



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:17 PM UTC

PDB ID : 7LJB / pdb_00007ljb
Title : Human TRAAK K⁺ channel mutant G158D in a K⁺ bound conductive conformation
Authors : Rietmeijer, R.A.; Brohawn, S.G.
Deposited on : 2021-01-28
Resolution : 2.97 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

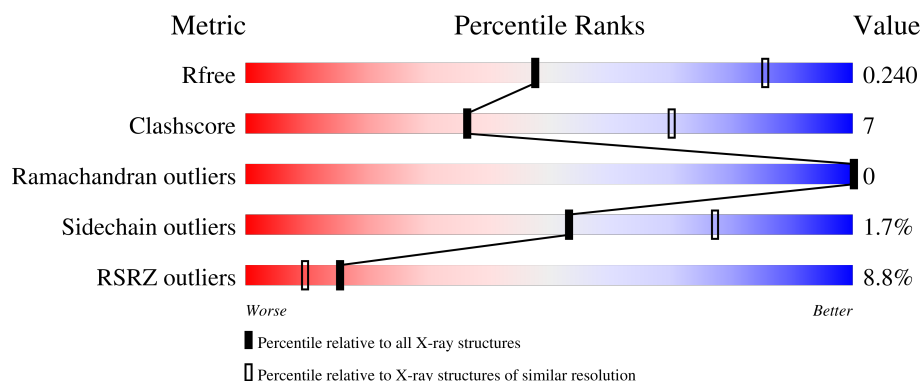
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.97 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3580 (3.00-2.96)
Clashscore	190562	3904 (3.00-2.96)
Ramachandran outliers	187476	3761 (3.00-2.96)
Sidechain outliers	187428	3764 (3.00-2.96)
RSRZ outliers	180081	3579 (3.00-2.96)

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	299	18% 72% 12% • 15%
1	B	299	5% 70% 13% • 16%
2	D	211	7% 83% 16% •
2	F	211	5% 81% 18% •
3	E	217	6% 81% 16% •

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Mol	Chain	Length	Quality of chain
3	G	217	7% 79% 17% ••

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 10586 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 Isoform 2 of Potassium channel subfamily K member 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	253	Total	C	N	O	S	0	0	0
			1967	1301	318	342	6			
1	B	251	Total	C	N	O	S	0	0	0
			1958	1293	317	342	6			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	104	GLN	ASN	engineered mutation	UNP Q9NYG8-2
A	108	GLN	ASN	engineered mutation	UNP Q9NYG8-2
A	158	ASP	GLY	engineered mutation	UNP Q9NYG8-2
A	291	SER	-	expression tag	UNP Q9NYG8-2
A	292	ASN	-	expression tag	UNP Q9NYG8-2
A	293	SER	-	expression tag	UNP Q9NYG8-2
A	294	LEU	-	expression tag	UNP Q9NYG8-2
A	295	GLU	-	expression tag	UNP Q9NYG8-2
A	296	VAL	-	expression tag	UNP Q9NYG8-2
A	297	LEU	-	expression tag	UNP Q9NYG8-2
A	298	PHE	-	expression tag	UNP Q9NYG8-2
A	299	GLN	-	expression tag	UNP Q9NYG8-2
B	104	GLN	ASN	engineered mutation	UNP Q9NYG8-2
B	108	GLN	ASN	engineered mutation	UNP Q9NYG8-2
B	158	ASP	GLY	engineered mutation	UNP Q9NYG8-2
B	291	SER	-	expression tag	UNP Q9NYG8-2
B	292	ASN	-	expression tag	UNP Q9NYG8-2
B	293	SER	-	expression tag	UNP Q9NYG8-2
B	294	LEU	-	expression tag	UNP Q9NYG8-2
B	295	GLU	-	expression tag	UNP Q9NYG8-2
B	296	VAL	-	expression tag	UNP Q9NYG8-2
B	297	LEU	-	expression tag	UNP Q9NYG8-2
B	298	PHE	-	expression tag	UNP Q9NYG8-2
B	299	GLN	-	expression tag	UNP Q9NYG8-2

- Molecule 2 is a protein called ANTI-TRAAK ANTIBODY 13E9 FAB FRAGMENT LIGHT CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	211	Total	C	N	O	S	0	0	0
			1616	1003	271	333	9			
2	F	211	Total	C	N	O	S	0	0	0
			1616	1003	271	333	9			

- Molecule 3 is a protein called ANTI-TRAAK ANTIBODY 13E9 FAB FRAGMENT HEAVY CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	211	Total	C	N	O	S	0	0	0
			1614	1026	261	319	8			
3	G	210	Total	C	N	O	S	0	0	0
			1605	1022	260	315	8			

- Molecule 4 is POTASSIUM ION (CCD ID: K) (formula: K) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	4	Total	K	0	0
			4	4		
4	B	2	Total	K	0	0
			2	2		

- Molecule 5 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Ca	0	0
			2	2		
5	G	1	Total	Ca	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	36	Total	O	0	0
			36	36		
6	B	35	Total	O	0	0
			35	35		
6	D	38	Total	O	0	0
			38	38		

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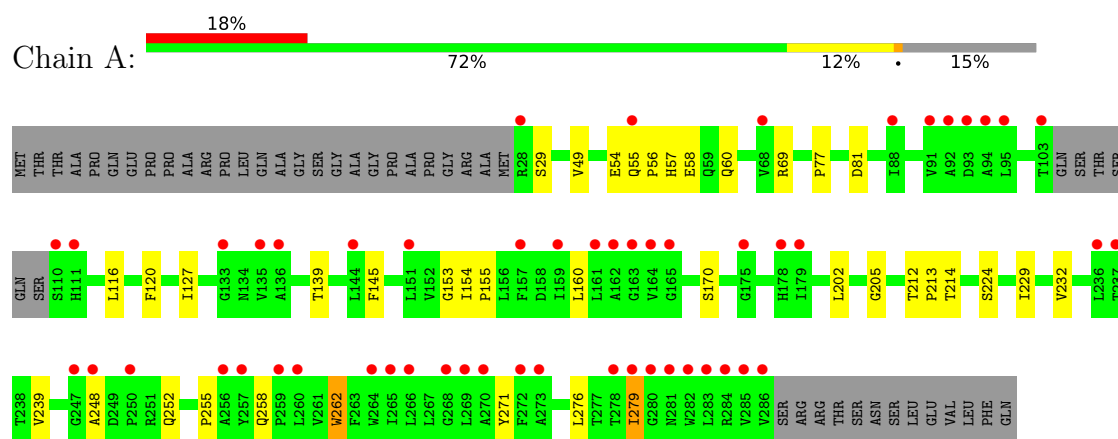
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	E	30	Total 30	O 30	0	0
6	F	34	Total 34	O 34	0	0
6	G	28	Total 28	O 28	0	0

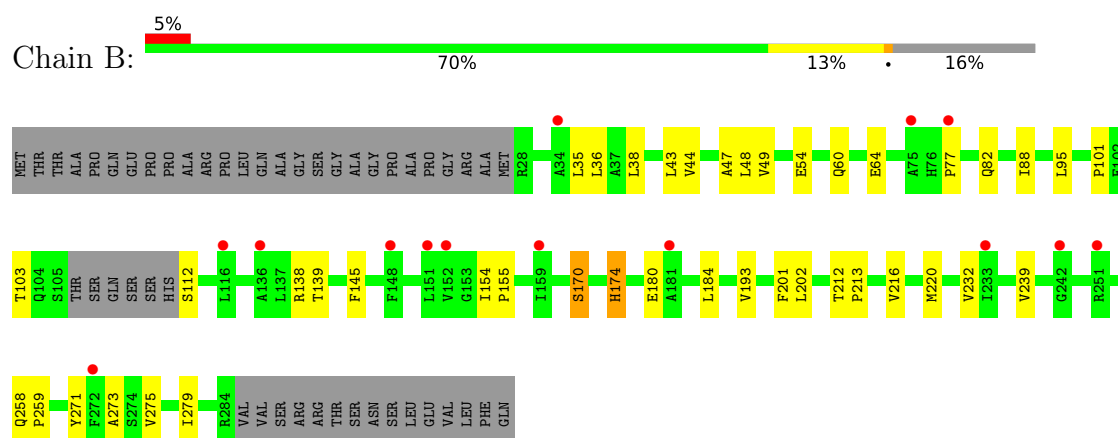
3 Residue-property plots [i](#)

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.

