



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 02:49 AM UTC

PDB ID : 8TYS / pdb_00008tys
Title : Adaptive mechanism of collagen IV scaffold assembly in Drosophila: crystal structure of tissue-extracted NC1 hexamer
Authors : Boudko, S.P.
Deposited on : 2023-08-25
Resolution : 2.90 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

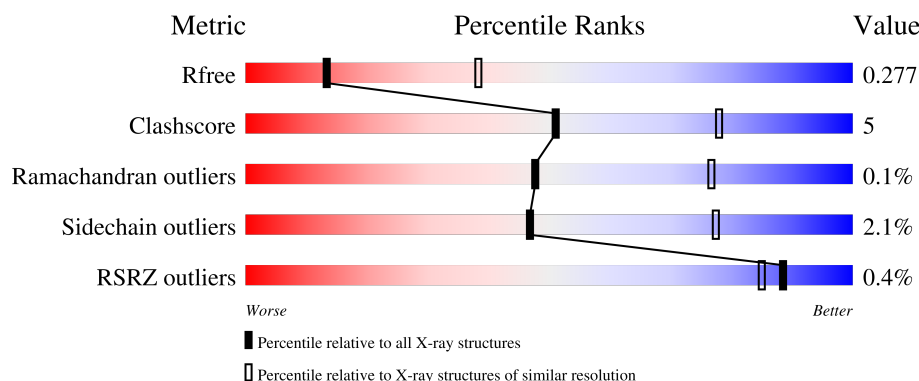
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

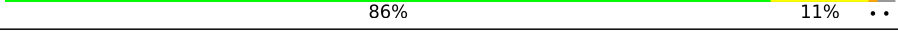
The reported resolution of this entry is 2.90 Å.

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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	230	 80% 17% .
1	C	230	 84% 13% ..
1	D	230	 82% 15% ..
1	F	230	 86% 11% ..
2	B	230	 84% 13% ..

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Mol	Chain	Length	Quality of chain
2	E	230	 87% 11% •

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10472 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 Collagen alpha-1(IV) chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	223	Total	C	N	O	S	0	0	0
			1719	1071	300	330	18			
1	C	226	Total	C	N	O	S	0	0	0
			1739	1087	301	333	18			
1	D	226	Total	C	N	O	S	0	0	0
			1740	1084	303	335	18			
1	F	226	Total	C	N	O	S	0	0	0
			1746	1090	303	335	18			

- Molecule 2 is a protein called Collagen IV, chain Viking.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	226	Total	C	N	O	S	0	0	0
			1763	1096	311	333	23			
2	E	225	Total	C	N	O	S	0	0	0
			1759	1094	310	332	23			

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		
3	C	1	Total	Cl	0	0
			1	1		
3	D	1	Total	Cl	0	0
			1	1		
3	F	1	Total	Cl	0	0
			1	1		

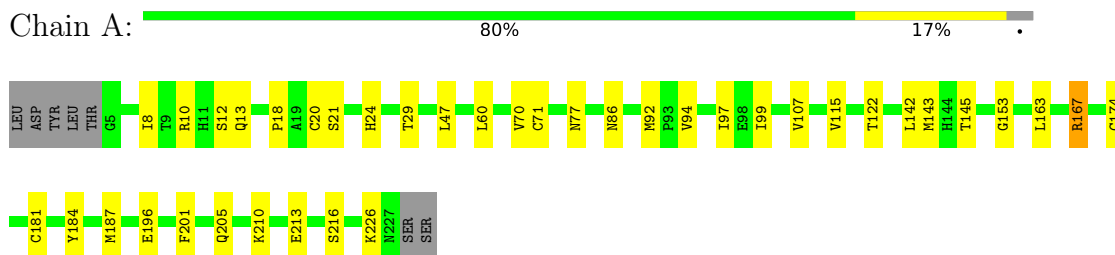
- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	1	Total 1	Ca 1	0	0
4	F	1	Total 1	Ca 1	0	0

