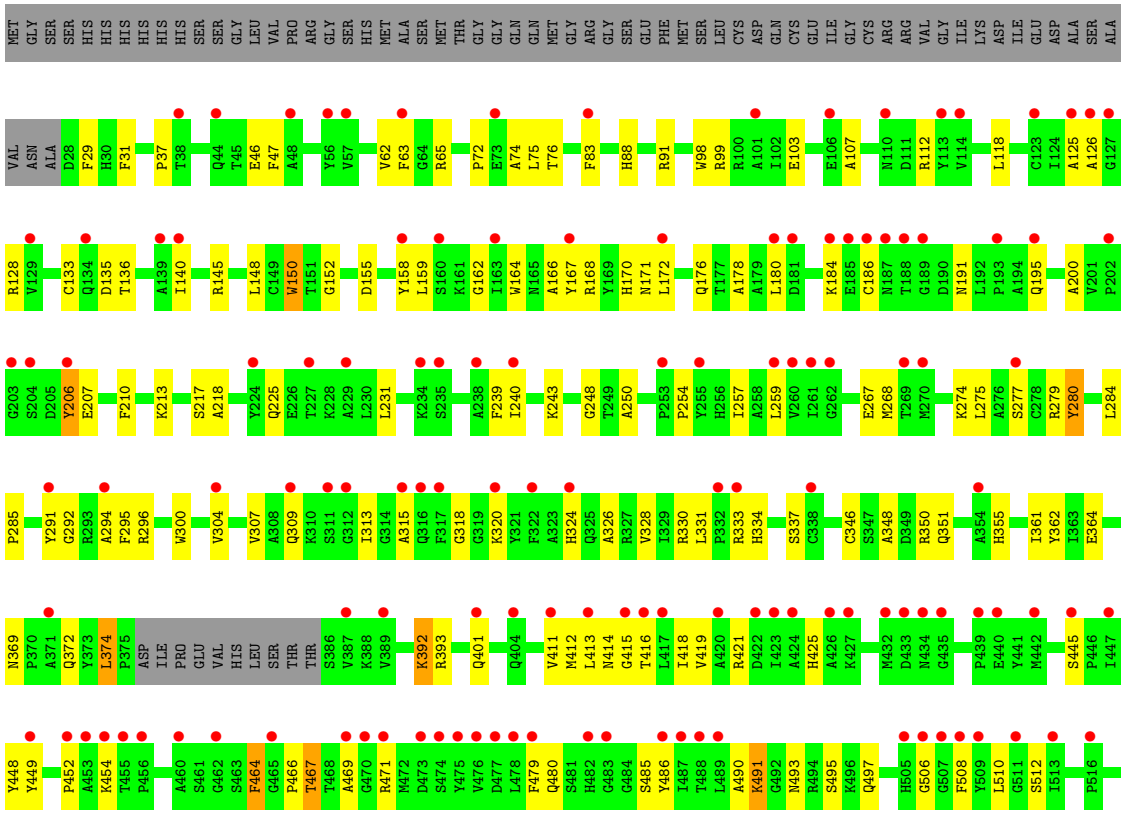


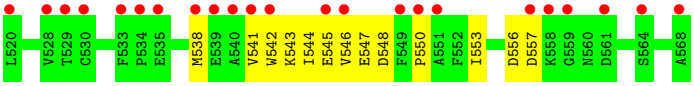
• Molecule 1: fumarate hydratase 2

Chain G:



• Molecule 1: fumarate hydratase 2




L520
V528
T529
C530
F533
P534
E535
M538
E539
A540
V541
W542
K543
I544
E545
V546
E547
D548
F549
P550
A551
F552
I553
D556
D557
K558
G559
N560
D561
S564
A568

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	159.09Å 66.07Å 238.09Å 90.00° 90.02° 90.00°	Depositor
Resolution (Å)	49.71 – 3.19 49.71 – 3.19	Depositor EDS
% Data completeness (in resolution range)	90.2 (49.71-3.19) 90.2 (49.71-3.19)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	714.55 (at 3.19Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.245 , 0.289 0.246 , 0.289	Depositor DCC
R_{free} test set	3752 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	65.6	Xtriage
Anisotropy	0.543	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 33.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.39$, $< L^2 > = 0.22$	Xtriage
Estimated twinning fraction	0.398 for h,-k,-l	Xtriage
Reported twinning fraction	0.500 for h,-k,-l	Depositor
Outliers	0 of 75107 reflections	Xtriage
F_o,F_c correlation	0.85	EDS
Total number of atoms	31246	wwPDB-VP
Average B, all atoms (Å^2)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.75% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: SF4, GOL

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	0/4024	0.67	1/5476 (0.0%)
1	B	0.39	0/4029	0.69	0/5489
1	C	0.34	0/3911	0.64	0/5329
1	D	0.35	0/3966	0.62	0/5399
1	E	0.36	0/3952	0.63	0/5380
1	F	0.36	0/4076	0.62	0/5542
1	G	0.36	0/3965	0.65	0/5401
1	H	0.38	1/3984 (0.0%)	0.65	0/5432
All	All	0.36	1/31907 (0.0%)	0.65	1/43448 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	150	TRP	CB-CG	-5.38	1.40	1.50

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	68	LEU	CA-CB-CG	5.32	127.53	115.30

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	3933	0	3563	90	0
1	B	3933	0	3571	97	0
1	C	3822	0	3400	123	0
1	D	3874	0	3531	91	0
1	E	3863	0	3537	102	0
1	F	3981	0	3721	115	0
1	G	3873	0	3489	107	0
1	H	3888	0	3506	124	0
2	A	8	0	0	1	0
2	B	8	0	0	2	0
2	C	8	0	0	5	0
2	D	8	0	0	0	0
2	E	8	0	0	1	0
2	F	8	0	0	3	0
2	G	8	0	0	0	0
2	H	8	0	0	0	0
3	B	6	0	8	2	0
3	E	6	0	8	1	0
4	A	1	0	0	0	0
4	D	1	0	0	0	0
4	F	1	0	0	0	0
All	All	31246	0	28334	792	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 13.

The worst 5 of 792 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:G:494:ARG:HD2	1:G:509:TYR:CD1	2.00	0.96
1:B:421:ARG:HH11	1:B:451:GLY:HA3	1.32	0.95
1:G:494:ARG:HD2	1:G:509:TYR:CE1	2.07	0.89
1:E:399:ARG:HD2	1:E:506:GLY:O	1.73	0.89
1:C:134:GLN:NE2	2:C:601:SF4:S4	2.48	0.87

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	535/604 (89%)	513 (96%)	20 (4%)	2 (0%)	34	69
1	B	530/604 (88%)	511 (96%)	17 (3%)	2 (0%)	34	69
1	C	528/604 (87%)	512 (97%)	16 (3%)	0	100	100
1	D	526/604 (87%)	508 (97%)	17 (3%)	1 (0%)	47	79
1	E	527/604 (87%)	506 (96%)	17 (3%)	4 (1%)	19	58
1	F	528/604 (87%)	510 (97%)	16 (3%)	2 (0%)	34	69
1	G	528/604 (87%)	513 (97%)	15 (3%)	0	100	100
1	H	527/604 (87%)	510 (97%)	16 (3%)	1 (0%)	47	79
All	All	4229/4832 (88%)	4083 (96%)	134 (3%)	12 (0%)	41	74

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	387	VAL
1	B	438	LEU
1	E	386	SER
1	E	395	ILE
1	H	374	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	363/492 (74%)	355 (98%)	8 (2%)	52	79

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	369/492 (75%)	363 (98%)	6 (2%)	62	84
1	C	347/492 (70%)	342 (99%)	5 (1%)	67	86
1	D	362/492 (74%)	353 (98%)	9 (2%)	47	77
1	E	363/492 (74%)	357 (98%)	6 (2%)	60	83
1	F	391/492 (80%)	383 (98%)	8 (2%)	55	80
1	G	357/492 (73%)	353 (99%)	4 (1%)	73	88
1	H	365/492 (74%)	358 (98%)	7 (2%)	57	81
All	All	2917/3936 (74%)	2864 (98%)	53 (2%)	59	82