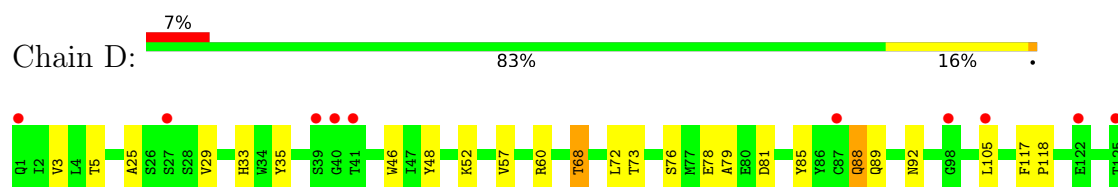
- Molecule 1: Isoform 2 of Potassium channel subfamily K member 4

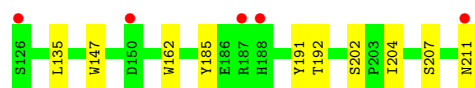


- Molecule 1: Isoform 2 of Potassium channel subfamily K member 4

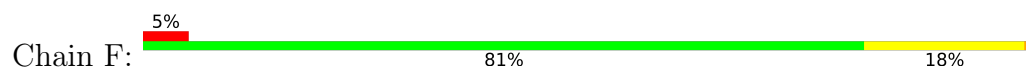


- Molecule 2: ANTI-TRAAK ANTIBODY 13E9 FAB FRAGMENT LIGHT CHAIN

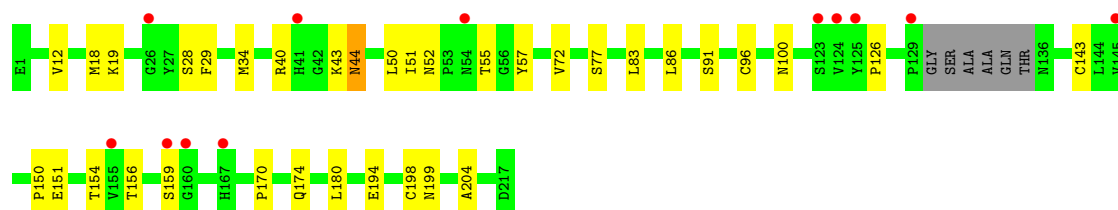
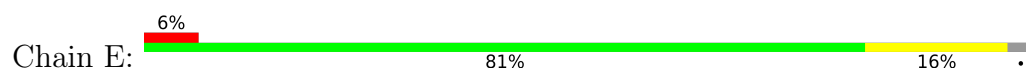




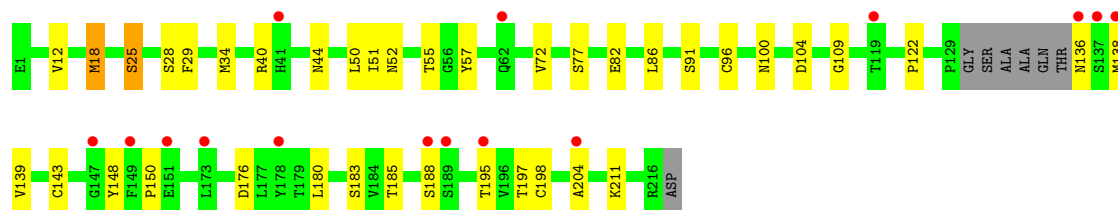
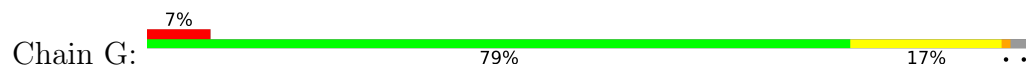
• Molecule 2: ANTI-TRAAK ANTIBODY 13E9 FAB FRAGMENT LIGHT CHAIN



• Molecule 3: ANTI-TRAAK ANTIBODY 13E9 FAB FRAGMENT HEAVY CHAIN



• Molecule 3: ANTI-TRAAK ANTIBODY 13E9 FAB FRAGMENT HEAVY CHAIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	80.14Å 137.31Å 96.30Å 90.00° 94.72° 90.00°	Depositor
Resolution (Å)	48.03 – 2.97 48.03 – 2.97	Depositor EDS
% Data completeness (in resolution range)	74.0 (48.03-2.97) 74.0 (48.03-2.97)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.25 (at 2.96Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.196 , 0.240 0.198 , 0.240	Depositor DCC
R_{free} test set	1575 reflections (2.15%)	wwPDB-VP
Wilson B-factor (Å ²)	91.9	Xtriage
Anisotropy	0.021	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 58.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	10586	wwPDB-VP
Average B, all atoms (Å ²)	107.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.40% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: K, CA

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	1.08	0/2017	1.71	11/2751 (0.4%)
1	B	1.08	0/2008	1.73	14/2737 (0.5%)
2	D	1.02	0/1655	1.36	1/2247 (0.0%)
2	F	1.04	0/1655	1.37	2/2247 (0.1%)
3	E	1.03	1/1656 (0.1%)	1.38	0/2260
3	G	1.04	1/1647 (0.1%)	1.36	3/2249 (0.1%)
All	All	1.05	2/10638 (0.0%)	1.51	31/14491 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	126	PRO	C-O	-5.61	1.18	1.23
3	G	25	SER	CA-CB	-5.12	1.45	1.53