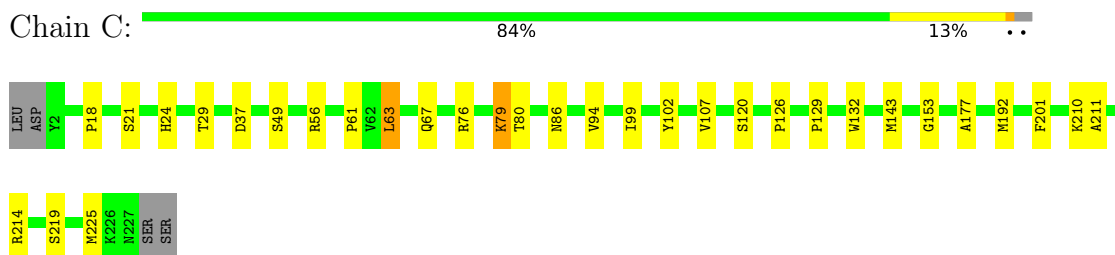
3 Residue-property plots [i](#)

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.

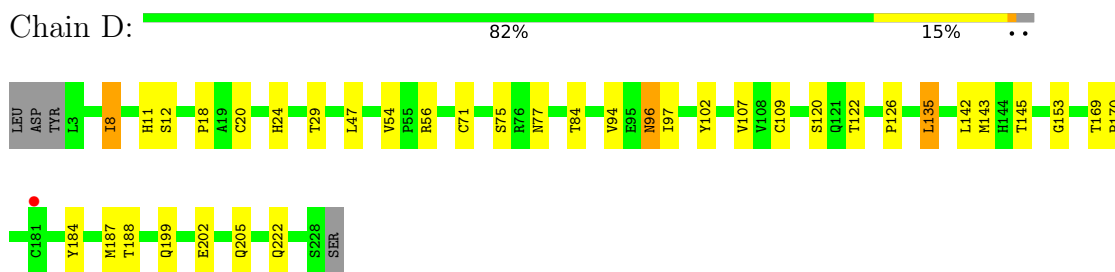
- Molecule 1: Collagen alpha-1(IV) chain



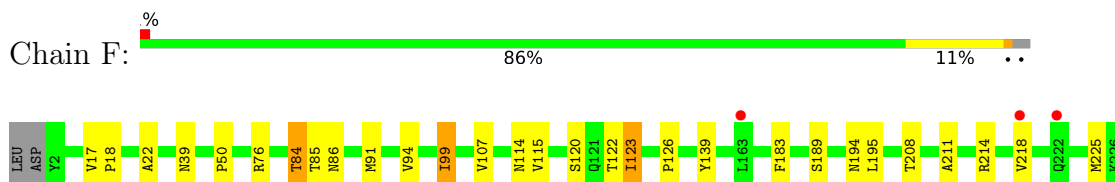
- Molecule 1: Collagen alpha-1(IV) chain



- Molecule 1: Collagen alpha-1(IV) chain

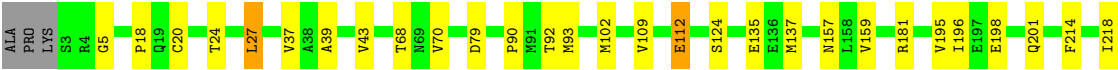
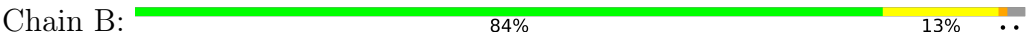


- Molecule 1: Collagen alpha-1(IV) chain

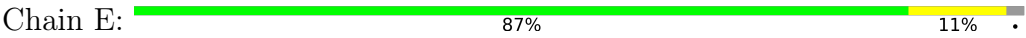




• Molecule 2: Collagen IV, chain Viking



• Molecule 2: Collagen IV, chain Viking



4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	145.21Å 145.21Å 106.49Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.63 – 2.90 40.63 – 2.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (40.63-2.90) 99.9 (40.63-2.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.54 (at 2.90Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.241 , 0.277 0.241 , 0.277	Depositor DCC
R_{free} test set	1335 reflections (4.70%)	wwPDB-VP
Wilson B-factor (Å ²)	76.6	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 27.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.045 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	10472	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.23% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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	0.08	0/1764	0.27	0/2402
1	C	0.08	0/1785	0.29	0/2432
1	D	0.09	0/1785	0.31	1/2431 (0.0%)
1	F	0.09	0/1792	0.29	0/2441
2	B	0.08	0/1805	0.28	0/2448
2	E	0.08	0/1801	0.28	0/2443
All	All	0.08	0/10732	0.29	1/14597 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	96	ASN	CB-CA-C	-5.32	110.00	117.23

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	1719	0	1611	32	0
1	C	1739	0	1628	20	0
1	D	1740	0	1634	25	0
1	F	1746	0	1638	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1763	0	1675	21	0
2	E	1759	0	1672	16	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	F	1	0	0	0	0
4	C	1	0	0	0	0
4	F	1	0	0	0	0
All	All	10472	0	9858	106	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 5.

