W O R L D W I D E
wwPDB
PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2022 – 06:20 am GMT

|		
PDB ID	:	7PU5
Title	:	Structure of SFPQ-NONO complex
Authors	:	Fribourg, S.
Deposited on	:	2021-09-28
Resolution	:	3.00 Å(reported)

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 3.00 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.
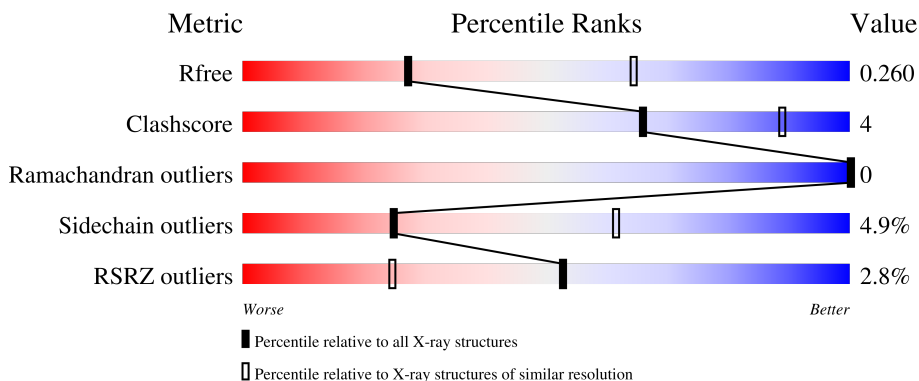
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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	259	2%; 81% 12% 7%
1	C	259	4%; 79% 14% 7%
1	E	259	%; 76% 15% 8%
1	G	259	4%; 78% 13% · 8%
1	I	259	4%; 81% 10% · 8%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	K	259	6%　　　　　77%　　　　　15%　　8%
2	B	259	79%　　　　　12%　　8%
2	D	259	2%　　　　　81%　　　　　11%　　8%
2	F	259	%　　　　　80%　　　　　11%　　8%
2	H	259	81%　　　　　11%　　7%
2	J	259	3%　　　　　80%　　　　　12%　　8%
2	L	259	2%　　　　　80%　　　　　12%　　7%

2 Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 23285 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 Non-POU domain-containing octamer-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	242	Total	C	N	O	S	0	0	0
			1963	1234	352	368	9			
1	C	242	Total	C	N	O	S	0	0	0
			1968	1238	353	368	9			
1	E	237	Total	C	N	O	S	0	0	0
			1929	1215	346	359	9			
1	G	237	Total	C	N	O	S	0	0	0
			1934	1219	347	359	9			
1	I	238	Total	C	N	O	S	0	0	0
			1930	1215	344	362	9			
1	K	239	Total	C	N	O	S	0	0	0
			1939	1221	346	363	9			

- Molecule 2 is a protein called Splicing factor, proline- and glutamine-rich.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	239	Total	C	N	O	S	0	0	0
			1932	1215	339	371	7			
2	D	239	Total	C	N	O	S	0	0	0
			1932	1215	339	371	7			
2	F	239	Total	C	N	O	S	0	0	0
			1932	1215	339	371	7			
2	H	240	Total	C	N	O	S	0	0	0
			1941	1220	340	374	7			
2	J	239	Total	C	N	O	S	0	0	0
			1932	1215	339	371	7			
2	L	240	Total	C	N	O	S	0	0	0
			1941	1220	340	374	7			

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).
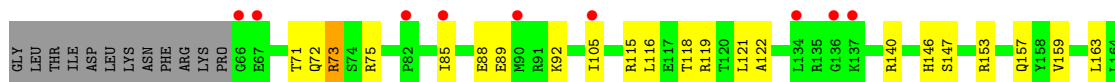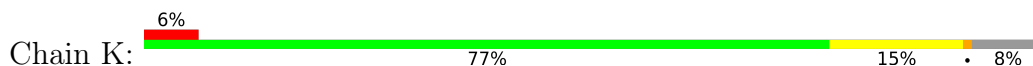
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total 2	Mg 2	0	0
3	D	2	Total 2	Mg 2	0	0
3	F	2	Total 2	Mg 2	0	0
3	H	2	Total 2	Mg 2	0	0
3	J	2	Total 2	Mg 2	0	0
3	K	1	Total 1	Mg 1	0	0
3	L	1	Total 1	Mg 1	0	0

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.

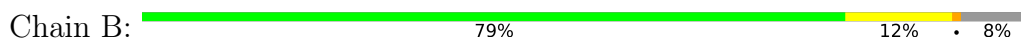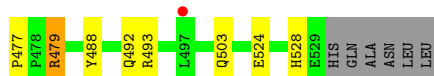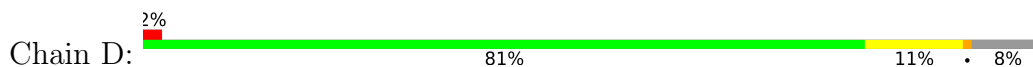• Molecule 1: Non-POU domain-containing octamer-binding protein

Chain A:

• Molecule 1: Non-POU domain-containing octamer-binding protein

Chain C:

• Molecule 1: Non-POU domain-containing octamer-binding protein
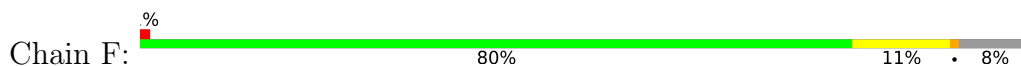
Chain E:

• Molecule 1: Non-POU domain-containing octamer-binding protein

Chain G:

L163 L164 E165 D182 D183 P187 K190 L205 T217 K239 P254 P255 R256 F257 A258 Y267 K272 I275 M298 E301 A302 A303 E306 H307 GLN VAL MET MET

• Molecule 1: Non-POU domain-containing octamer-binding protein

Chain I:

4%

81% 10% • 8%

GLY LEU THR ILE ASP LEU LYS ASN PHE ARG LYS PRO G66 E67 R73 S74 R75 L81 P82 I85 E88 D108 LYS G110 R115 T118 R119 T120 L121 P133 L134 R135 L139 R142 R153 V159 L163 L164 E165 D183 R186 L205 L214

T217 R251 P255 R256 F263 Y267 R270 W271 K272 A273 L274 I275 E278 Q281 L296 E301 R304 HIS GLU HIS GLN VAL MET LEU MET

• Molecule 1: Non-POU domain-containing octamer-binding protein

Chain K:

6%

77% 15% • 8%

GLY LEU THR ILE ASP LEU LYS ASN PHE ARG LYS PRO G66 E67 T71 Q72 R73 S74 R75 P82 I85 E88 E89 M90 R91 K92 I105 R115 L116 E117 T118 R119 T120 L121 A122 L134 R135 G136 K137 R140 H146 S147 R153 Q157 Y158 V159 L163 L164

E165 V181 D182 D183 R184 G185 R186 P187 E194 L205 L215 T216 T217 P218 P219 R220 P254 P255 R256 F263 Y267 L274 I275 E276 K279 Q280 L296 M300 E301 A302 A303 R304 HIS GLU HIS GLN VAL MET LEU MET
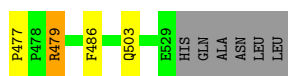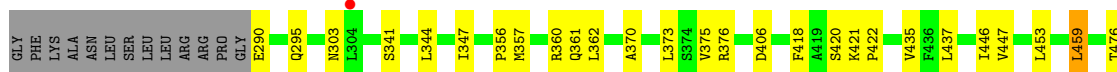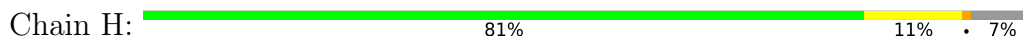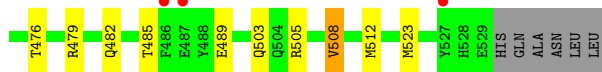
• Molecule 2: Splicing factor, proline- and glutamine-rich