5 of 53 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	144	LYS
1	F	274	LYS
1	H	392	LYS
1	E	206	TYR
1	E	464	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	F	87	HIS
1	F	170	HIS
1	F	324	HIS
1	H	480	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

10 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	GOL	E	602	-	5,5,5	0.94	0	5,5,5	1.16	1 (20%)
2	SF4	F	601	1	0,12,12	-	-	-		
2	SF4	E	601	1	0,12,12	-	-	-		
2	SF4	A	601	1	0,12,12	-	-	-		
2	SF4	D	601	1	0,12,12	-	-	-		
2	SF4	H	601	1	0,12,12	-	-	-		
2	SF4	G	601	1	0,12,12	-	-	-		
3	GOL	B	602	-	5,5,5	0.98	0	5,5,5	0.94	0
2	SF4	B	601	1	0,12,12	-	-	-		
2	SF4	C	601	1	0,12,12	-	-	-		

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	SF4	F	601	1	-	-	0/6/5/5
2	SF4	E	601	1	-	-	0/6/5/5
2	SF4	A	601	1	-	-	0/6/5/5
2	SF4	D	601	1	-	-	0/6/5/5
3	GOL	B	602	-	-	2/4/4/4	-
2	SF4	G	601	1	-	-	0/6/5/5
3	GOL	E	602	-	-	2/4/4/4	-
2	SF4	H	601	1	-	-	0/6/5/5
2	SF4	B	601	1	-	-	0/6/5/5
2	SF4	C	601	1	-	-	0/6/5/5

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	E	602	GOL	C3-C2-C1	-2.01	103.91	111.70

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	602	GOL	C1-C2-C3-O3
3	B	602	GOL	O1-C1-C2-O2
3	B	602	GOL	O1-C1-C2-C3
3	E	602	GOL	O2-C2-C3-O3

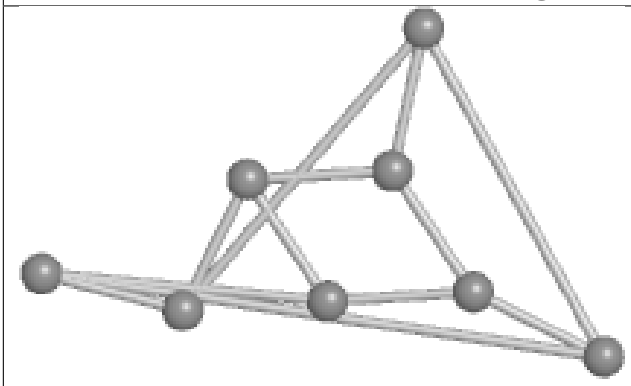
There are no ring outliers.

7 monomers are involved in 15 short contacts:

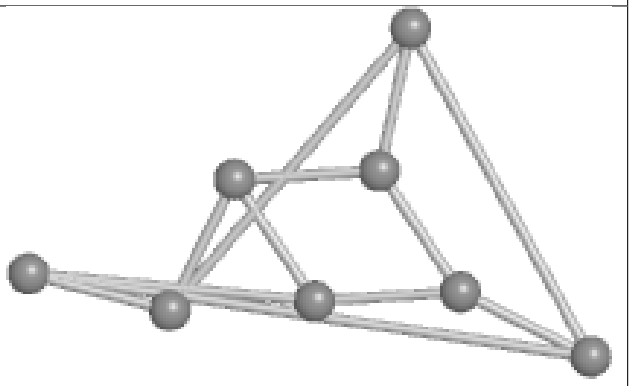
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	602	GOL	1	0
2	F	601	SF4	3	0
2	E	601	SF4	1	0
2	A	601	SF4	1	0
3	B	602	GOL	2	0
2	B	601	SF4	2	0
2	C	601	SF4	5	0

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 then 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.