All (106) 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:D:199:GLN:HB2	1:D:202:GLU:HG3	1.65	0.77
1:F:94:VAL:HG23	1:F:99:ILE:HG22	1.72	0.72
2:B:137:MET:HE3	2:B:225:ARG:HD2	1.72	0.71
2:B:93:MET:SD	2:E:211:LYS:NZ	2.67	0.67
2:B:198:GLU:OE1	2:B:201:GLN:NE2	2.29	0.65
2:E:24:THR:HG22	2:E:113:THR:HB	1.79	0.65
2:B:124:SER:HA	2:B:195:VAL:HG13	1.83	0.61
2:B:20:CYS:HB3	2:B:24:THR:HG23	1.83	0.61
1:A:13:GLN:O	1:A:167:ARG:NH2	2.35	0.59
2:E:37:VAL:HB	2:E:79:ASP:HB2	1.84	0.59
2:B:27:LEU:HD11	2:B:112:GLU:HB3	1.85	0.58
1:D:56:ARG:NH2	1:F:195:LEU:O	2.35	0.58
1:C:143:MET:HA	1:C:153:GLY:HA2	1.87	0.57
1:A:122:THR:HG23	1:A:196:GLU:HB3	1.86	0.57
1:D:29:THR:HG22	1:D:107:VAL:HG23	1.88	0.56
2:B:137:MET:HB2	2:B:223:VAL:HG23	1.88	0.56
1:A:18:PRO:HG2	1:A:107:VAL:HG12	1.88	0.55
1:A:70:VAL:HG22	1:C:210:LYS:HG2	1.89	0.54
2:B:181:ARG:NH2	1:F:76:ARG:O	2.35	0.54
2:B:135:GLU:OE2	2:B:227:ARG:NH2	2.41	0.53
1:A:77:ASN:HB2	1:D:77:ASN:HB2	1.91	0.53
1:F:115:VAL:HG22	1:F:225:MET:HB2	1.91	0.52
2:E:90:PRO:HB2	2:E:92:THR:HG22	1.91	0.52
1:A:20:CYS:HB3	1:A:24:HIS:HB2	1.90	0.52
1:A:184:TYR:HD2	1:A:187:MET:HE3	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:12:SER:HB3	1:A:18:PRO:HD3	1.93	0.51
1:D:120:SER:OG	1:D:122:THR:OG1	2.24	0.51
1:A:8:ILE:HG12	1:A:115:VAL:HG11	1.93	0.51
1:D:184:TYR:HD2	1:D:187:MET:HE3	1.76	0.51
1:D:20:CYS:HB3	1:D:24:HIS:HB2	1.94	0.50
1:A:29:THR:HG22	1:A:107:VAL:HG23	1.92	0.50
2:E:124:SER:HA	2:E:195:VAL:HG13	1.94	0.49
1:F:120:SER:HB3	1:F:126:PRO:HB3	1.94	0.49
1:A:97:ILE:HD13	1:C:201:PHE:HB2	1.94	0.49
2:B:37:VAL:HB	2:B:79:ASP:HB2	1.93	0.49
1:D:12:SER:HB3	1:D:18:PRO:HD3	1.96	0.48
2:B:18:PRO:HG2	2:B:109:VAL:HG22	1.96	0.48
1:C:21:SER:HB3	1:C:24:HIS:CE1	2.49	0.48
1:A:210:LYS:NZ	1:F:91:MET:HB3	2.29	0.47
1:C:94:VAL:HG23	1:C:99:ILE:HG12	1.96	0.47
1:A:153:GLY:HA3	2:B:43:VAL:HG11	1.96	0.47
1:C:120:SER:HB3	1:C:126:PRO:HB3	1.96	0.47
1:D:126:PRO:O	1:D:222:GLN:NE2	2.46	0.46
1:A:174:CYS:HA	1:A:181:CYS:HA	1.98	0.46
1:D:199:GLN:HB3	2:E:99:ARG:HH22	1.81	0.46
1:A:86:ASN:HB3	1:A:167:ARG:NH1	2.30	0.46
1:A:71:CYS:SG	1:C:214:ARG:HD2	2.55	0.46
1:F:211:ALA:HA	1:F:214:ARG:NH1	2.30	0.46
1:A:210:LYS:HZ1	1:F:91:MET:HB3	1.82	0.46
1:F:39:ASN:OD1	1:F:76:ARG:NH1	2.46	0.46
1:A:94:VAL:HG22	1:A:99:ILE:HG22	1.98	0.45
1:D:96:ASN:HB3	1:D:97:ILE:HD12	1.98	0.45