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	68	THR	CA-CB-OG1	-5.92	100.72	109.60
1	B	239	VAL	N-CA-C	-5.56	105.30	110.53
1	A	239	VAL	N-CA-C	-5.54	105.32	110.53
1	A	153	GLY	CA-C-N	5.52	124.74	120.33
1	A	153	GLY	C-N-CA	5.52	124.74	120.33
1	B	170	SER	CA-C-N	5.51	127.61	120.44
1	B	170	SER	C-N-CA	5.51	127.61	120.44
3	G	176	ASP	CA-CB-CG	5.51	118.11	112.60
1	A	262	TRP	CA-C-N	5.47	127.61	120.28
1	A	262	TRP	C-N-CA	5.47	127.61	120.28
2	F	98	GLY	CA-C-N	5.42	128.08	120.28
2	F	98	GLY	C-N-CA	5.42	128.08	120.28
1	B	174	HIS	CA-C-N	5.31	125.73	119.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	174	HIS	C-N-CA	5.31	125.73	119.94
3	G	136	ASN	CA-CB-CG	5.30	117.90	112.60
3	G	109	GLY	CA-C-O	-5.25	118.60	122.23
1	A	29	SER	CA-C-N	5.23	127.23	120.44
1	A	29	SER	C-N-CA	5.23	127.23	120.44
1	B	279	ILE	CA-C-N	5.23	125.78	119.98
1	B	279	ILE	C-N-CA	5.23	125.78	119.98
1	B	64	GLU	CA-C-O	-5.22	115.02	120.55
1	B	103	THR	CA-C-N	5.22	130.12	122.77
1	B	103	THR	C-N-CA	5.22	130.12	122.77
1	A	279	ILE	CA-C-N	5.18	125.73	119.98
1	A	279	ILE	C-N-CA	5.18	125.73	119.98
1	A	170	SER	CA-C-N	5.11	127.08	120.44
1	A	170	SER	C-N-CA	5.11	127.08	120.44
1	B	273	ALA	CA-C-N	5.05	127.04	120.28
1	B	273	ALA	C-N-CA	5.05	127.04	120.28
1	B	180	GLU	CA-C-N	5.04	127.29	120.38
1	B	180	GLU	C-N-CA	5.04	127.29	120.38

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	1967	0	1986	31	0
1	B	1958	0	1978	29	0
2	D	1616	0	1542	22	0
2	F	1616	0	1542	33	0
3	E	1614	0	1586	27	1
3	G	1605	0	1582	29	0
4	A	4	0	0	0	0
4	B	2	0	0	0	0
5	A	2	0	0	0	0
5	G	1	0	0	0	1
6	A	36	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	35	0	0	0	0
6	D	38	0	0	7	0
6	E	30	0	0	1	0
6	F	34	0	0	1	0
6	G	28	0	0	2	0
All	All	10586	0	10216	147	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 7.