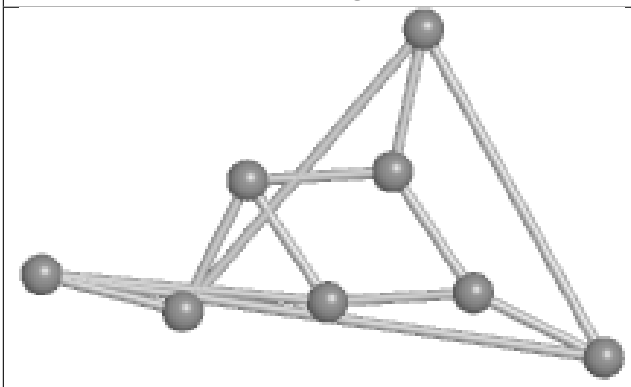
Ligand SF4 F 601



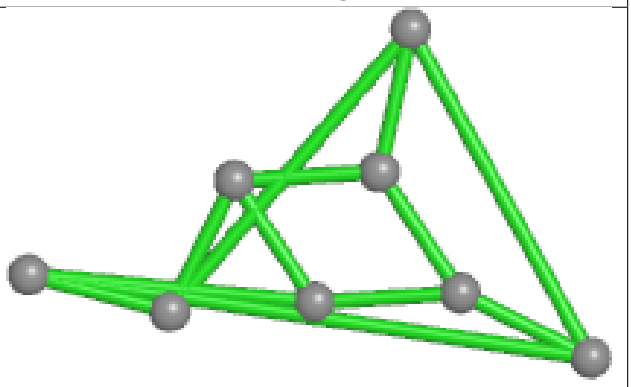
Bond lengths



Bond angles

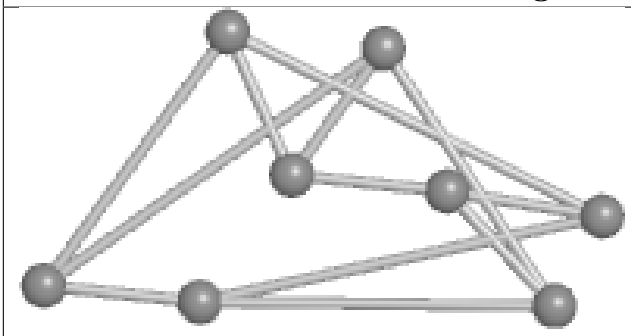


Torsions

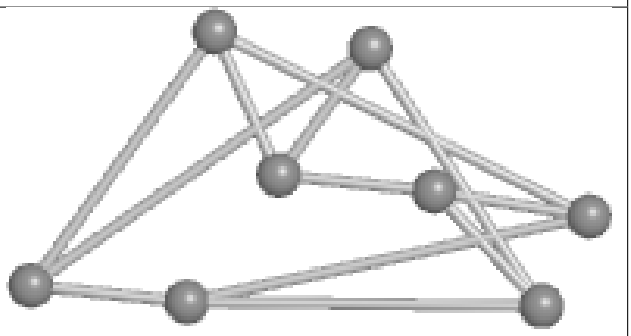


Rings

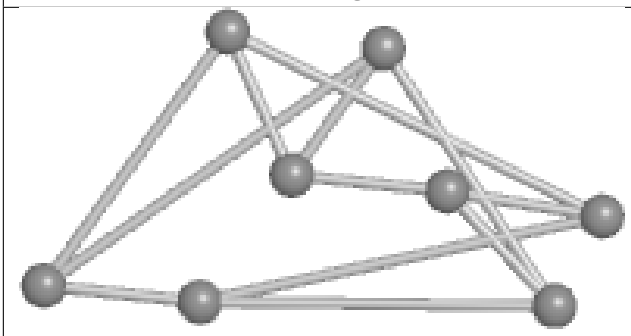
Ligand SF4 E 601



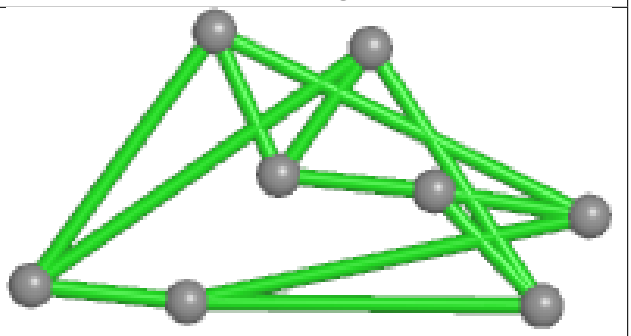
Bond lengths



Bond angles

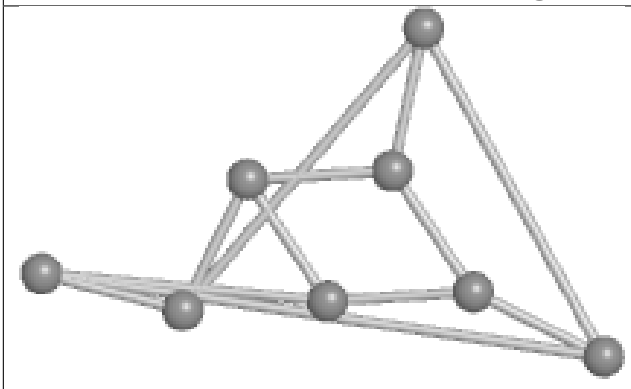


Torsions

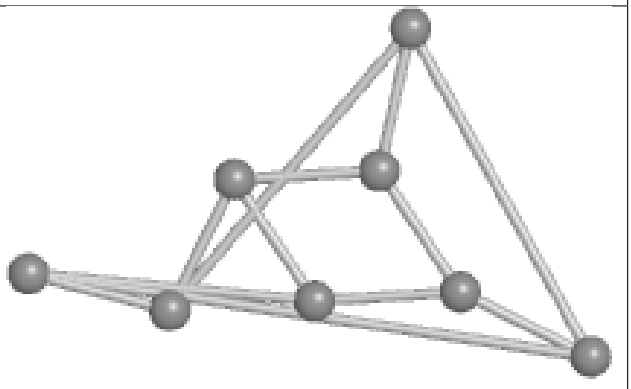


Rings

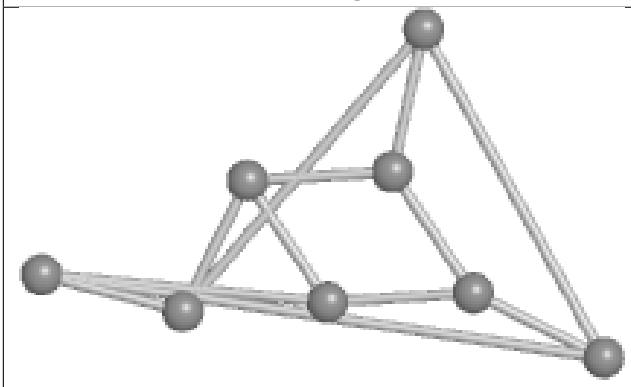
Ligand SF4 A 601



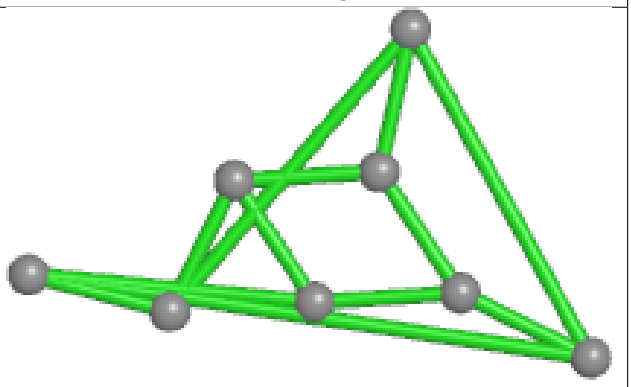
Bond lengths



Bond angles

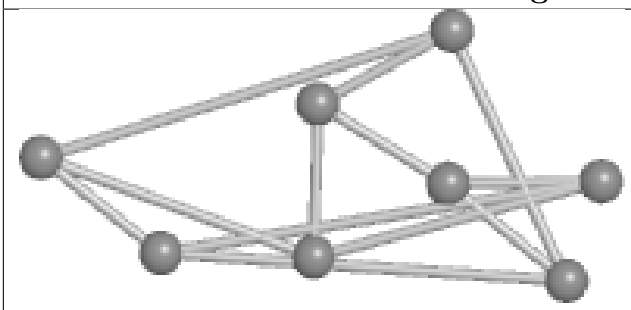


Torsions

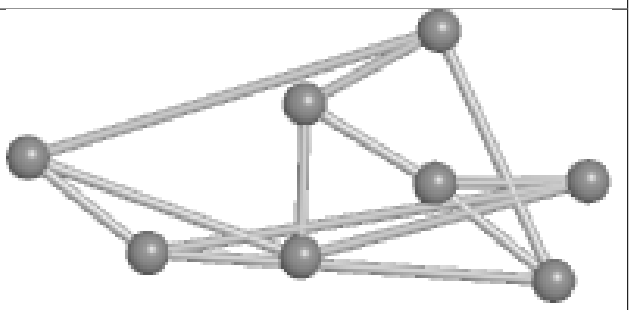


Rings

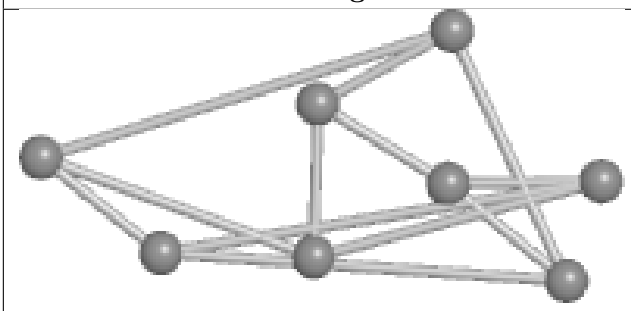
Ligand SF4 D 601



Bond lengths



Bond angles



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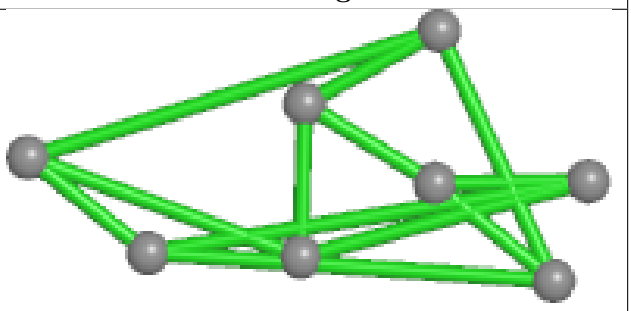
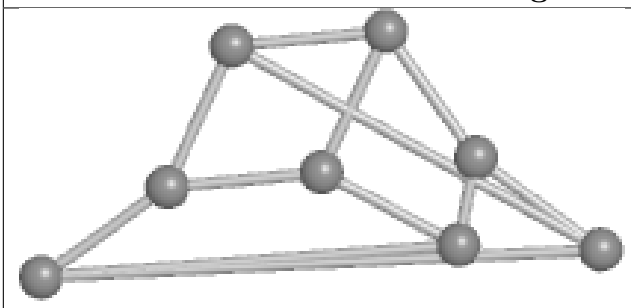
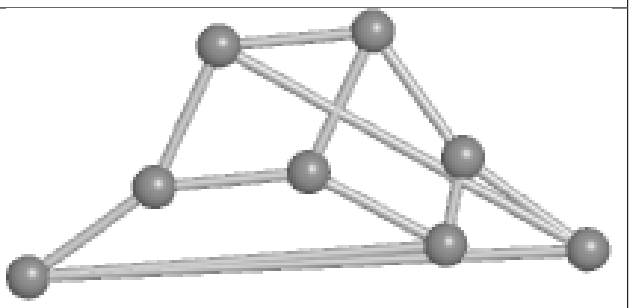