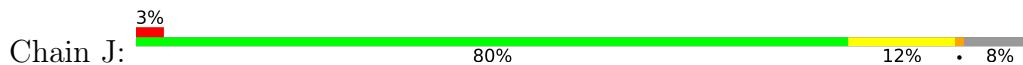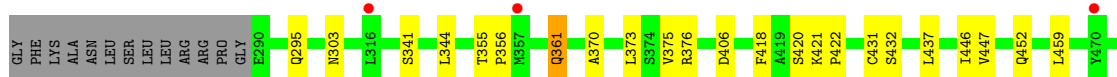Chain B:

79% 12% • 8%

GLY PHE LYS ALA ASN LEU SER LEU LEU ARG ARG PRO GLY GLU K291 Q295 N303 F313 K319 S341 L344 I347 A370 L373 S374 V375 R376 N377 D406 R407 F418 K421 P422 V435 R443 I446 V447 Q452 E473 T476 P477 P478

R479 E487 R493 Q503 Q504 R505 V508 E524 H528 E529 HIS GLN ALA ASN LEU LEU

• Molecule 2: Splicing factor, proline- and glutamine-rich

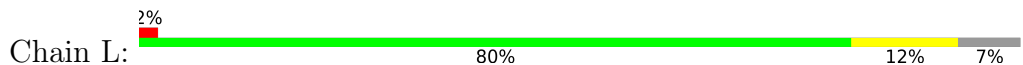Chain D:

2%

81% 11% • 8%

GLY PHE LYS ALA ASN LEU SER LEU LEU ARG ARG PRO GLY GLU K291 Q295 N303 L304 I328 K332 P356 Q361 L362 A370 L373 S374 V375 R376 D406 T411 F418 K421 P422 V435 F436 L437 R443 P444 V445 I446 V447 Q452 E473

P477 P478 R479 Y488 Q492 R493 L497 Q503 E524 H528 E529 HIS GLN ALA ASN LEU LEU

• Molecule 2: Splicing factor, proline- and glutamine-rich

Chain F:

%

80% 11% • 8%

GLY PHE LYS ALA ASN LEU SER LEU LEU ARG ARG PRO GLY GLU K291 Q295 N303 D307 I347 T355 P356 M357 R358 Q361 A370 L373 S374 V375 R376 D406 F418 A419 S420 K421 P422 V435 F436 L437 V445 I446 V447 Q452 L453 L459 E473

P477 P478 R479 F486 Y490 R493 Q503 A526 E529 HIS GLN ALA ASN LEU LEU

• Molecule 2: Splicing factor, proline- and glutamine-rich

Chain H:
81% 11% 7%

GLY PHE LYS ALA ASN LEU SER LEU LEU ARG ARG PRO GLY E290 Q295 N303 L304 S341 L344 I347 P356 M357 R360 Q361 L362 A370 L373 S374 V375 R376 D406 F418 A419 S420 K421 P422 V435 F436 L437 I446 V447 L453 L459 T476

P477 P478 R479 F486 Q503 E529 HIS GLN ALA ASN LEU LEU

• Molecule 2: Splicing factor, proline- and glutamine-rich

Chain J:
3% 80% 12% 8%

GLY PHE LYS ALA ASN LEU SER LEU LEU ARG ARG PRO GLY GLU K291 Q295 F313 L352 T355 P356 Q361 A370 L373 S374 V375 R376 Y381 D406 F418 A419 S420 K421 P422 L437 L438 T439 T440 T441 P442 I446 V447 Q452 P468 M469 Y470 Q471

T476 R479 Q482 T485 F486 E487 Y488 E489 Q503 Q504 R505 V508 M512 M523 Y527 H528 E529 HIS GLN ALA ASN LEU LEU

• Molecule 2: Splicing factor, proline- and glutamine-rich

Chain L:
2% 80% 12% 7%

GLY PHE LYS ALA ASN LEU SER LEU LEU ARG ARG PRO GLY E290 Q295 N303 L316 S341 L344 T355 P356 M357 Q361 A370 L373 S374 V375 R376 D406 F418 A419 S420 K421 P422 C431 S432 L437 I446 V447 Q452 L459 Y470

T476 R479 F480 A481 T485 F486 E489 Y490 R493 D498 Q503 L519 M523 E529 HIS GLN ALA ASN LEU LEU

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	467.00Å　66.82Å　126.89Å	Depositor
a, b, c, α, β, γ	90.00°　105.89°　90.00°	
Resolution (Å)	48.45　–　3.00	Depositor
	48.45　–　3.00	EDS
% Data completeness	77.2 (48.45-3.00)	Depositor
(in resolution range)	77.2 (48.45-3.00)	EDS
R_{merge}	0.13	Depositor
R_{sym}	0.15	Depositor
$< I/\sigma(I) >$ [1]	1.53 (at 3.01Å)	Xtriage
Refinement program	BUSTER 2.10.4 (16-JUL-2021)	Depositor
R, R_{free}	0.223　,　0.255	Depositor
	0.226　,　0.260	DCC
R_{free} test set	2903 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å^2)	80.7	Xtriage
Anisotropy	0.046	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	(Not available) , (Not available)	EDS
L-test for twinning[2]	$< |L| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.022 for -h-2*l,-k,l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	23285	wwPDB-VP
Average B, all atoms (Å^2)	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 59.10 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.8551e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

---

[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: MG

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	0.37	0/2001	0.54	0/2686
1	C	0.39	0/2006	0.53	0/2692
1	E	0.41	0/1966	0.55	0/2639
1	G	0.40	0/1971	0.54	0/2645
1	I	0.38	0/1965	0.55	0/2636
1	K	0.37	0/1975	0.56	0/2650
2	B	0.38	0/1970	0.52	0/2648
2	D	0.37	0/1970	0.50	0/2648
2	F	0.39	0/1970	0.52	0/2648
2	H	0.39	0/1979	0.52	0/2660
2	J	0.38	0/1970	0.52	0/2648
2	L	0.37	0/1979	0.52	0/2660
All	All	0.39	0/23722	0.53	0/31860

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	1963	0	1945	20	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1968	0	1957	15	0
1	E	1929	0	1917	20	0
1	G	1934	0	1927	19	0
1	I	1930	0	1923	15	0
1	K	1939	0	1937	22	0
2	B	1932	0	1903	24	0
2	D	1932	0	1903	17	0
2	F	1932	0	1903	22	0
2	H	1941	0	1909	18	0
2	J	1932	0	1903	21	0
2	L	1941	0	1909	22	0
3	B	2	0	0	0	0
3	D	2	0	0	0	0
3	F	2	0	0	0	0
3	H	2	0	0	0	0
3	J	2	0	0	0	0
3	K	1	0	0	0	0
3	L	1	0	0	0	0
All	All	23285	0	23036	183	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 4.