All (147) 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)
2:D:76:SER:O	6:D:301:HOH:O	2.03	0.77
1:A:276:LEU:HA	1:A:279:ILE:HG22	1.68	0.76
1:A:77:PRO:HA	3:E:100:ASN:HD21	1.50	0.76
3:G:139:VAL:HG23	3:G:188:SER:HB3	1.70	0.73
1:B:77:PRO:HA	3:G:100:ASN:ND2	2.03	0.73
3:E:156:THR:OG1	3:E:199:ASN:HB2	1.90	0.72
1:B:77:PRO:HA	3:G:100:ASN:HD21	1.55	0.70
3:E:28:SER:HB2	3:G:28:SER:HB2	1.72	0.70
1:A:248:ALA:HB1	1:A:262:TRP:HE1	1.59	0.68
1:A:276:LEU:HA	1:A:279:ILE:CG2	2.25	0.67
2:F:35:TYR:HE2	2:F:88:GLN:HB2	1.60	0.66
3:G:34:MET:CE	3:G:96:CYS:HB2	2.25	0.66
2:F:111:ALA:O	6:F:301:HOH:O	2.13	0.66
3:E:18:MET:HG2	3:E:19:LYS:N	2.13	0.64
1:B:216:VAL:O	1:B:220:MET:HG2	1.97	0.64
2:F:99:ALA:HA	3:G:44:ASN:HB3	1.81	0.63
2:F:160:ASN:ND2	2:F:174:MET:HE1	2.14	0.62
3:E:34:MET:CE	3:E:96:CYS:HB2	2.30	0.61
1:A:77:PRO:HA	3:E:100:ASN:ND2	2.16	0.61
3:G:29:PHE:HB2	3:G:77:SER:HB2	1.83	0.60
1:A:139:THR:OG1	1:B:54:GLU:OE2	2.15	0.60
2:F:79:ALA:HA	2:F:105:LEU:HD11	1.83	0.59
1:A:69:ARG:NH1	1:A:81:ASP:OD1	2.35	0.58
3:G:25:SER:HA	6:G:421:HOH:O	2.03	0.58
1:A:116:LEU:HD21	1:B:48:LEU:HD23	1.85	0.58
1:B:212:THR:HB	1:B:213:PRO:HD3	1.85	0.58
3:E:29:PHE:HB2	3:E:77:SER:HB2	1.85	0.57
1:A:205:GLY:HA3	1:A:271:TYR:CZ	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:212:THR:HB	1:A:213:PRO:HD3	1.86	0.57
3:E:44:ASN:N	3:E:44:ASN:OD1	2.38	0.57
2:F:134:PHE:CE2	3:G:183:SER:HB3	2.40	0.57
1:A:60:GLN:HB3	1:B:138:ARG:NH1	2.20	0.56
3:E:12:VAL:HG21	3:E:86:LEU:CD1	2.34	0.56
1:A:252:GLN:OE1	1:A:252:GLN:N	2.38	0.56
2:F:89:GLN:HE21	2:F:92:ASN:H	1.54	0.56
1:A:202:LEU:HA	1:A:271:TYR:OH	2.06	0.55
2:F:45:ARG:HD3	3:G:104:ASP:HA	1.88	0.55
1:B:202:LEU:HA	1:B:271:TYR:OH	2.07	0.54
1:A:127:ILE:CD1	1:B:43:LEU:HD21	2.38	0.54
1:A:55:GLN:N	1:A:56:PRO:HD2	2.23	0.54
2:F:89:GLN:NE2	2:F:92:ASN:H	2.06	0.54
2:F:134:PHE:CE2	3:G:183:SER:CB	2.91	0.54
3:G:34:MET:HE1	3:G:96:CYS:HB2	1.88	0.53
3:G:195:THR:HA	6:G:406:HOH:O	2.08	0.53
1:B:201:PHE:HE1	1:B:275:VAL:HG22	1.73	0.53
2:D:3:VAL:HA	6:D:320:HOH:O	2.08	0.53
2:D:29:VAL:HG11	2:D:89:GLN:HG3	1.90	0.52
3:E:40:ARG:NH1	3:E:91:SER:O	2.43	0.52
2:D:35:TYR:O	2:D:85:TYR:HA	2.10	0.52
2:F:35:TYR:O	2:F:85:TYR:HA	2.09	0.52
6:D:331:HOH:O	3:E:44:ASN:HB3	2.10	0.51
2:F:72:LEU:C	2:F:72:LEU:HD23	2.36	0.51
2:D:25:ALA:O	2:D:68:THR:OG1	2.27	0.51
3:E:159:SER:H	3:E:199:ASN:ND2	2.09	0.50
2:F:123:GLN:HE22	2:F:130:SER:HB2	1.77	0.50
2:F:72:LEU:HD23	2:F:73:THR:N	2.26	0.49
3:G:12:VAL:HG21	3:G:86:LEU:CD1	2.42	0.49
2:D:79:ALA:HA	2:D:105:LEU:HD21	1.94	0.49
2:F:135:LEU:HD12	2:F:135:LEU:N	2.27	0.49
1:A:248:ALA:CB	1:A:262:TRP:HE1	2.26	0.49
3:G:52:ASN:HB3	3:G:55:THR:OG1	2.13	0.49
2:F:46:TRP:O	2:F:57:VAL:HG21	2.13	0.48
3:G:195:THR:HG22	3:G:197:THR:HG23	1.95	0.48
1:A:276:LEU:HD13	1:A:279:ILE:HG21	1.94	0.48
2:D:135:LEU:N	2:D:135:LEU:HD12	2.28	0.48
2:F:149:ILE:HG22	2:F:191:TYR:CE1	2.48	0.48
1:A:252:GLN:HA	1:A:255:PRO:HG3	1.95	0.48
2:D:72:LEU:HD23	2:D:73:THR:N	2.29	0.48
3:E:174:GLN:NE2	6:E:303:HOH:O	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:127:ILE:HD13	1:B:43:LEU:HD21	1.94	0.48
3:E:50:LEU:C	3:E:50:LEU:HD12	2.40	0.47
6:D:331:HOH:O	3:E:44:ASN:CB	2.62	0.47
1:A:49:VAL:HG11	1:B:145:PHE:CE2	2.50	0.47
3:G:180:LEU:HD12	3:G:180:LEU:C	2.40	0.47
1:B:44:VAL:O	1:B:48:LEU:HG	2.15	0.47
2:D:35:TYR:HE2	2:D:88:GLN:CB	2.28	0.47
3:E:150:PRO:HD2	3:E:204:ALA:CB	2.45	0.47
3:G:12:VAL:HG21	3:G:86:LEU:HD12	1.95	0.47
1:B:95:LEU:HD21	1:B:101:PRO:HG3	1.97	0.47
3:E:180:LEU:C	3:E:180:LEU:HD12	2.40	0.47
2:F:149:ILE:HG13	2:F:149:ILE:O	2.15	0.46
2:D:46:TRP:O	2:D:57:VAL:HG21	2.15	0.46
3:G:138:MET:HE3	3:G:185:THR:HG22	1.98	0.46
1:A:258:GLN:OE1	1:A:258:GLN:HA	2.15	0.46
1:A:54:GLU:OE2	1:B:139:THR:OG1	2.33	0.46
3:G:40:ARG:NH1	3:G:91:SER:O	2.45	0.46
3:G:18:MET:O	3:G:82:GLU:HA	2.15	0.45
3:G:50:LEU:C	3:G:50:LEU:HD12	2.41	0.45
2:D:78:GLU:OE1	6:D:302:HOH:O	2.21	0.45
2:D:162:TRP:O	3:E:170:PRO:HG2	2.16	0.45
3:E:12:VAL:HG21	3:E:86:LEU:HD12	1.98	0.45
6:D:317:HOH:O	3:E:43:LYS:HA	2.17	0.45
2:F:46:TRP:CD2	2:F:57:VAL:HG22	2.51	0.45
2:F:47:ILE:HG12	2:F:53:LEU:HD12	1.99	0.45
2:F:192:THR:HG22	2:F:207:SER:OG	2.17	0.45
1:A:224:SER:C	6:A:403:HOH:O	2.60	0.45
2:D:60:ARG:HD2	2:D:81:ASP:OD2	2.17	0.45
3:E:52:ASN:HB3	3:E:55:THR:OG1	2.18	0.44
1:A:58:GLU:OE2	1:B:112:SER:HA	2.17	0.44
2:D:117:PHE:HA	2:D:118:PRO:HD3	1.86	0.44
1:B:154:ILE:N	1:B:155:PRO:HD2	2.33	0.44
3:E:51:ILE:HA	3:E:57:TYR:O	2.18	0.44
1:A:160:LEU:HD11	1:B:36:LEU:HA	2.00	0.44
2:F:35:TYR:HE2	2:F:88:GLN:CB	2.30	0.44
1:A:154:ILE:N	1:A:155:PRO:HD2	2.33	0.43
2:D:48:TYR:O	2:D:52:LYS:HB2	2.18	0.43
1:B:38:LEU:C	1:B:38:LEU:HD23	2.43	0.43
2:D:147:TRP:N	6:D:304:HOH:O	2.46	0.43
2:F:3:VAL:HB	2:F:26:SER:HB3	1.99	0.43
2:D:89:GLN:NE2	2:D:92:ASN:H	2.15	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:51:ILE:HA	3:G:57:TYR:O	2.18	0.43
1:B:170:SER:O	1:B:174:HIS:HB2	2.18	0.43
2:F:35:TYR:CE2	2:F:88:GLN:HB2	2.48	0.43
2:D:60:ARG:NH1	2:D:81:ASP:OD1	2.52	0.43
2:F:139:TYR:CD1	2:F:140:PRO:HA	2.53	0.43
3:G:122:PRO:HB3	3:G:148:TYR:HB3	2.00	0.43
1:B:95:LEU:CD2	1:B:101:PRO:HG3	2.48	0.43
3:E:28:SER:CB	3:G:28:SER:HB2	2.43	0.43
2:F:123:GLN:HE22	2:F:130:SER:CB	2.32	0.43
2:F:24:SER:HA	2:F:68:THR:O	2.19	0.42
1:A:120:PHE:HA	1:B:47:ALA:HB2	2.01	0.42
1:B:258:GLN:HB3	1:B:259:PRO:HD3	2.00	0.42
2:D:192:THR:HG22	2:D:207:SER:OG	2.19	0.42
1:A:214:THR:HG21	1:A:229:ILE:HG12	2.02	0.42
1:A:276:LEU:CA	1:A:279:ILE:HG22	2.45	0.42
3:E:83:LEU:HB3	3:E:86:LEU:HD21	2.01	0.42
1:A:57:HIS:O	1:B:138:ARG:NH1	2.53	0.41
3:E:12:VAL:HG21	3:E:86:LEU:HD13	2.02	0.41
2:F:21:MET:HE1	2:F:85:TYR:CD1	2.55	0.41
2:F:89:GLN:CD	2:F:89:GLN:C	2.87	0.41
2:F:29:VAL:O	2:F:70:TYR:OH	2.36	0.41
2:F:48:TYR:O	2:F:52:LYS:HB2	2.21	0.41
1:A:145:PHE:CZ	1:B:49:VAL:HG11	2.56	0.41
1:B:60:GLN:HA	1:B:60:GLN:OE1	2.20	0.41
3:G:150:PRO:HD2	3:G:204:ALA:CB	2.51	0.41
1:B:35:LEU:HD12	1:B:35:LEU:HA	1.87	0.41
2:D:72:LEU:HD23	2:D:72:LEU:C	2.45	0.41
1:B:82:GLN:OE1	3:G:50:LEU:HD21	2.21	0.41
2:F:44:LYS:HB2	2:F:44:LYS:HE3	1.76	0.41
2:D:33:HIS:HD2	2:D:88:GLN:HG3	1.86	0.40
3:G:29:PHE:CD2	3:G:77:SER:HA	2.56	0.40
2:D:185:TYR:HA	2:D:191:TYR:OH	2.21	0.40
3:E:34:MET:HE1	3:E:96:CYS:HB2	2.01	0.40
3:E:51:ILE:HD13	3:E:72:VAL:HG13	2.02	0.40
2:F:191:TYR:HB2	2:F:208:PHE:CE2	2.56	0.40
1:B:184:LEU:HG	1:B:193:VAL:HG11	2.02	0.40
3:G:51:ILE:HD13	3:G:72:VAL:HG13	2.04	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)
3:E:194:GLU:OE2	5:G:301:CA:CA[2_556]	1.65	0.55