1:A:13:GLN:HB3	1:A:167:ARG:HH21	1.81	0.45
1:A:226:LYS:NZ	2:B:112:GLU:OE2	2.42	0.45
1:A:210:LYS:HG2	2:B:70:VAL:HG12	1.98	0.45
1:C:129:PRO:HB2	1:C:132:TRP:CD1	2.52	0.45
2:E:139:THR:HG22	2:E:222:THR:HG23	1.98	0.45
1:A:10:ARG:HH22	1:A:21:SER:HG	1.62	0.45
1:A:13:GLN:HB3	1:A:167:ARG:NH2	2.32	0.44
1:F:84:THR:HG22	1:F:85:THR:H	1.82	0.44
1:A:184:TYR:OH	1:D:75:SER:O	2.23	0.44
2:E:159:VAL:HG21	1:F:50:PRO:HG2	2.00	0.44
1:C:61:PRO:HD2	1:C:80:THR:HG21	2.00	0.44
1:D:142:LEU:HG	1:D:143:MET:HG3	1.99	0.44
2:E:116:ARG:NH2	1:F:114:ASN:OD1	2.51	0.44
1:F:122:THR:HA	1:F:194:ASN:OD1	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:213:GLU:O	1:A:216:SER:OG	2.35	0.44
1:D:84:THR:HG22	1:D:170:PRO:C	2.43	0.43
1:D:153:GLY:HA3	2:E:43:VAL:HG11	2.00	0.43
1:A:47:LEU:HD23	1:A:163:LEU:HD21	1.99	0.43
2:B:90:PRO:HB2	2:B:92:THR:HG22	1.99	0.43
1:D:205:GLN:O	1:D:205:GLN:HG2	2.18	0.43
1:D:145:THR:OG1	1:D:188:THR:OG1	2.36	0.43
2:B:196:ILE:O	1:C:56:ARG:HD3	2.19	0.43
1:D:135:LEU:HD23	1:D:135:LEU:HA	1.87	0.43
1:D:8:ILE:HG23	1:D:109:CYS:HB2	2.00	0.42
2:E:142:SER:HB2	2:E:193:LEU:HB2	2.01	0.42
1:D:18:PRO:HG2	1:D:107:VAL:HG12	2.01	0.42
1:F:84:THR:HG21	1:F:183:PHE:HZ	1.84	0.42
1:C:37:ASP:CG	1:C:79:LYS:HE2	2.44	0.42
1:D:11:HIS:NE2	1:D:47:LEU:O	2.51	0.42
1:A:145:THR:HG21	2:B:39:ALA:HB3	2.02	0.42
2:B:218:ILE:HD13	1:C:63:LEU:HD21	2.01	0.42
1:C:76:ARG:HA	2:E:177:HIS:CE1	2.55	0.42
1:F:139:TYR:HB3	1:F:218:VAL:HG11	2.01	0.42
1:C:24:HIS:CE1	1:C:225:MET:HE1	2.54	0.42
1:C:192:MET:HB2	1:C:219:SER:HB3	2.02	0.42
1:D:145:THR:HG21	2:E:39:ALA:HB3	2.02	0.42
1:D:120:SER:HG	1:D:122:THR:HG1	1.62	0.41
2:B:157:ASN:OD1	2:B:159:VAL:HG12	2.19	0.41
1:C:177:ALA:HB3	2:E:179:HIS:CE1	2.55	0.41
1:C:37:ASP:HB3	1:C:79:LYS:HG2	2.01	0.41
1:A:205:GLN:OE1	1:A:205:GLN:N	2.38	0.41
1:A:142:LEU:HG	1:A:143:MET:HG3	2.02	0.41
1:F:123:ILE:HG23	1:F:194:ASN:ND2	2.35	0.41
2:E:93:MET:HE2	2:E:93:MET:HB3	1.96	0.41
1:A:92:MET:HG2	1:F:208:THR:OG1	2.21	0.41
1:C:29:THR:HG22	1:C:107:VAL:HG23	2.03	0.41
1:D:71:CYS:SG	1:F:214:ARG:HD2	2.61	0.41
1:A:226:LYS:HD2	2:B:5:GLY:HA3	2.02	0.41
1:F:18:PRO:HG2	1:F:107:VAL:HG12	2.02	0.40
1:D:94:VAL:HG11	1:D:102:TYR:HE2	1.87	0.40
1:C:18:PRO:HG2	1:C:107:VAL:HG12	2.03	0.40
2:E:95:PRO:HA	2:E:183:ASN:HB2	2.02	0.40
1:A:201:PHE:CE2	2:B:102:MET:HG2	2.57	0.40
1:C:94:VAL:HG11	1:C:102:TYR:CE2	2.56	0.40