The worst 5 of 183 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:216:THR:O	2:B:479:ARG:NH2	1.96	0.98
1:I:251:ARG:NH1	2:J:381:TYR:O	2.10	0.85
2:B:479:ARG:NH1	2:B:487:GLU:OE2	2.11	0.83
1:C:85:ILE:HG23	1:C:105:ILE:HD11	1.65	0.77
1:E:85:ILE:HG23	1:E:105:ILE:HD11	1.65	0.77

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	240/259 (93%)	236 (98%)	4 (2%)	0	100	100
1	C	240/259 (93%)	235 (98%)	5 (2%)	0	100	100
1	E	233/259 (90%)	230 (99%)	3 (1%)	0	100	100
1	G	233/259 (90%)	229 (98%)	4 (2%)	0	100	100
1	I	234/259 (90%)	231 (99%)	3 (1%)	0	100	100
1	K	237/259 (92%)	234 (99%)	3 (1%)	0	100	100
2	B	237/259 (92%)	232 (98%)	5 (2%)	0	100	100
2	D	237/259 (92%)	230 (97%)	7 (3%)	0	100	100
2	F	237/259 (92%)	231 (98%)	6 (2%)	0	100	100
2	H	238/259 (92%)	232 (98%)	6 (2%)	0	100	100
2	J	237/259 (92%)	232 (98%)	5 (2%)	0	100	100
2	L	238/259 (92%)	233 (98%)	5 (2%)	0	100	100
All	All	2841/3108 (91%)	2785 (98%)	56 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2   Protein sidechains   ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	210/227 (92%)	200 (95%)	10 (5%)	25	62
1	C	211/227 (93%)	196 (93%)	15 (7%)	14	46
1	E	207/227 (91%)	191 (92%)	16 (8%)	13	42
1	G	208/227 (92%)	196 (94%)	12 (6%)	20	55
1	I	207/227 (91%)	197 (95%)	10 (5%)	25	62
1	K	208/227 (92%)	195 (94%)	13 (6%)	18	51
2	B	205/221 (93%)	194 (95%)	11 (5%)	22	57

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	205/221 (93%)	198 (97%)	7 (3%)	37	72
2	F	205/221 (93%)	199 (97%)	6 (3%)	42	76
2	H	206/221 (93%)	199 (97%)	7 (3%)	37	72
2	J	205/221 (93%)	197 (96%)	8 (4%)	32	69
2	L	206/221 (93%)	199 (97%)	7 (3%)	37	72
All	All	2483/2688 (92%)	2361 (95%)	122 (5%)	25	61

5 of 122 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	301	GLU
1	K	183	ASP
1	G	183	ASP
1	K	165	GLU
2	L	432	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
2	J	295	GLN
2	L	295	GLN
2	D	295	GLN
1	E	72	GLN
2	F	295	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 12 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	242/259 (93%)	0.27	6 (2%) 57	29	67, 89, 125, 138	0
1	C	242/259 (93%)	0.28	10 (4%) 37	14	57, 85, 126, 141	0
1	E	237/259 (91%)	0.16	3 (1%) 77	51	60, 81, 124, 136	0
1	G	237/259 (91%)	0.28	10 (4%) 36	14	56, 83, 138, 151	0
1	I	238/259 (91%)	0.39	11 (4%) 32	12	64, 93, 135, 162	0
1	K	239/259 (92%)	0.41	16 (6%) 17	5	65, 102, 139, 213	0
2	B	239/259 (92%)	0.17	1 (0%) 92	79	46, 91, 120, 148	0
2	D	239/259 (92%)	0.10	4 (1%) 70	41	50, 84, 115, 143	0
2	F	239/259 (92%)	0.12	3 (1%) 77	51	43, 80, 112, 139	0
2	H	240/259 (92%)	0.15	1 (0%) 92	79	55, 85, 117, 142	0
2	J	239/259 (92%)	0.25	8 (3%) 46	20	52, 85, 133, 140	0
2	L	240/259 (92%)	0.25	6 (2%) 57	29	63, 98, 139, 144	0
All	All	2871/3108 (92%)	0.24	79 (2%) 53	25	43, 88, 130, 213	0

The worst 5 of 79 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	109	LYS	6.3
1	C	85	ILE	5.5
1	I	67	GLU	4.3
1	I	134	LEU	4.3
1	K	66	GLY	4.3