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	249/299 (83%)	243 (98%)	6 (2%)	0	100	100
1	B	247/299 (83%)	241 (98%)	6 (2%)	0	100	100
2	D	209/211 (99%)	197 (94%)	12 (6%)	0	100	100
2	F	209/211 (99%)	202 (97%)	7 (3%)	0	100	100
3	E	207/217 (95%)	198 (96%)	9 (4%)	0	100	100
3	G	206/217 (95%)	196 (95%)	10 (5%)	0	100	100
All	All	1327/1454 (91%)	1277 (96%)	50 (4%)	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	205/243 (84%)	204 (100%)	1 (0%)	81	89
1	B	205/243 (84%)	203 (99%)	2 (1%)	68	83
2	D	184/184 (100%)	179 (97%)	5 (3%)	39	70
2	F	184/184 (100%)	182 (99%)	2 (1%)	65	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	E	187/190 (98%)	182 (97%)	5 (3%)	39	70
3	G	186/190 (98%)	182 (98%)	4 (2%)	45	73
All	All	1151/1234 (93%)	1132 (98%)	19 (2%)	53	77

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	232	VAL
1	B	88	ILE
1	B	232	VAL
2	D	5	THR
2	D	88	GLN
2	D	202	SER
2	D	204	ILE
2	D	211	ASN
3	E	44	ASN
3	E	143	CYS
3	E	151	GLU
3	E	154	THR
3	E	198	CYS
2	F	21	MET
2	F	44	LYS
3	G	18	MET
3	G	143	CYS
3	G	198	CYS
3	G	211	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	GLN
1	A	76	HIS
1	B	57	HIS
1	B	76	HIS
2	D	88	GLN
2	D	144	ASN
2	D	189	ASN
3	E	136	ASN
3	E	199	ASN
2	F	123	GLN

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Mol	Chain	Res	Type
2	F	144	ASN
2	F	189	ASN
3	G	174	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 9 ligands modelled in this entry, 9 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	253/299 (84%)	1.06	53 (20%) 2 2	66, 133, 202, 240	0
1	B	251/299 (83%)	0.46	14 (5%) 30 18	65, 133, 199, 230	0
2	D	211/211 (100%)	0.13	15 (7%) 22 13	59, 90, 119, 137	0
2	F	211/211 (100%)	0.09	10 (4%) 36 22	65, 94, 139, 163	0
3	E	211/217 (97%)	-0.01	12 (5%) 29 17	60, 83, 112, 160	0
3	G	210/217 (96%)	0.05	15 (7%) 22 13	60, 87, 125, 174	0
All	All	1347/1454 (92%)	0.32	119 (8%) 15 10	59, 97, 183, 240	0

All (119) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	269	LEU	11.6
1	A	161	LEU	9.9
2	F	201	THR	9.6
1	A	270	ALA	8.2
1	B	148	PHE	8.0
2	F	1	GLN	7.7
2	F	202	SER	6.7
3	G	136	ASN	6.5
1	A	268	GLY	6.2
1	B	75	ALA	5.8
1	A	265	ILE	5.7
1	B	152	VAL	5.7
1	B	116	LEU	5.4
1	A	264	TRP	5.4
1	A	273	ALA	5.3
1	A	236	LEU	5.0
2	D	40	GLY	4.9
1	A	256	ALA	4.9
3	G	151	GLU	4.9

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Mol	Chain	Res	Type	RSRZ
2	F	92	ASN	4.8
3	E	159	SER	4.7
2	D	187	ARG	4.6
1	A	151	LEU	4.5
3	E	41	HIS	4.4
2	F	93	SER	4.3
1	A	103	THR	4.2
1	A	272	PHE	4.2
1	A	165	GLY	4.1
2	D	122	GLU	4.1
2	F	203	PRO	4.0
1	A	179	ILE	3.9
1	A	247	GLY	3.9
1	B	151	LEU	3.8
2	D	150	ASP	3.6
1	B	159	ILE	3.6
2	D	39	SER	3.6
1	A	266	LEU	3.6
1	A	280	GLY	3.5
1	A	136	ALA	3.5
1	A	286	VAL	3.5
1	A	159	ILE	3.4
1	B	34	ALA	3.4
1	A	157	PHE	3.4
3	G	178	TYR	3.4
1	A	260	LEU	3.3
1	A	162	ALA	3.2
1	A	135	VAL	3.2
1	A	133	GLY	3.2
3	G	189	SER	3.2
1	A	175	GLY	3.2
3	E	123	SER	3.2
1	A	88	ILE	3.2
3	E	145	VAL	3.2
1	A	283	LEU	3.1
1	A	55	GLN	3.1
1	A	163	GLY	3.1
3	E	160	GLY	3.1
3	G	137	SER	3.0
1	A	111	HIS	3.0
1	A	284	ARG	3.0
2	D	105	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	257	TYR	3.0
1	A	281	ASN	3.0
1	A	259	PRO	3.0
1	A	144	LEU	2.9
2	D	27	SER	2.9
1	A	278	THR	2.9
3	G	173	LEU	2.9
1	A	68	VAL	2.8
3	G	41	HIS	2.8
1	A	110	SER	2.8
1	A	92	ALA	2.8
2	D	211	ASN	2.8
3	G	62	GLN	2.8
2	D	41	THR	2.8
1	A	91	VAL	2.7
1	B	251	ARG	2.7
2	F	200	SER	2.7
1	B	272	PHE	2.7
3	E	26	GLY	2.6
3	G	149	PHE	2.6
3	G	204	ALA	2.6
2	D	125	THR	2.6
3	G	188	SER	2.5
1	B	136	ALA	2.5
2	F	160	ASN	2.5
1	B	181	ALA	2.5
1	A	237	THR	2.5
3	E	125	TYR	2.4
3	G	119	THR	2.4
2	F	145	VAL	2.4
1	A	95	LEU	2.3
1	B	242	GLY	2.3
2	D	1	GLN	2.3
2	D	126	SER	2.3
1	A	248	ALA	2.2
3	E	54	ASN	2.2
1	A	164	VAL	2.2
1	A	282	TRP	2.2
1	A	28	ARG	2.1
3	E	129	PRO	2.1
3	G	195	THR	2.1
2	D	87	CYS	2.1

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Mol	Chain	Res	Type	RSRZ
3	E	167	HIS	2.1
1	A	250	PRO	2.1
1	A	279	ILE	2.1
3	G	138	MET	2.1
2	D	98	GLY	2.1
2	F	196	THR	2.1
3	E	124	VAL	2.1
3	E	155	VAL	2.1
1	A	94	ALA	2.1
1	A	178	HIS	2.0
1	A	285	VAL	2.0
1	B	77	PRO	2.0
3	G	147	GLY	2.0
1	A	93	ASP	2.0
1	B	233	ILE	2.0
2	D	188	HIS	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.