Rings

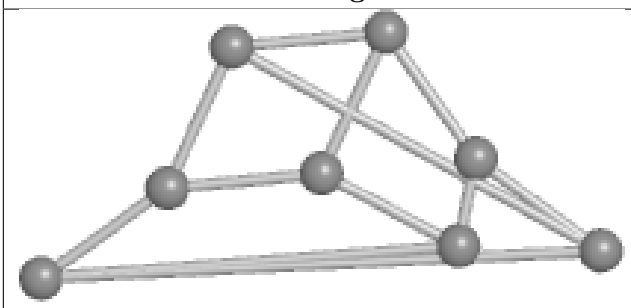
Ligand SF4 H 601



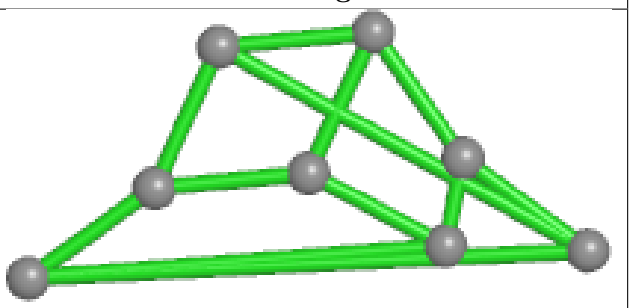
Bond lengths



Bond angles

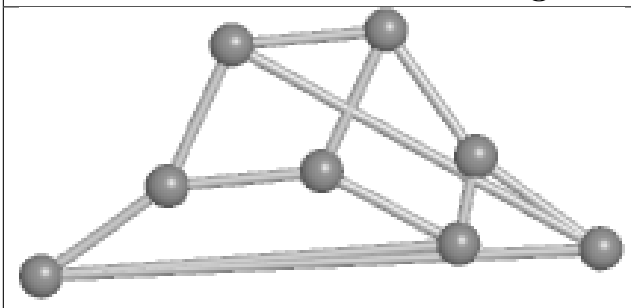


Torsions

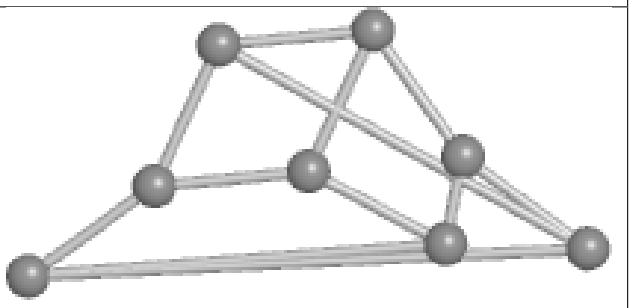


Rings

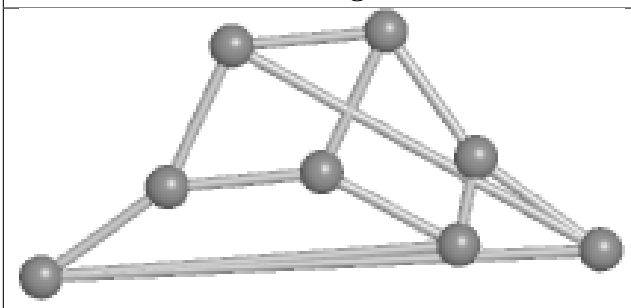
Ligand SF4 G 601



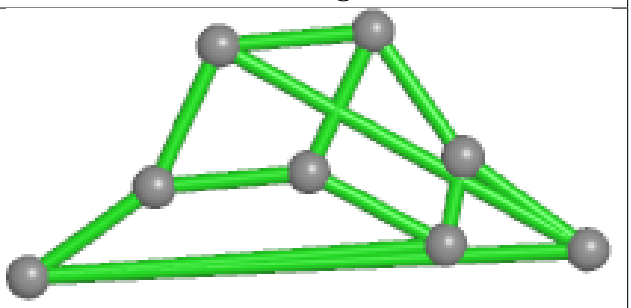
Bond lengths



Bond angles

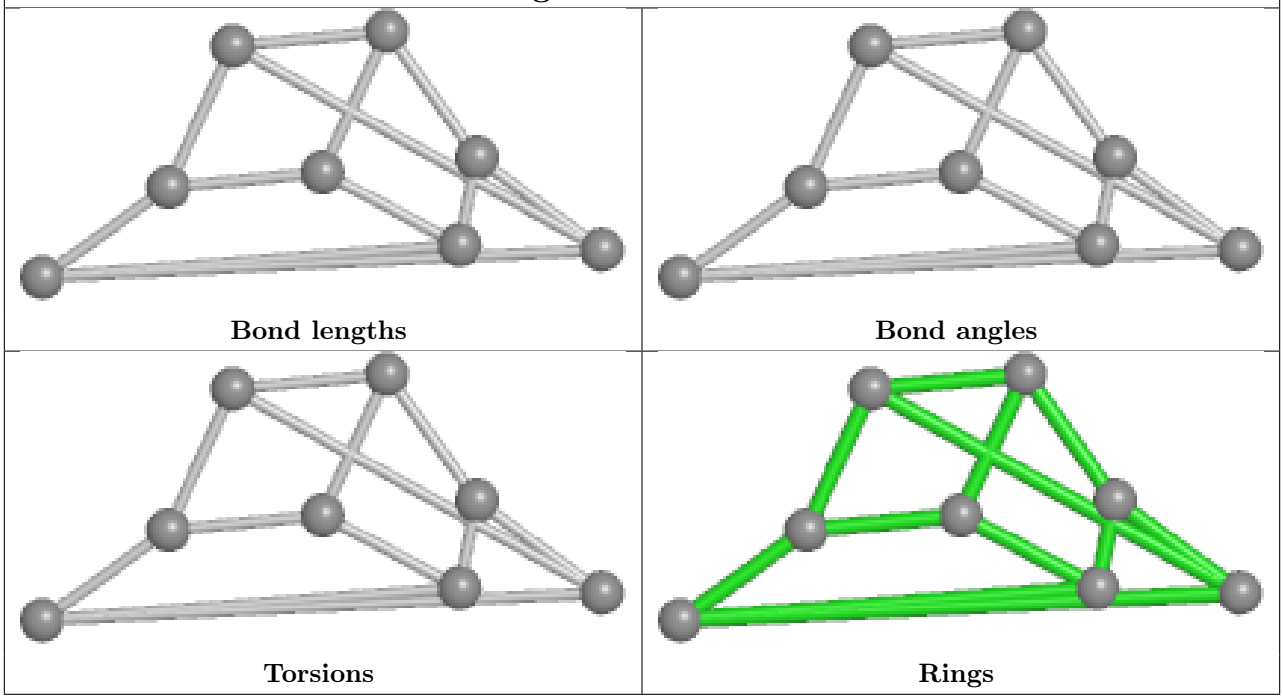


Torsions

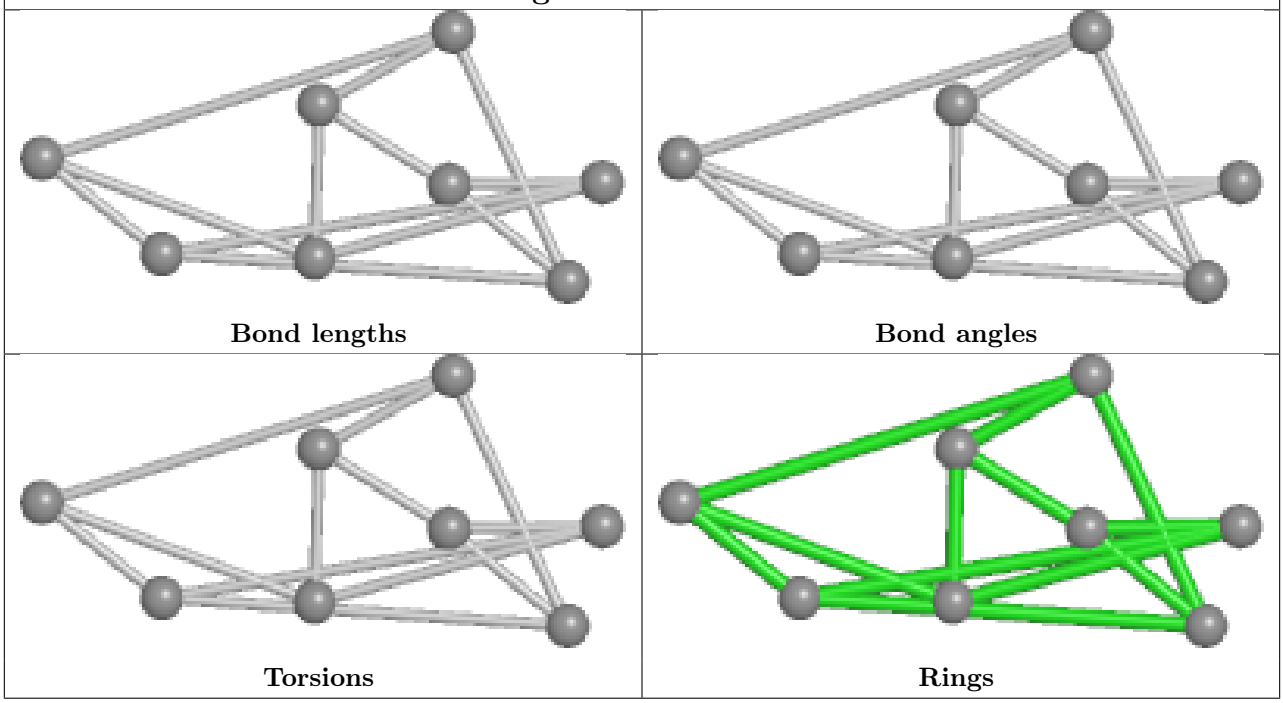


Rings

Ligand SF4 B 601



Ligand SF4 C 601



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, 95^{th} 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	539/604 (89%)	1.50	133 (24%)	0	0	23, 58, 89, 106	0
1	B	534/604 (88%)	1.39	121 (22%)	0	0	24, 50, 79, 89	0
1	C	532/604 (88%)	1.68	173 (32%)	0	0	37, 80, 91, 100	0
1	D	530/604 (87%)	1.66	168 (31%)	0	0	29, 72, 89, 102	0
1	E	531/604 (87%)	1.76	177 (33%)	0	0	34, 65, 92, 103	0
1	F	531/604 (87%)	1.28	118 (22%)	0	0	34, 57, 71, 81	0
1	G	532/604 (88%)	1.71	173 (32%)	0	0	28, 66, 91, 102	0
1	H	531/604 (87%)	1.52	153 (28%)	0	0	22, 65, 88, 111	0