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 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, 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
3	MG	F	601	1/1	0.90	0.14	52,52,52,52	0
3	MG	H	602	1/1	0.90	0.19	62,62,62,62	0
3	MG	H	601	1/1	0.91	0.19	60,60,60,60	0
3	MG	D	601	1/1	0.91	0.16	70,70,70,70	0
3	MG	L	601	1/1	0.91	0.17	78,78,78,78	0
3	MG	F	602	1/1	0.92	0.12	48,48,48,48	0
3	MG	J	601	1/1	0.92	0.11	71,71,71,71	0
3	MG	B	602	1/1	0.92	0.21	41,41,41,41	0
3	MG	K	401	1/1	0.93	0.20	62,62,62,62	0
3	MG	J	602	1/1	0.95	0.18	45,45,45,45	0
3	MG	D	602	1/1	0.95	0.35	41,41,41,41	0
3	MG	B	601	1/1	0.95	0.14	82,82,82,82	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.
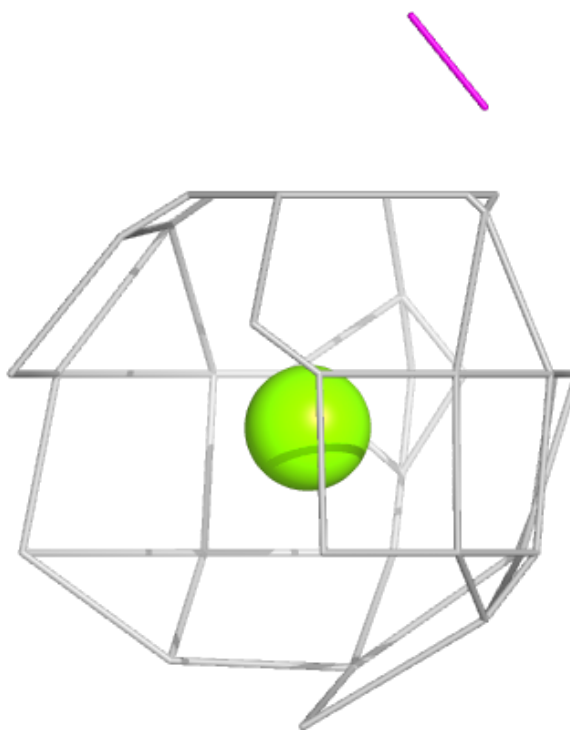