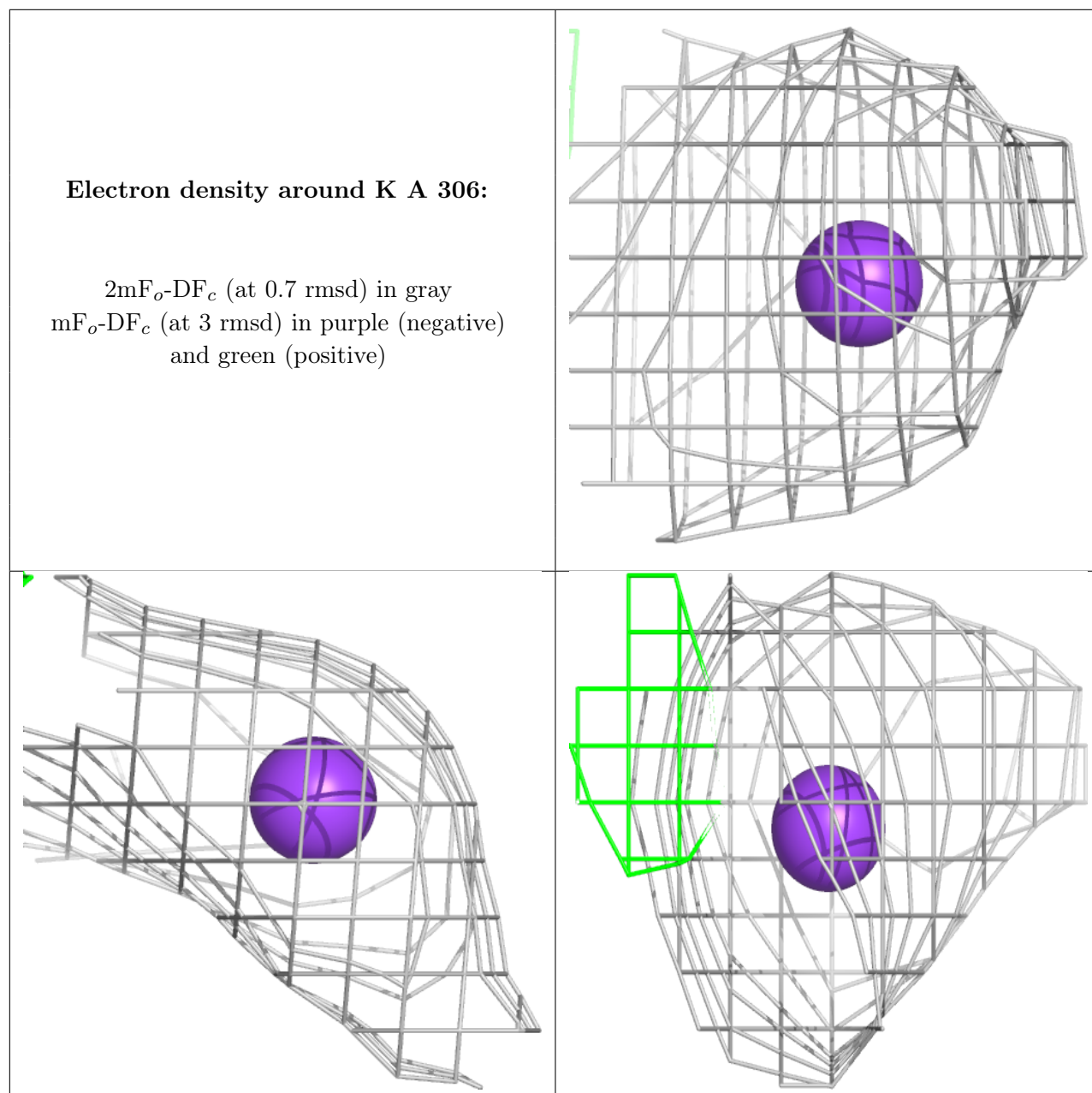
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	K	A	306	1/1	0.77	0.10	113,113,113,113	0
4	K	A	303	1/1	0.93	0.17	99,99,99,99	0
4	K	A	301	1/1	0.96	0.11	103,103,103,103	0
5	CA	G	301	1/1	0.96	0.07	100,100,100,100	0
5	CA	A	305	1/1	0.97	0.04	113,113,113,113	0
5	CA	A	304	1/1	0.98	0.04	99,99,99,99	0
4	K	A	302	1/1	0.99	0.02	111,111,111,111	0

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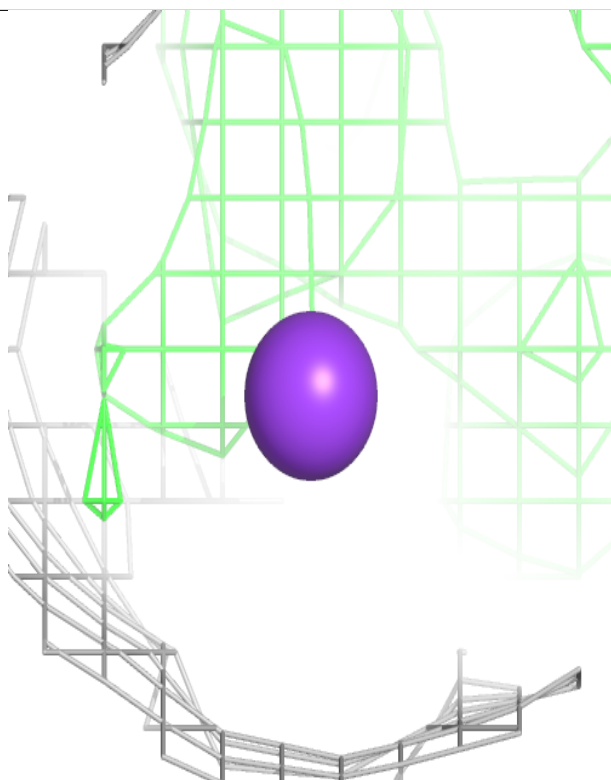
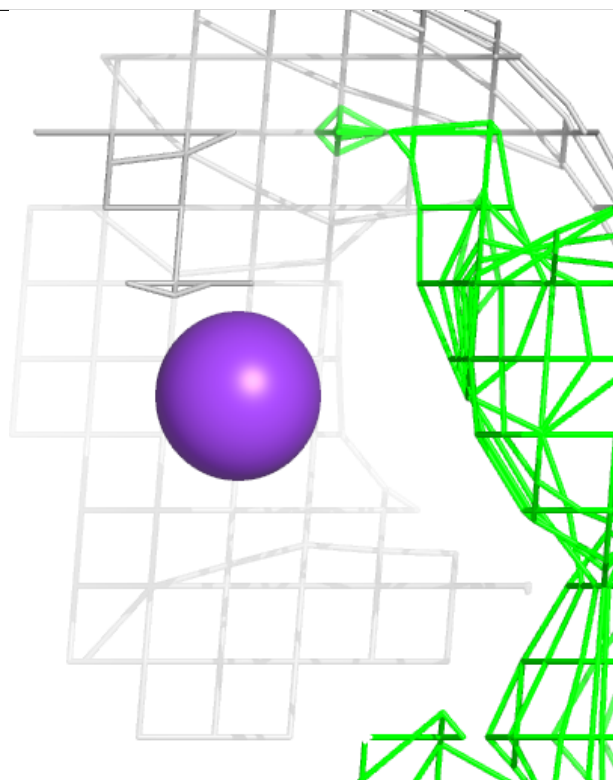
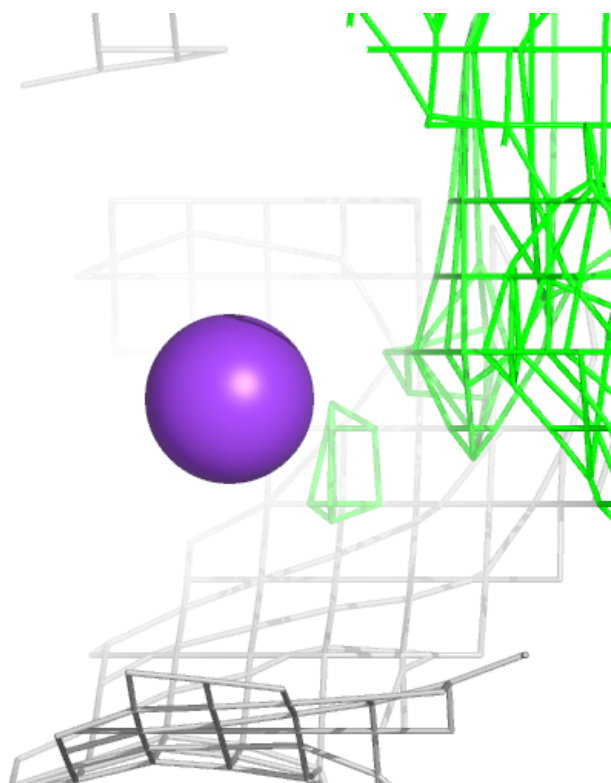
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	K	B	301	1/1	0.99	0.02	92,92,92,92	0
4	K	B	302	1/1	0.99	0.04	103,103,103,103	0

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.