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	221/230 (96%)	209 (95%)	12 (5%)	0	100	100
1	C	224/230 (97%)	212 (95%)	11 (5%)	1 (0%)	30	59
1	D	224/230 (97%)	210 (94%)	14 (6%)	0	100	100
1	F	224/230 (97%)	212 (95%)	11 (5%)	1 (0%)	30	59
2	B	224/230 (97%)	218 (97%)	6 (3%)	0	100	100
2	E	223/230 (97%)	219 (98%)	4 (2%)	0	100	100
All	All	1340/1380 (97%)	1280 (96%)	58 (4%)	2 (0%)	48	77

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	211	ALA
1	F	22	ALA

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	190/197 (96%)	188 (99%)	2 (1%)	65	88
1	C	191/197 (97%)	186 (97%)	5 (3%)	40	73
1	D	193/197 (98%)	189 (98%)	4 (2%)	47	77
1	F	193/197 (98%)	187 (97%)	6 (3%)	35	69
2	B	197/200 (98%)	193 (98%)	4 (2%)	48	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	E	197/200 (98%)	194 (98%)	3 (2%)	57 84
All	All	1161/1188 (98%)	1137 (98%)	24 (2%)	47 77

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

Mol	Chain	Res	Type
1	A	60	LEU
1	A	167	ARG
2	B	27	LEU
2	B	68	THR
2	B	112	GLU
2	B	214	PHE
1	C	49	SER
1	C	63	LEU
1	C	67	GLN
1	C	79	LYS
1	C	86	ASN
1	D	8	ILE
1	D	54	VAL
1	D	135	LEU
1	D	169	THR
2	E	68	THR
2	E	102	MET
2	E	135	GLU
1	F	17	VAL
1	F	84	THR
1	F	86	ASN
1	F	99	ILE
1	F	123	ILE
1	F	189	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	25	ASN
2	B	69	ASN
1	C	68	ASN
1	C	206	GLN
2	E	49	GLN
2	E	69	ASN
1	F	13	GLN

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Mol	Chain	Res	Type
1	F	67	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 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 [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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	223/230 (96%)	0.14	0	100	100	51, 80, 102, 120	0
1	C	226/230 (98%)	0.05	0	100	100	45, 81, 104, 118	0
1	D	226/230 (98%)	0.32	1 (0%)	88	85	54, 89, 114, 124	0
1	F	226/230 (98%)	0.35	3 (1%)	75	67	43, 82, 119, 137	0
2	B	226/230 (98%)	-0.16	0	100	100	41, 63, 95, 111	0
2	E	225/230 (97%)	-0.05	1 (0%)	88	85	47, 70, 102, 116	0
All	All	1352/1380 (97%)	0.11	5 (0%)	88	85	41, 77, 110, 137	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	218	VAL	3.5
1	D	181	CYS	2.9
1	F	163	LEU	2.2
2	E	224	CYS	2.1
1	F	222	GLN	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