Electron density around MG F 601:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
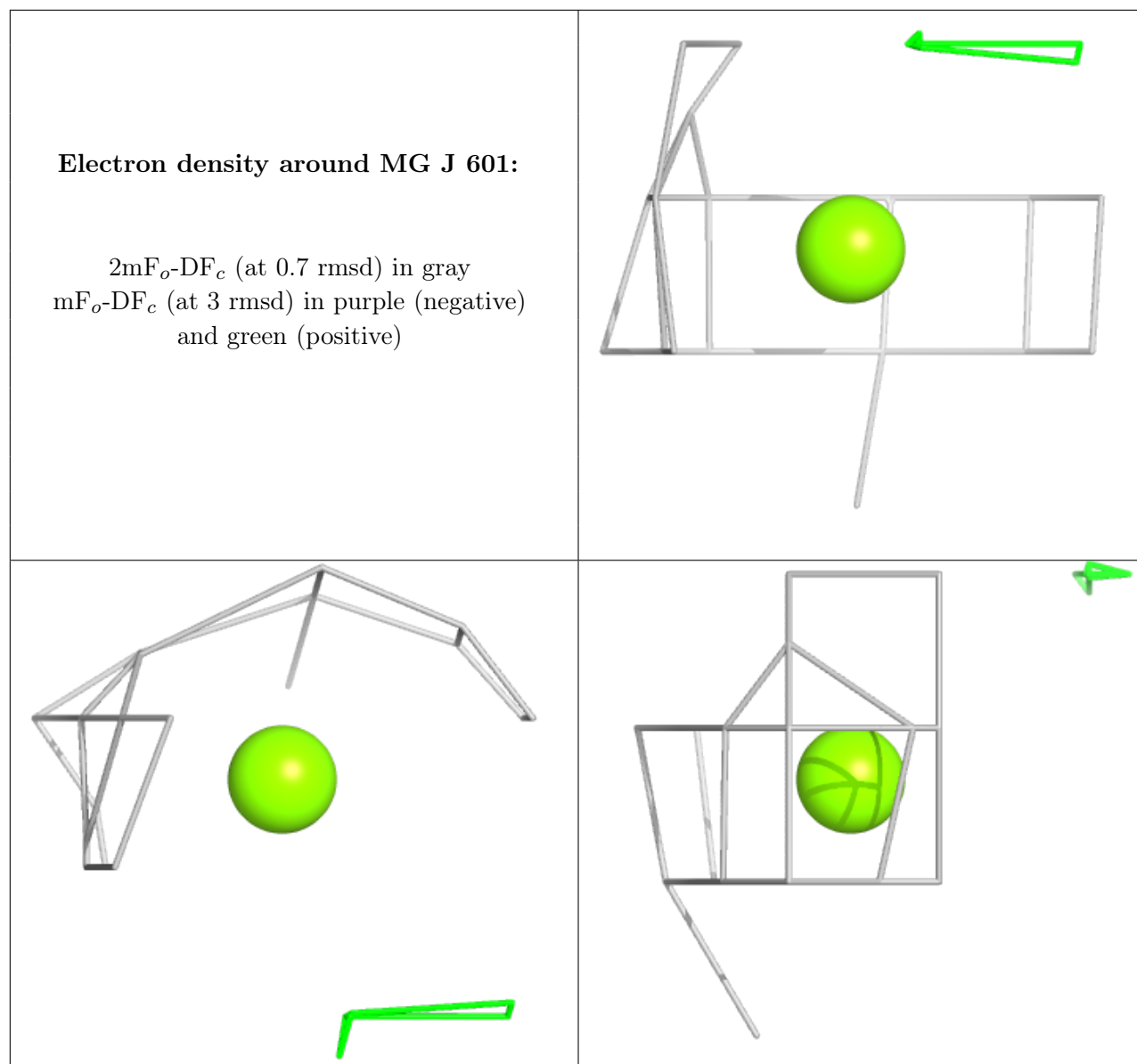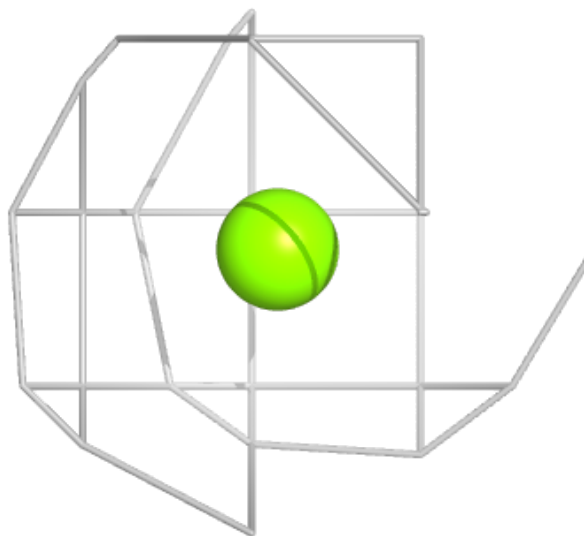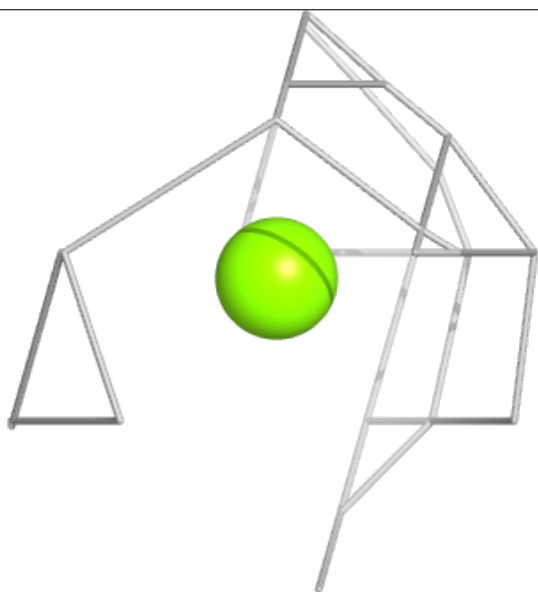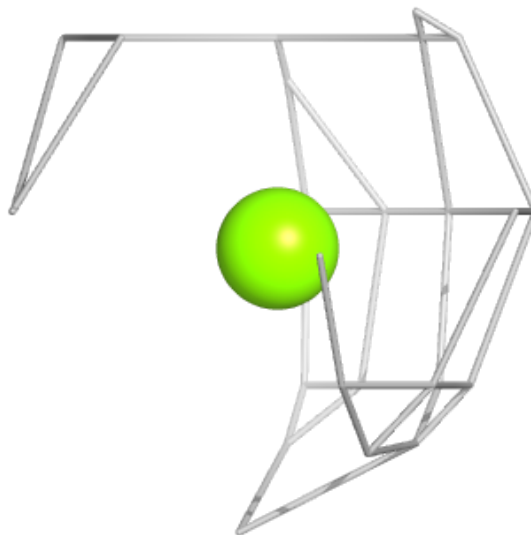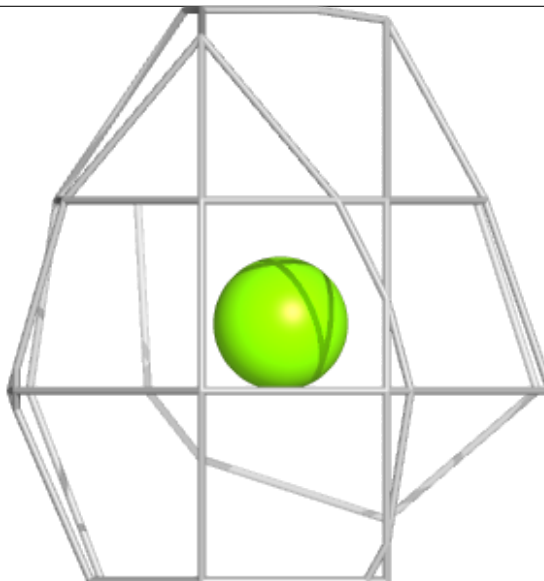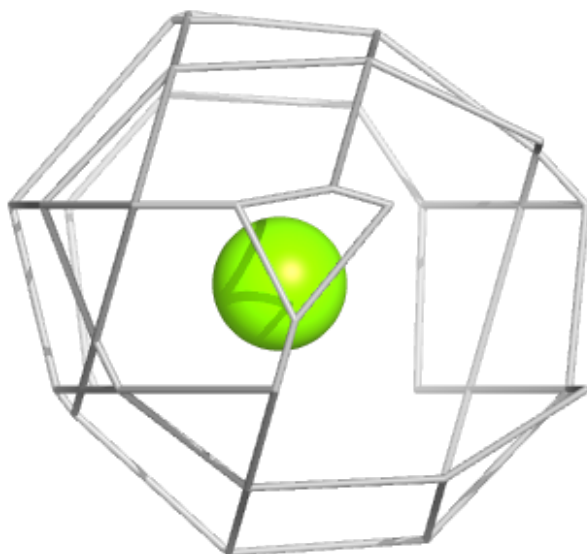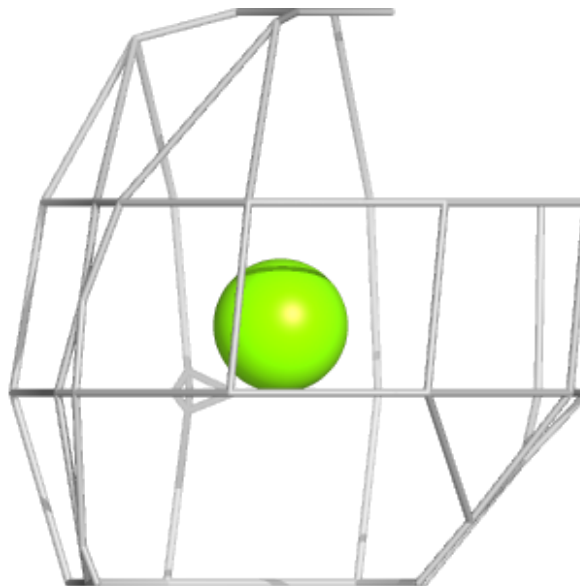and green (positive)
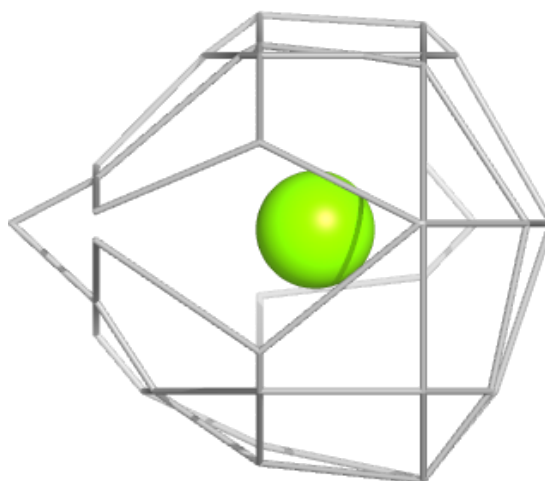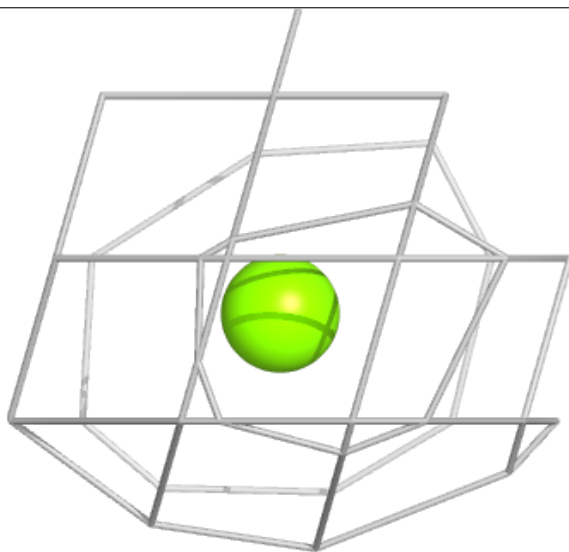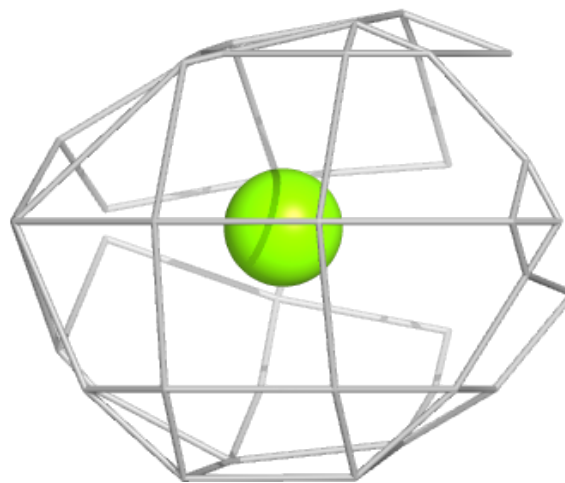
Electron density around MG H 602:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)
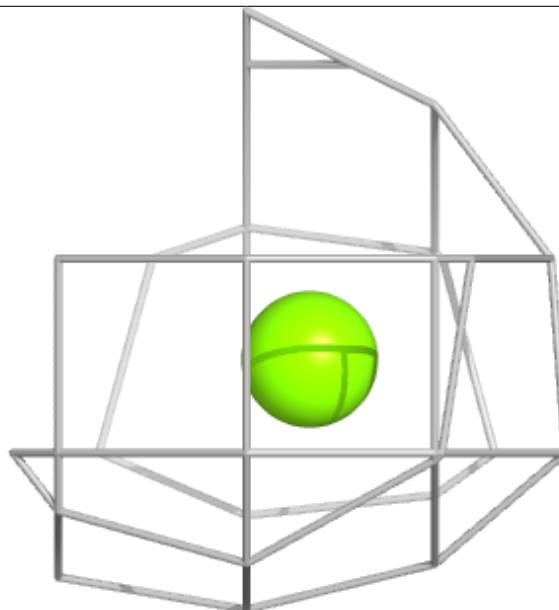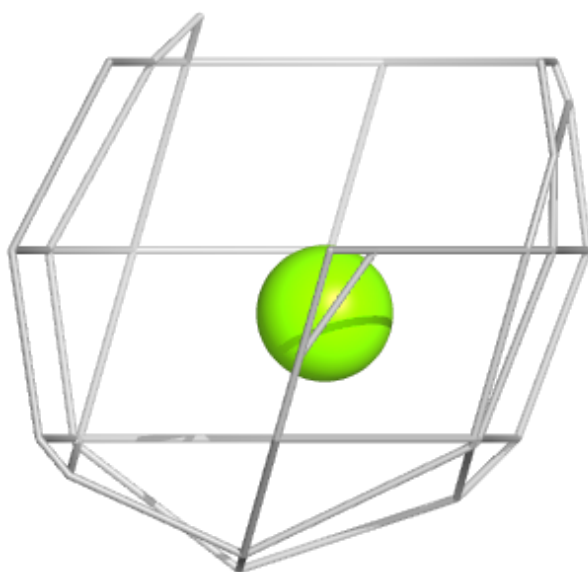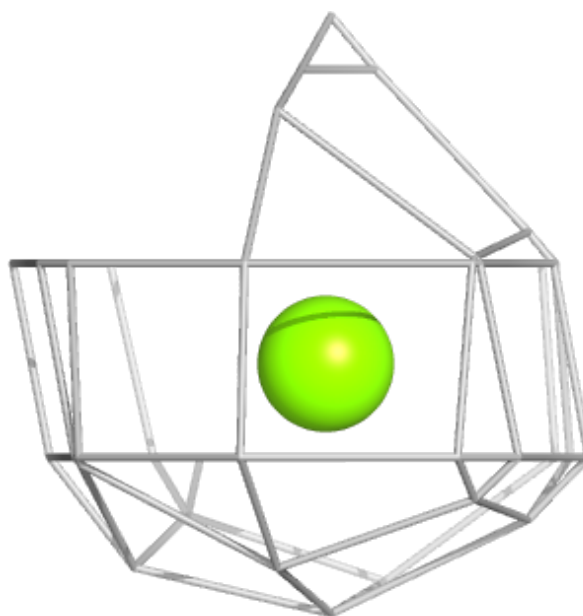
Electron density around MG H 601:

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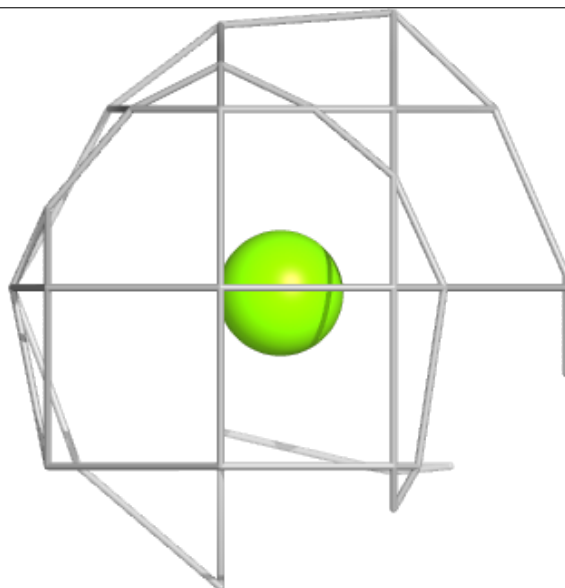$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
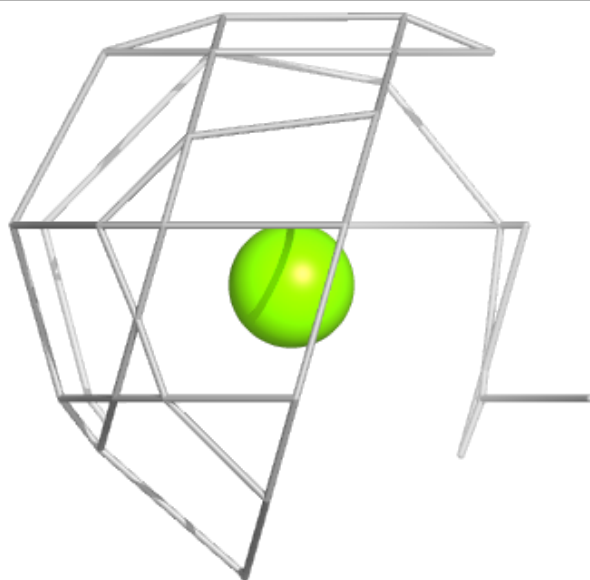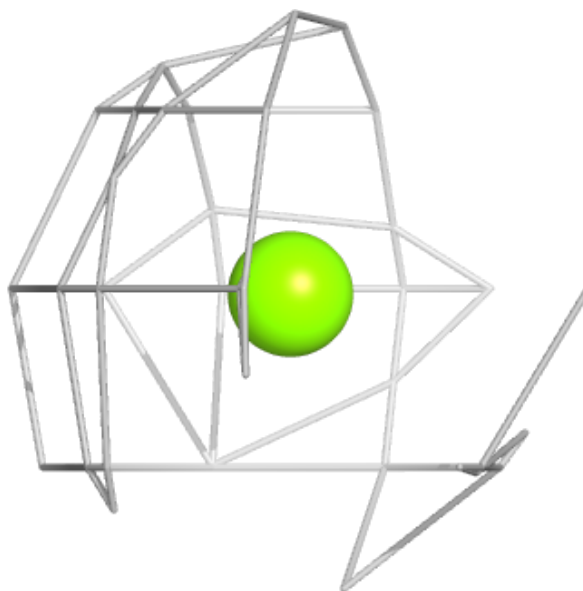and green (positive)