All	All	4260/4832 (88%)	1.56	1216 (28%)	0	0	22, 64, 89, 111	0

The worst 5 of 1216 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	194	ALA	13.7
1	C	437	PRO	12.8
1	E	489	LEU	12.8
1	E	547	GLU	12.7
1	A	480	GLN	12.7

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

There are no monosaccharides in this entry.

6.4 Ligands (i)

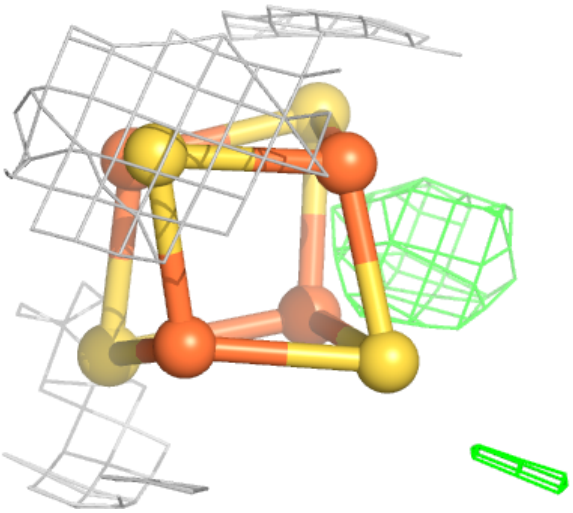
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

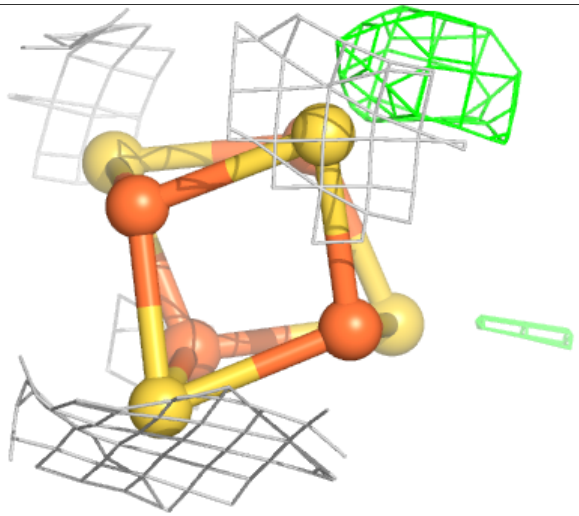
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	GOL	E	602	6/6	0.65	0.26	58,59,65,65	0
3	GOL	B	602	6/6	0.66	0.36	35,37,41,41	0
2	SF4	C	601	8/8	0.88	0.14	80,84,105,116	0
2	SF4	F	601	8/8	0.89	0.13	51,77,94,94	0
2	SF4	E	601	8/8	0.90	0.13	55,69,89,96	0
2	SF4	G	601	8/8	0.90	0.16	48,80,92,96	0
2	SF4	H	601	8/8	0.91	0.12	65,70,94,94	0
2	SF4	B	601	8/8	0.93	0.18	29,40,52,74	0
2	SF4	A	601	8/8	0.93	0.13	53,65,77,81	0
2	SF4	D	601	8/8	0.95	0.16	52,59,78,85	0

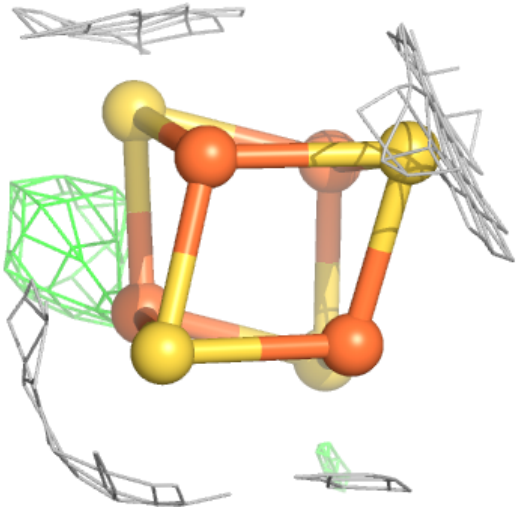
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around SF4 C 601:

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

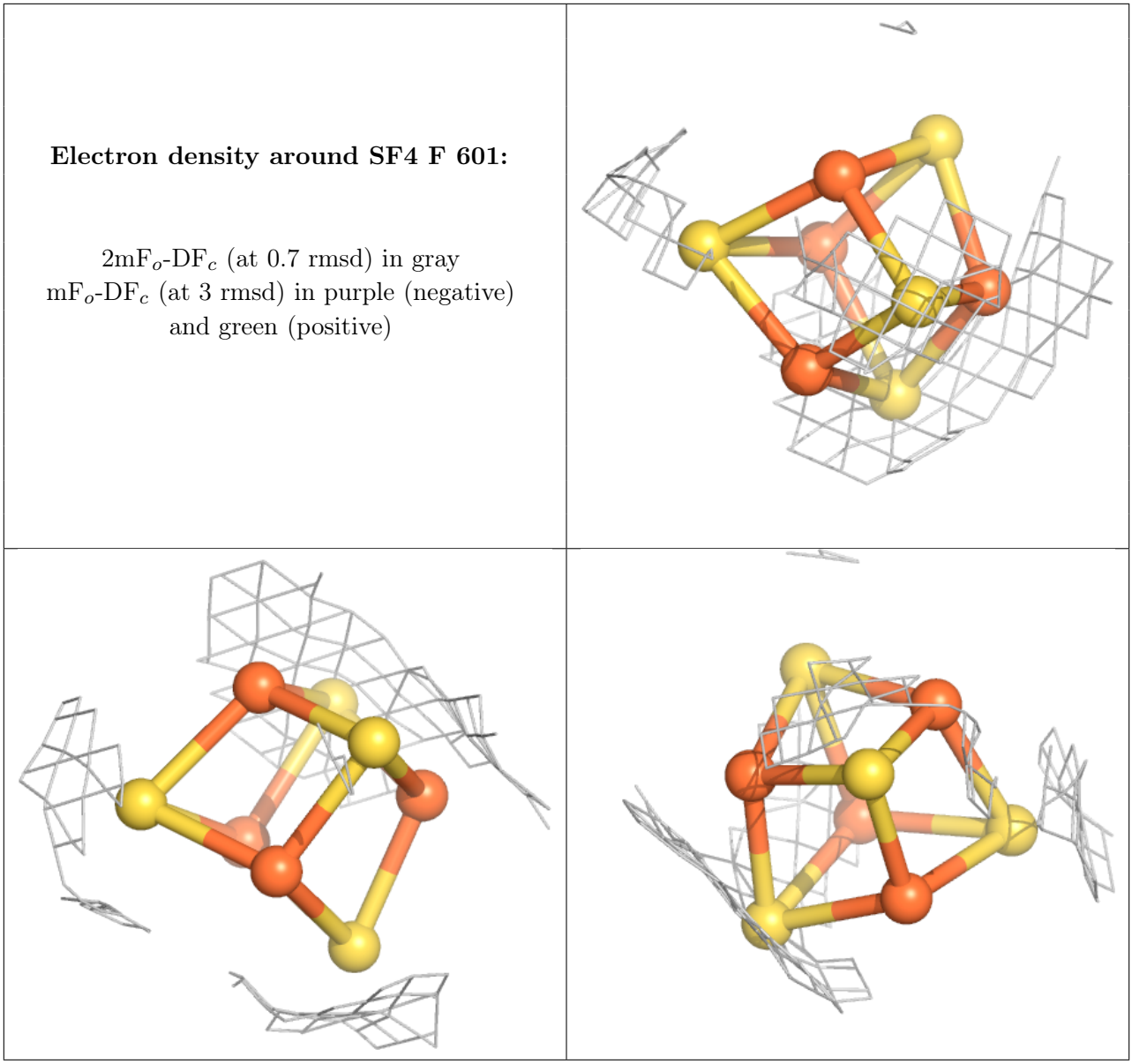






Electron density around SF4 F 601:

$2mF_o$-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 E 601:

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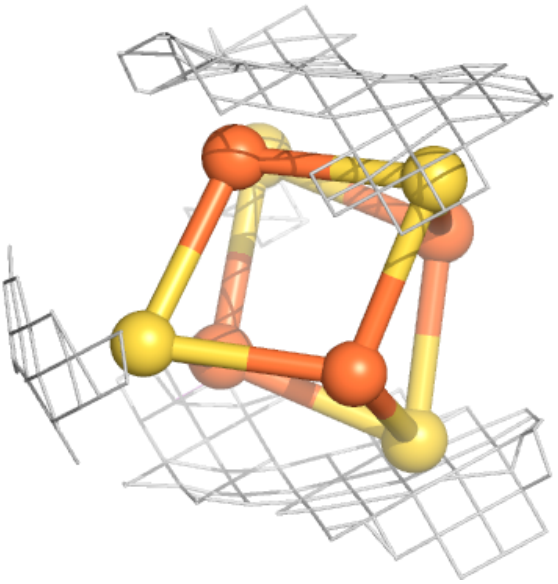
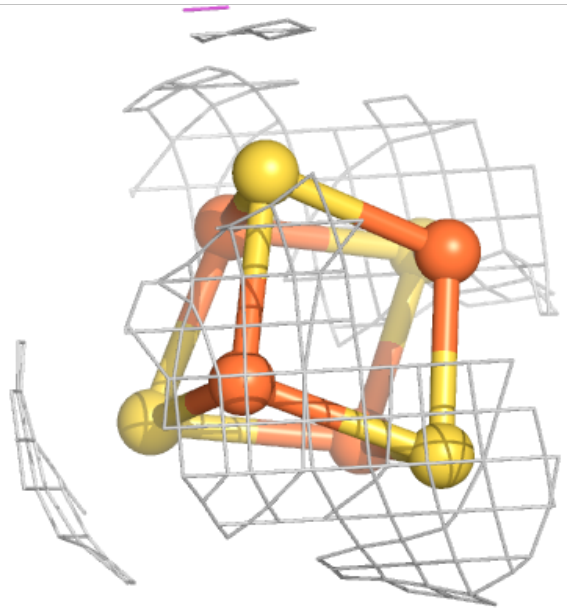
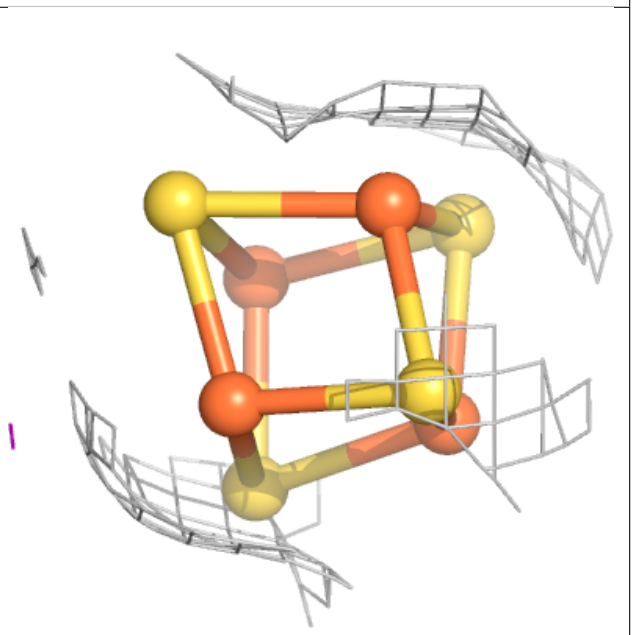
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