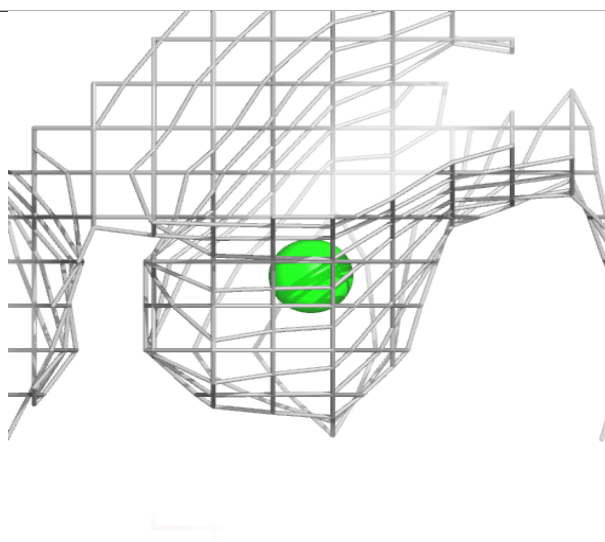
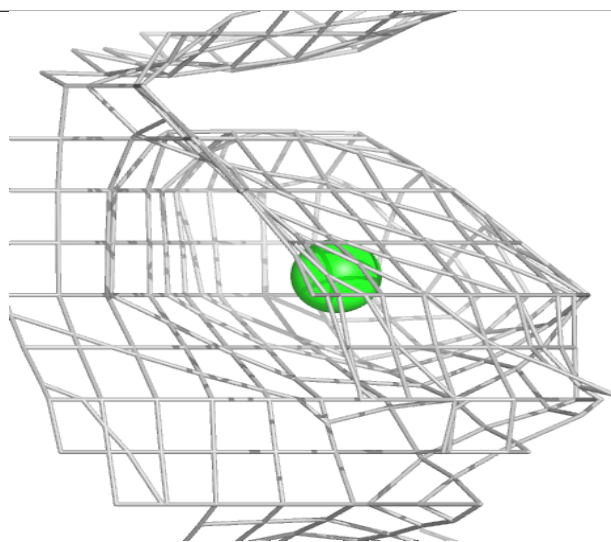
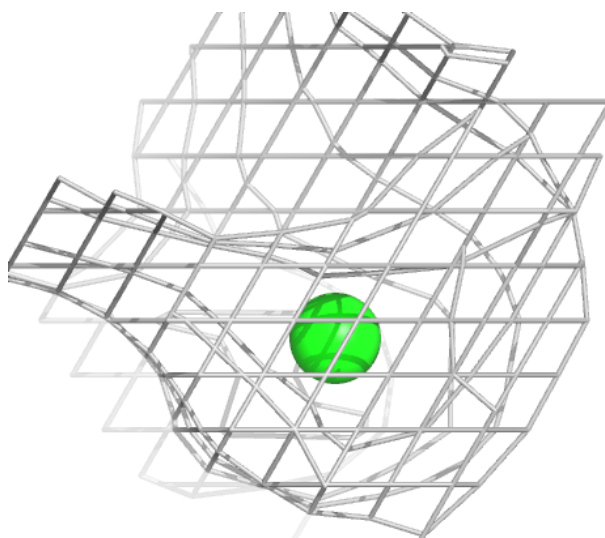
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	CL	D	301	1/1	0.83	0.09	85,85,85,85	0
3	CL	A	301	1/1	0.91	0.12	69,69,69,69	0
3	CL	C	301	1/1	0.93	0.07	57,57,57,57	0
4	CA	C	302	1/1	0.93	0.11	62,62,62,62	0
3	CL	F	301	1/1	0.94	0.07	54,54,54,54	0
4	CA	F	302	1/1	0.94	0.18	74,74,74,74	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.