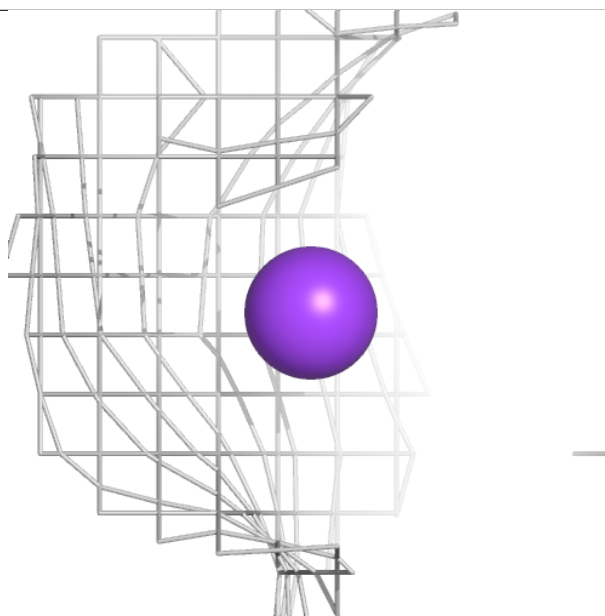
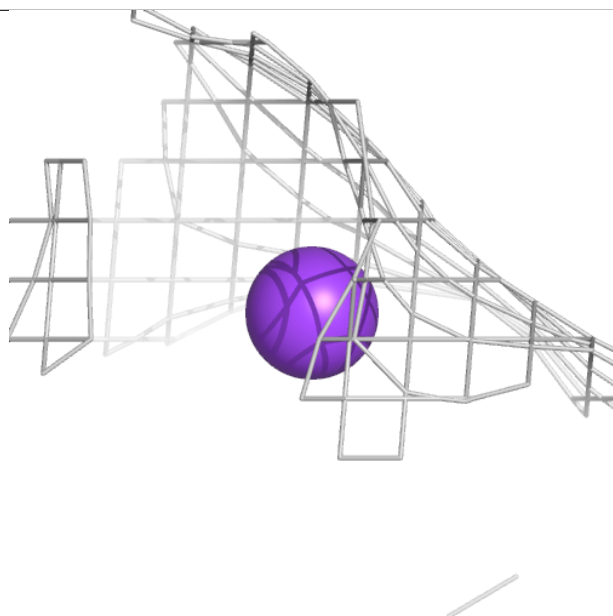
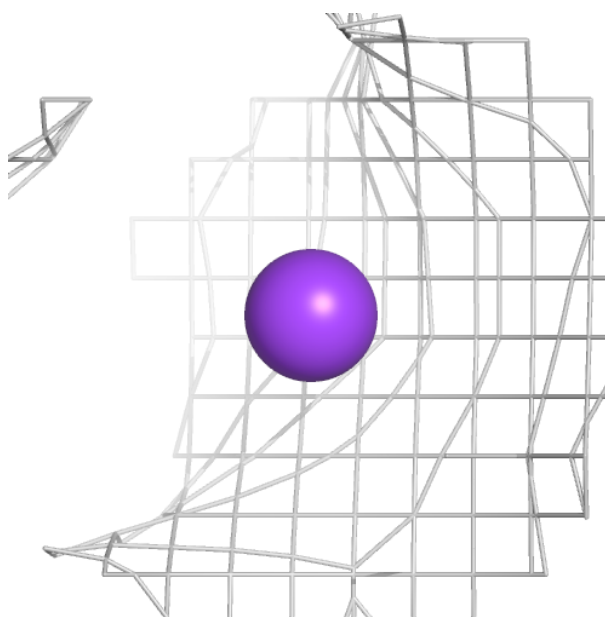
Electron density around K A 303:

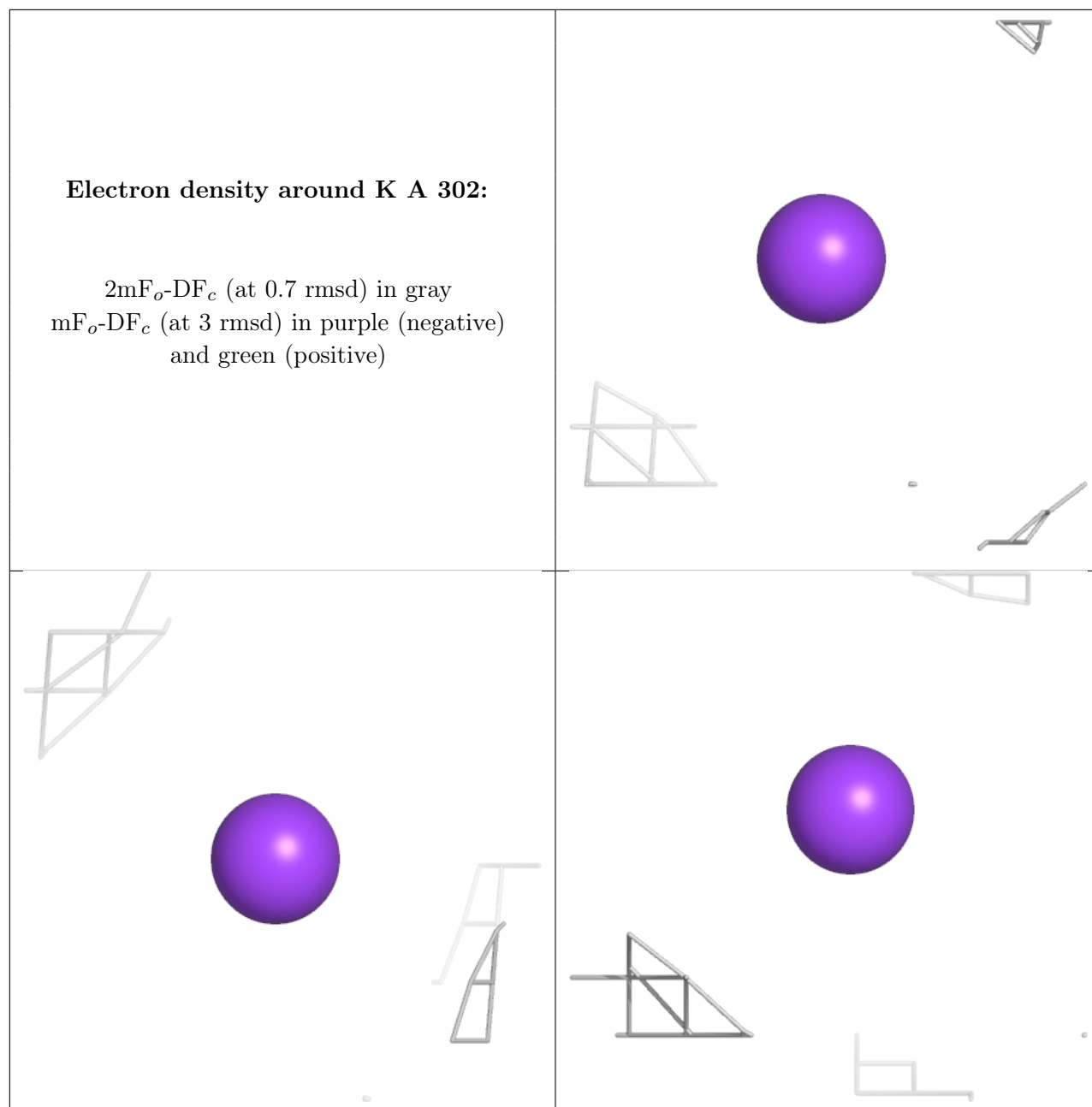
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around K A 301:

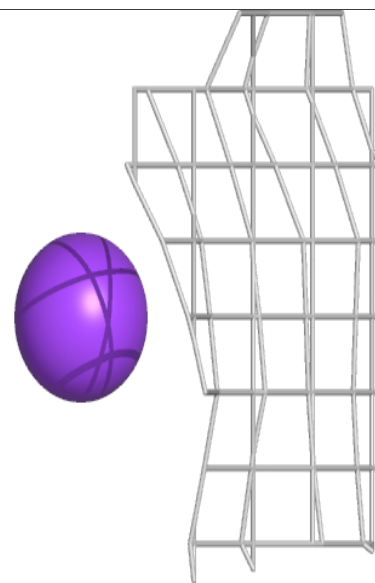
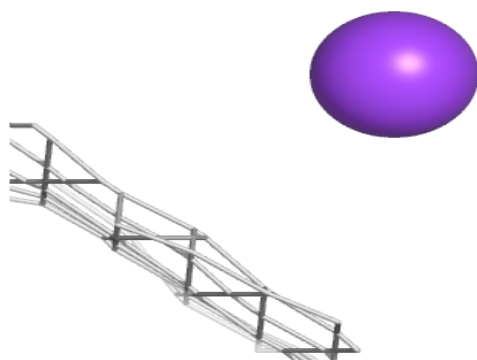
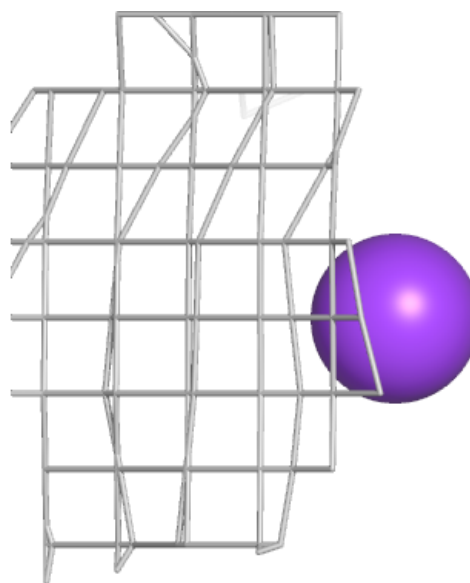
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

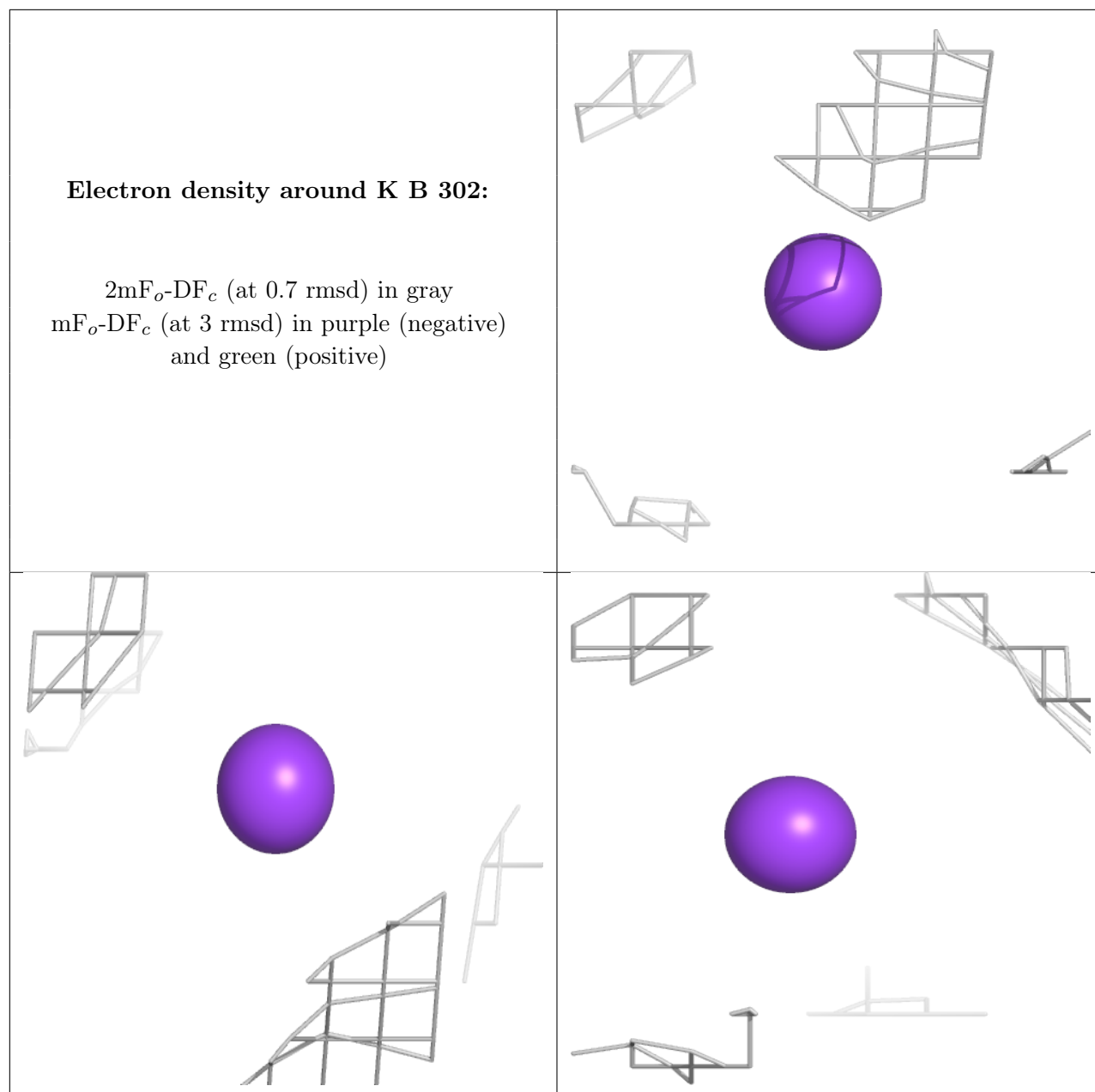




Electron density around K B 301:

$2mF_o-DF_c$ (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.