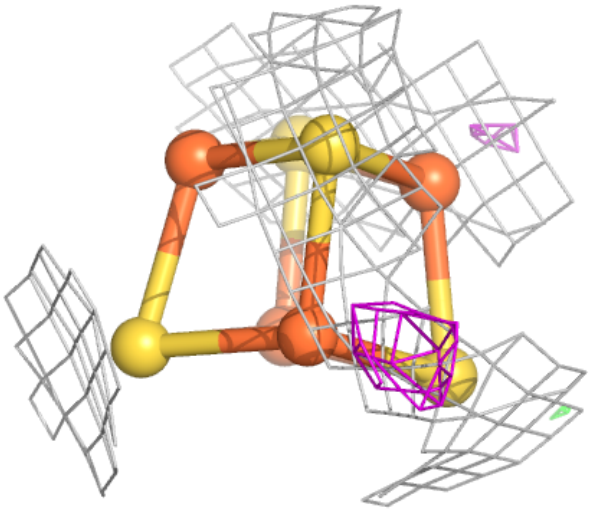


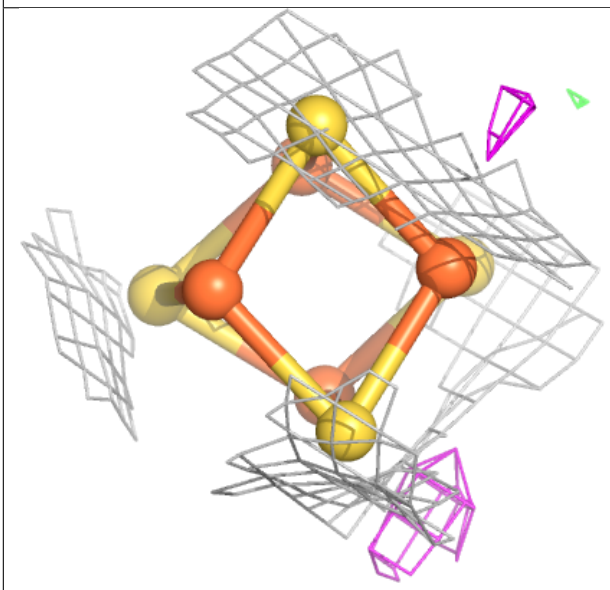


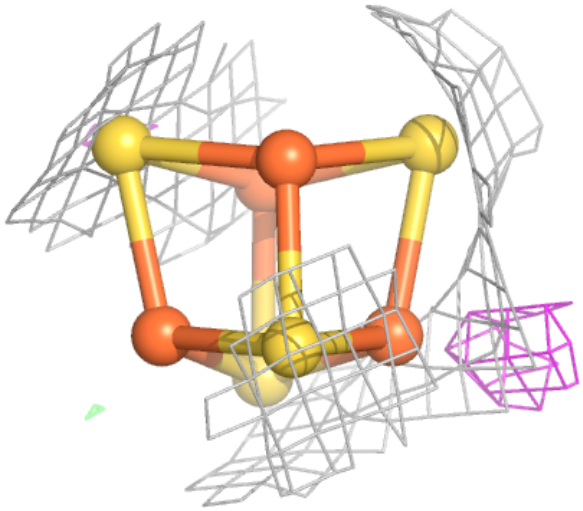


Electron density around SF4 G 601:

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

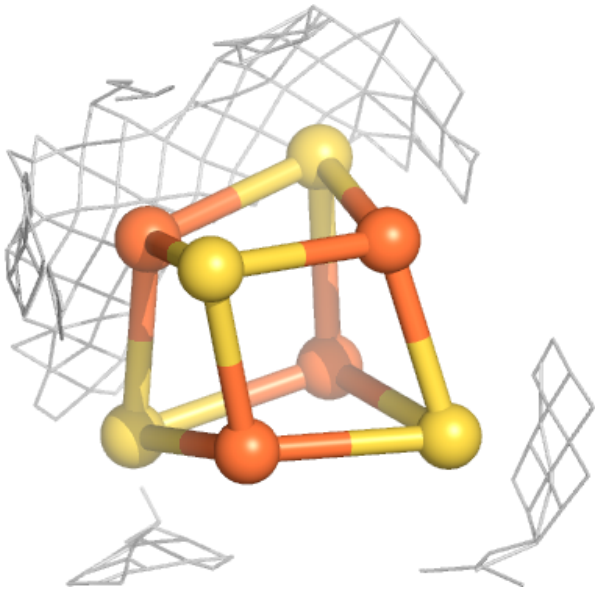


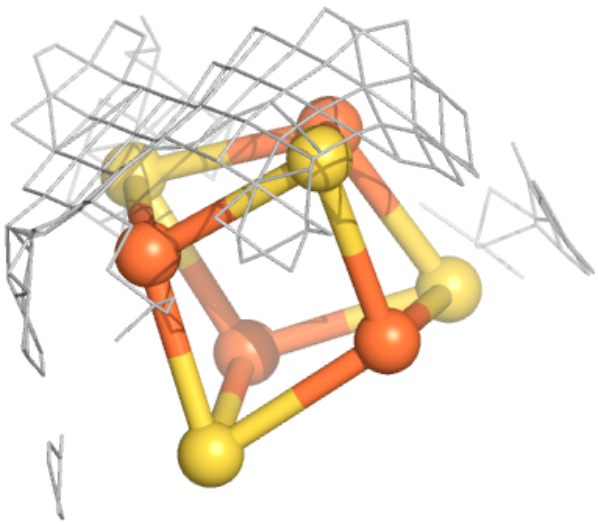


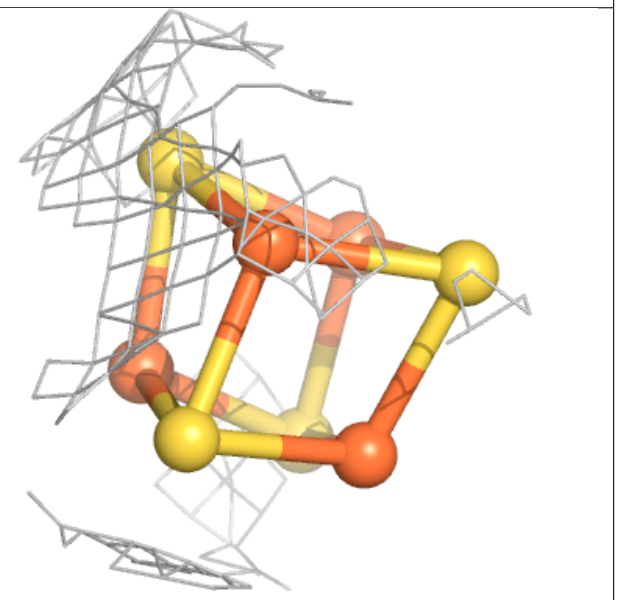


Electron density around SF4 H 601:

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

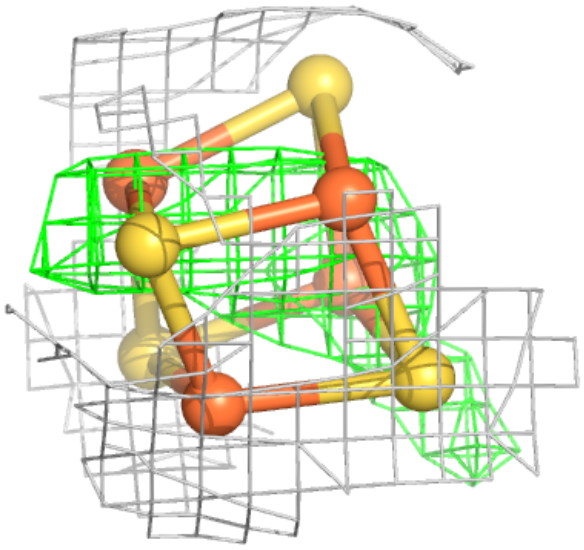


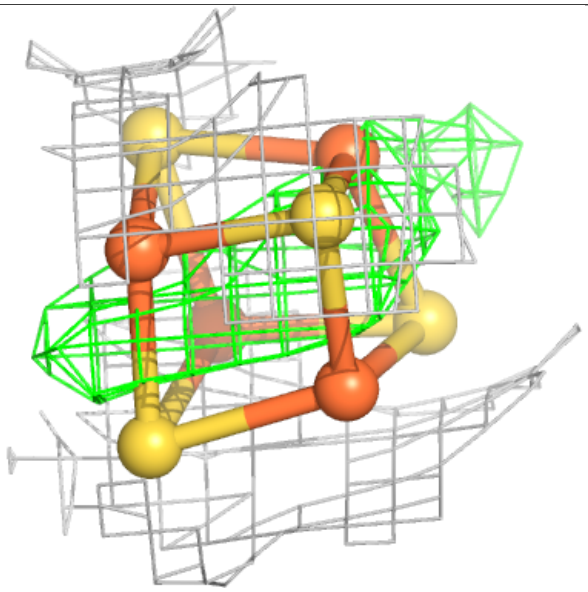


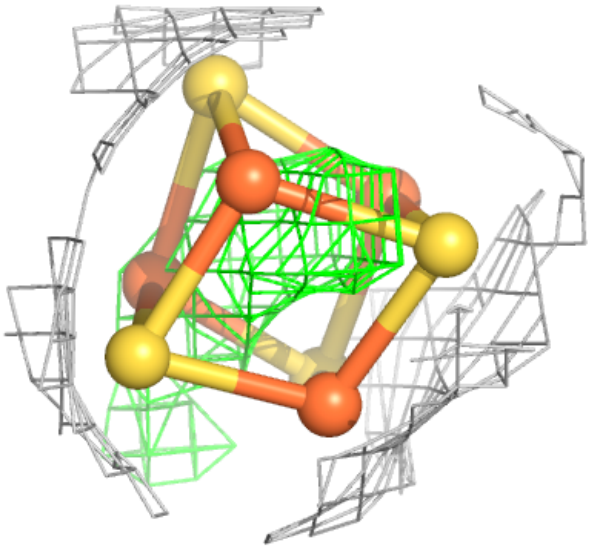


Electron density around SF4 B 601:

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

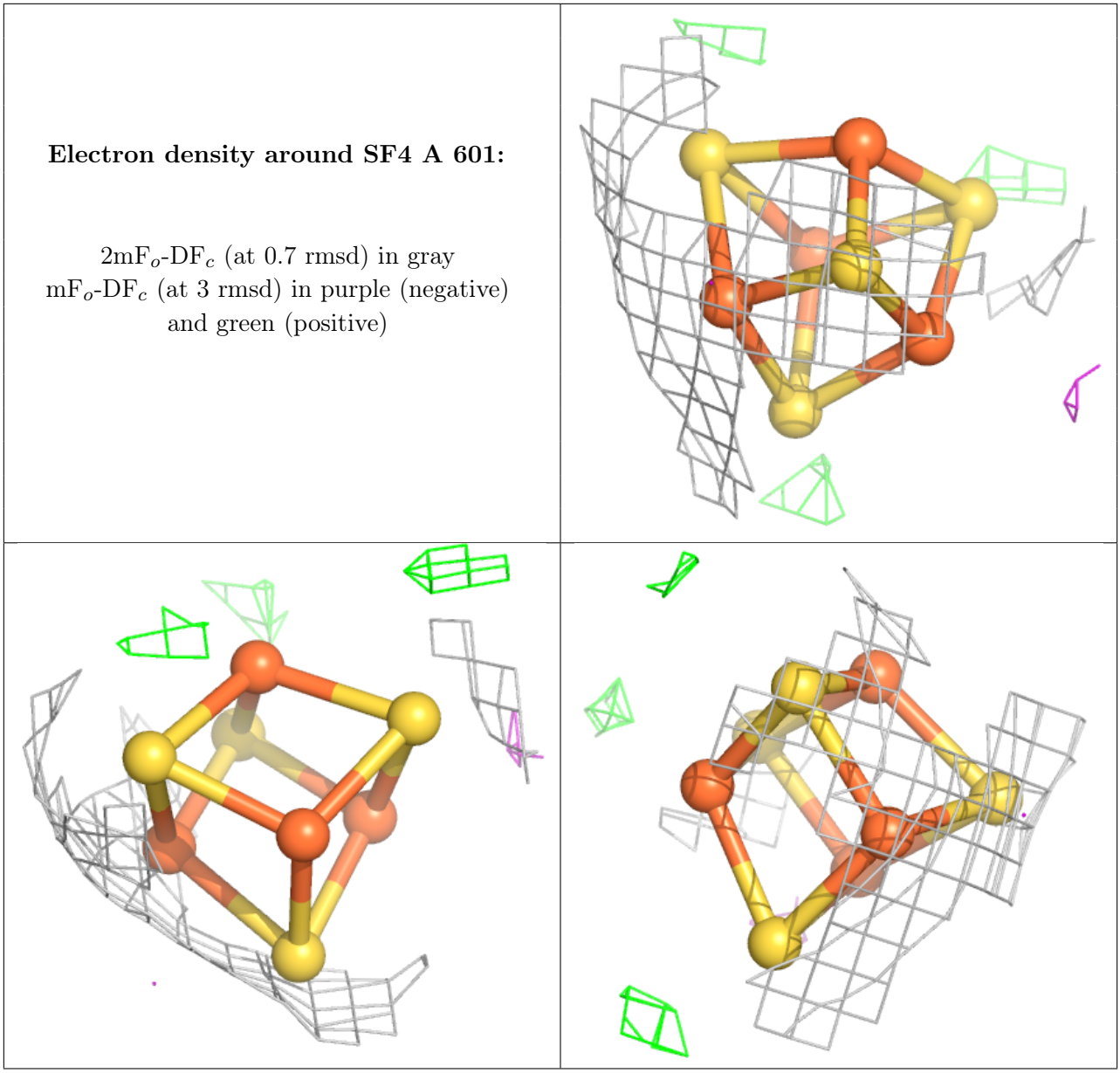






Electron density around SF4 A 601:

$2mF_o$-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 D 601:

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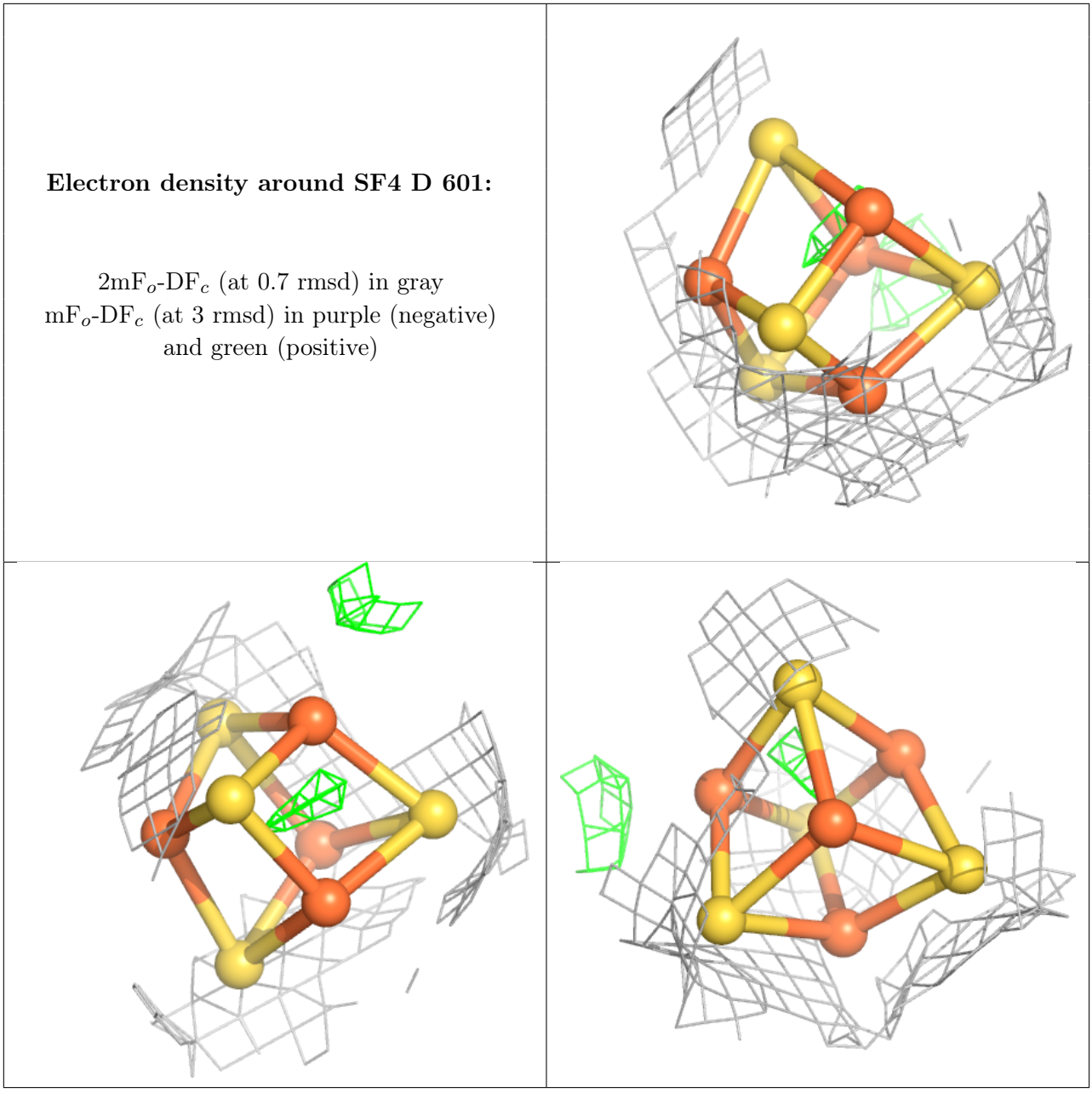
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



6.5 Other polymers

There are no such residues in this entry.