Electron density around MG D 601:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
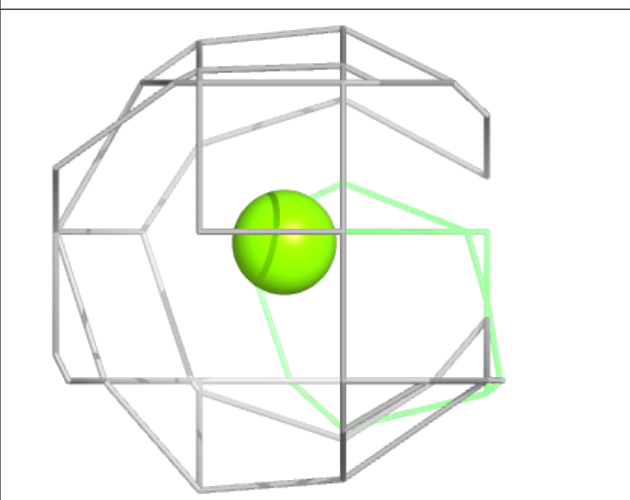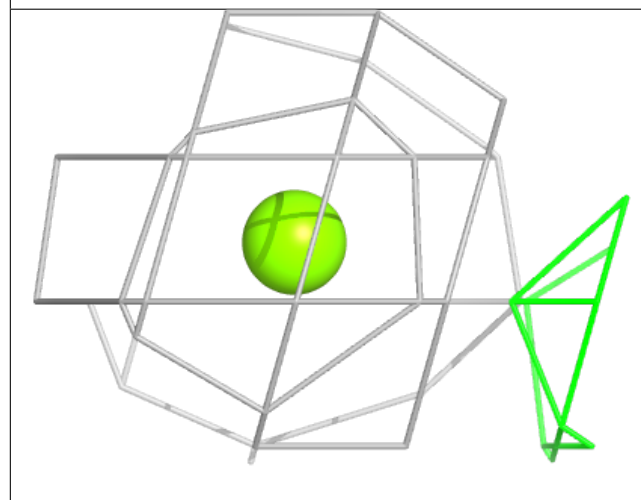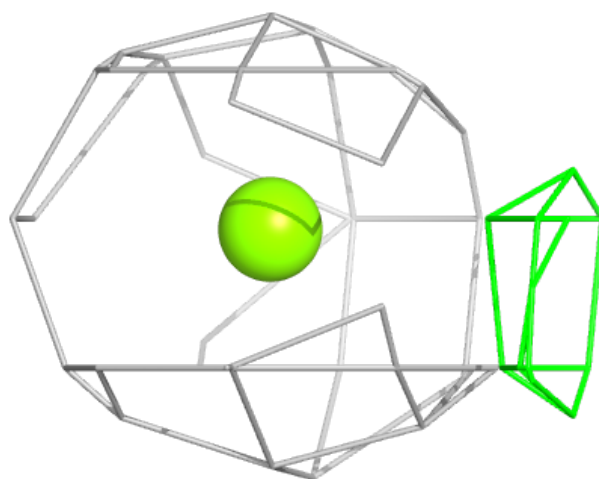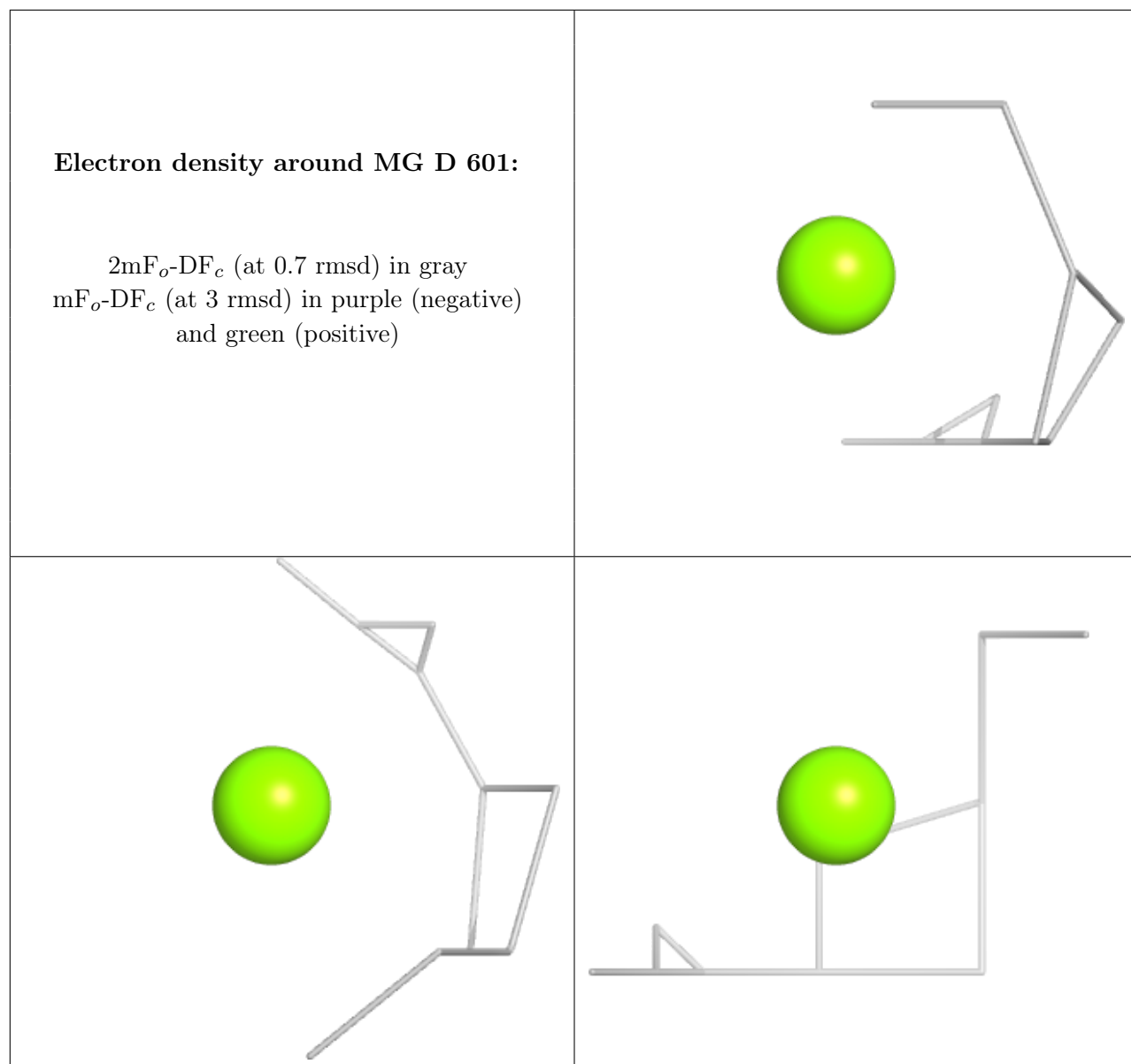
Electron density around MG L 601:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)
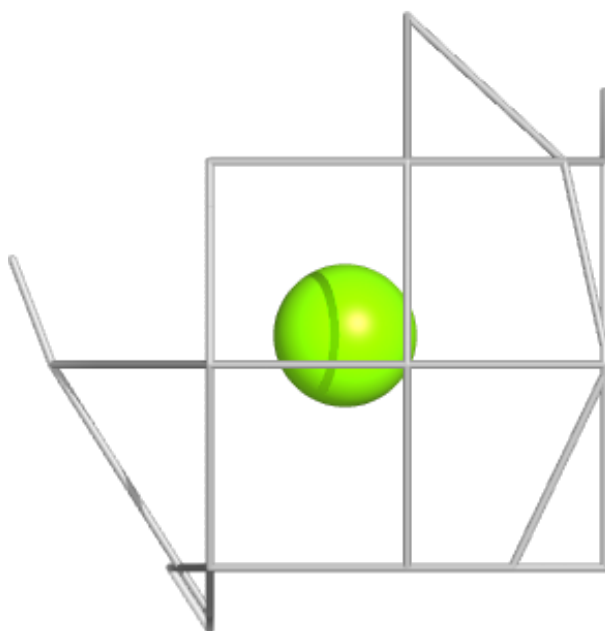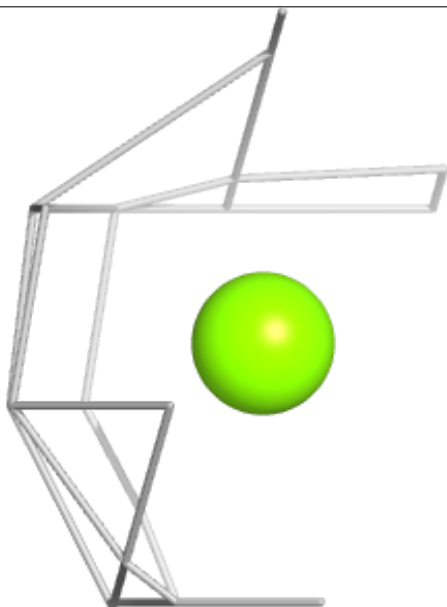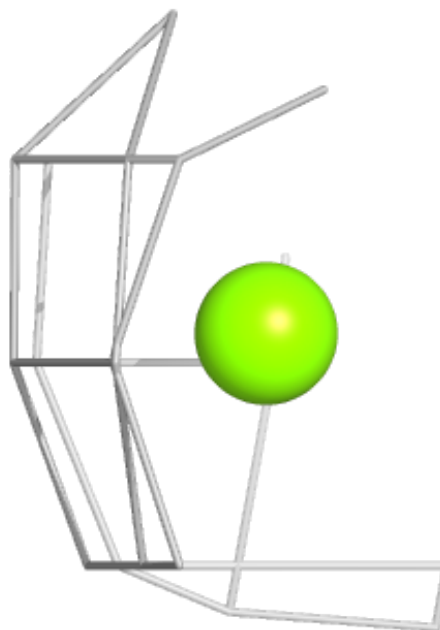
Electron density around MG F 602:

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

Electron density around MG J 601:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
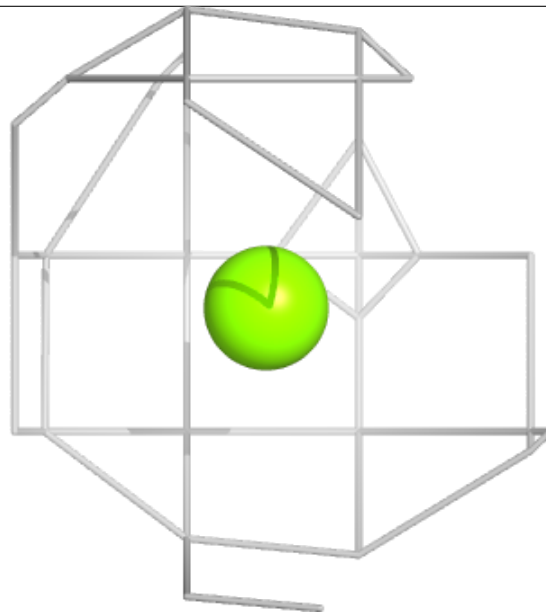$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
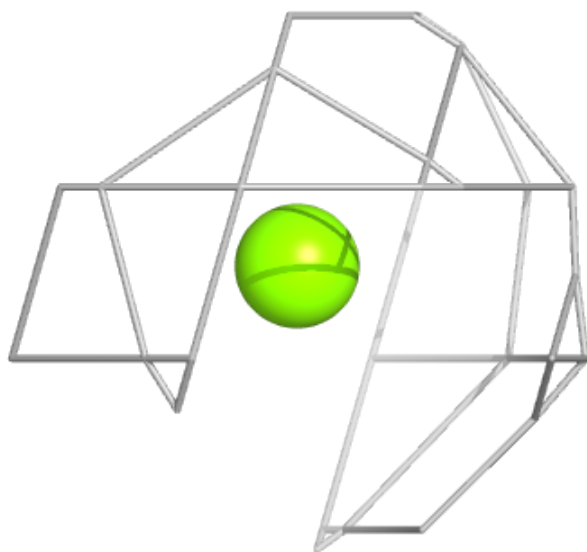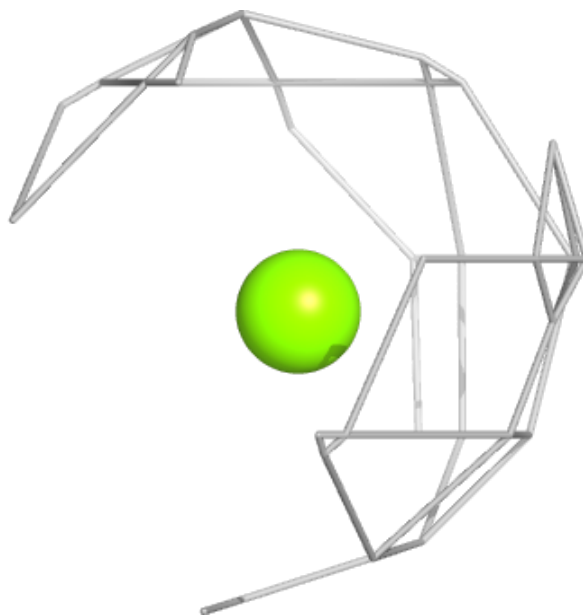and green (positive)
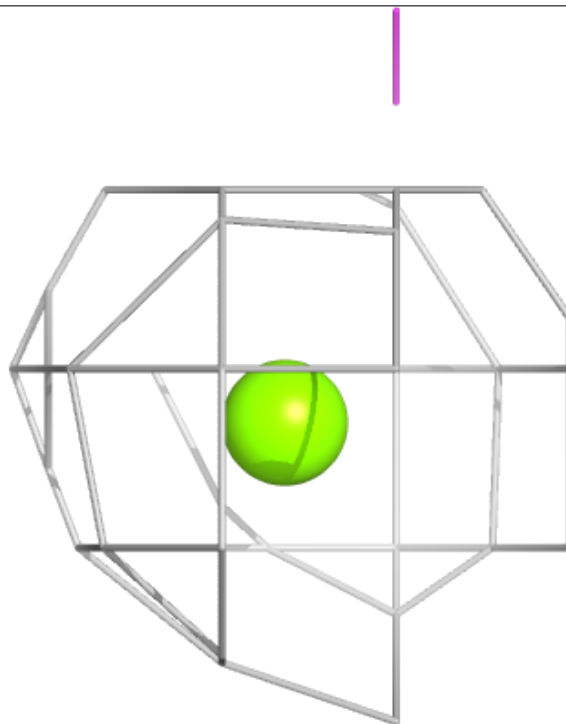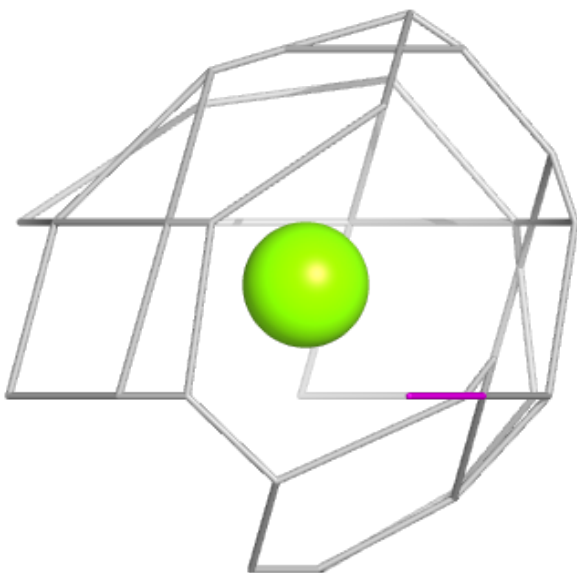
Electron density around MG B 602:

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

Electron density around MG K 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 MG J 602:

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

Electron density around MG D 602:
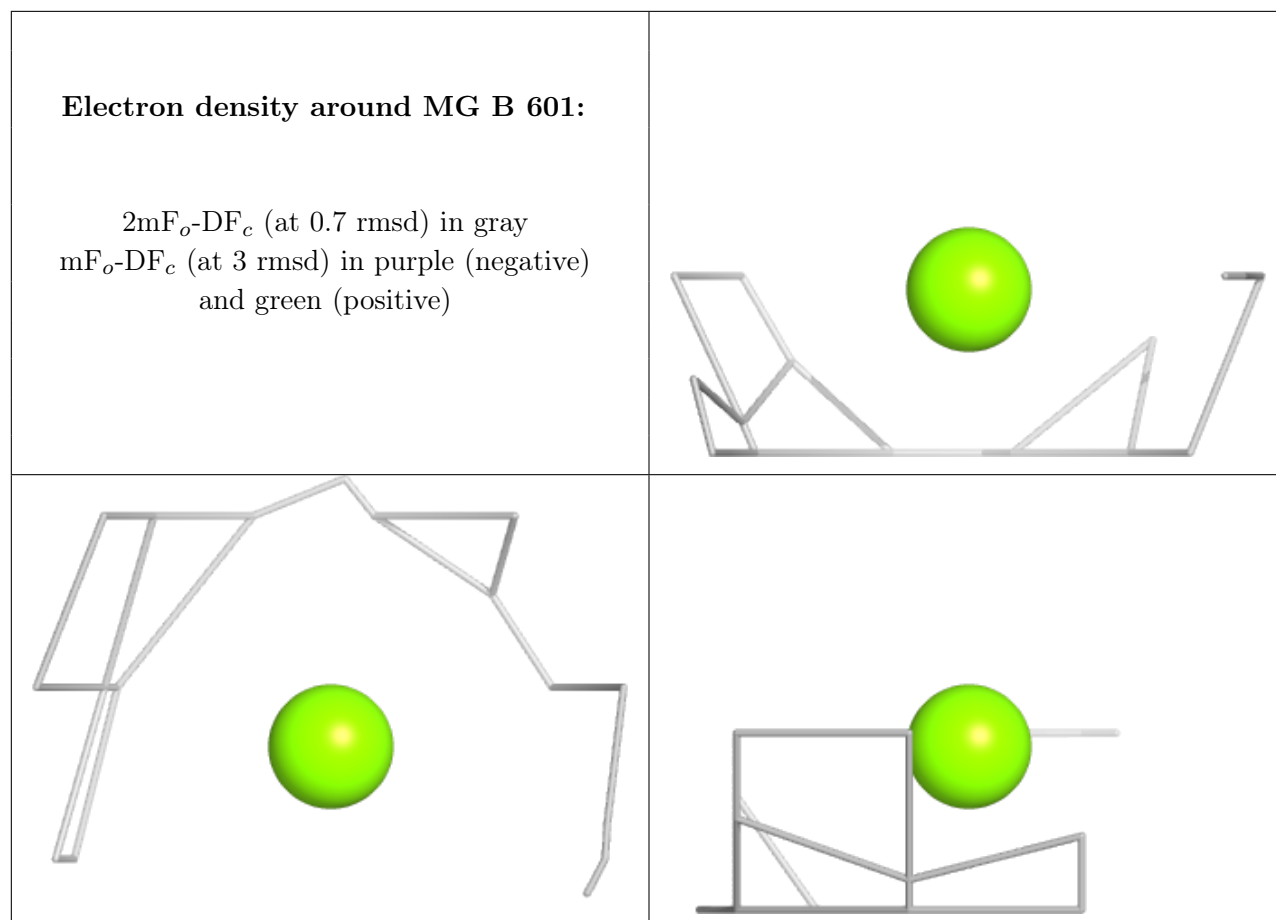
$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)

Electron density around MG 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)

6.5 Other polymers ⓘ

There are no such residues in this entry.