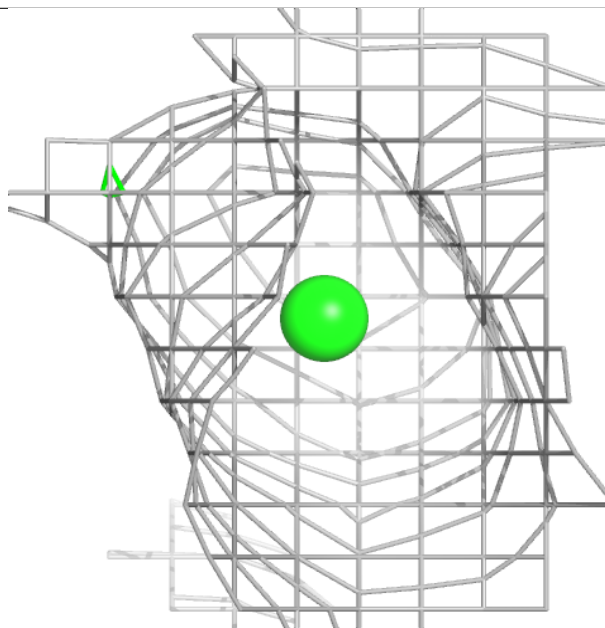
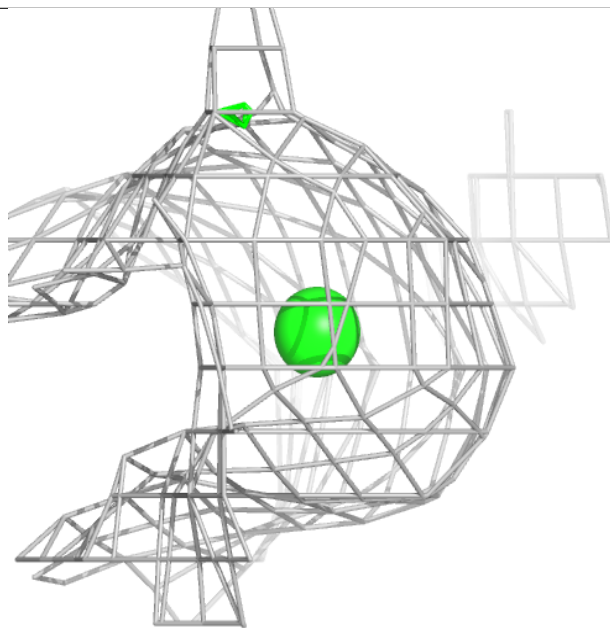
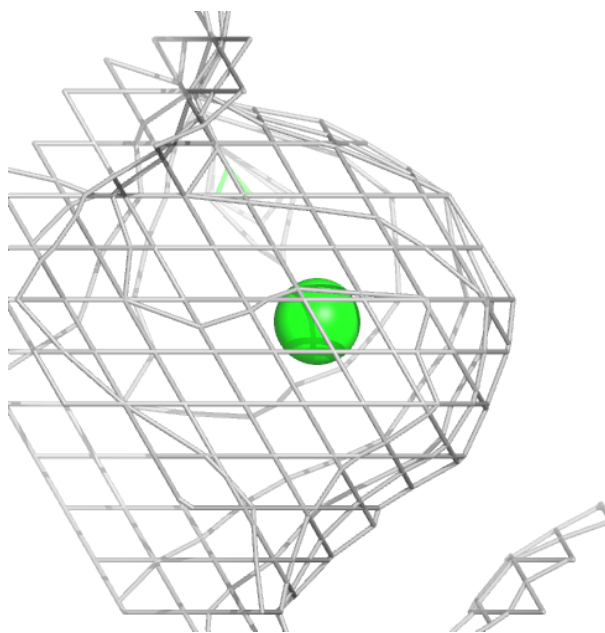
Electron density around CL D 301:

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



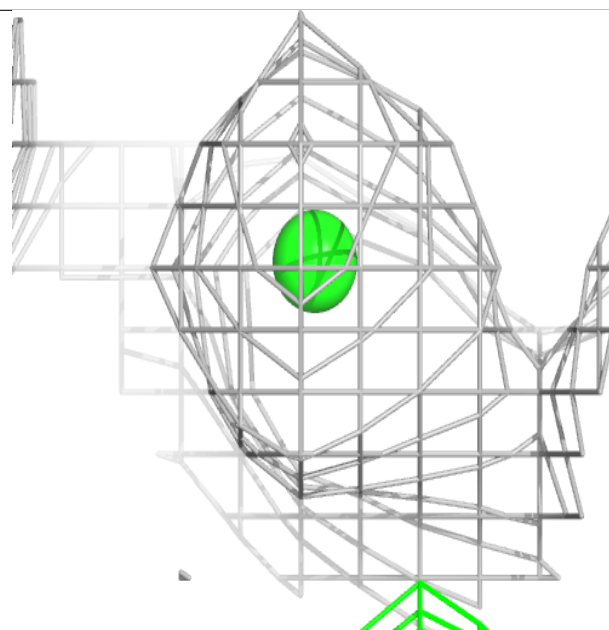
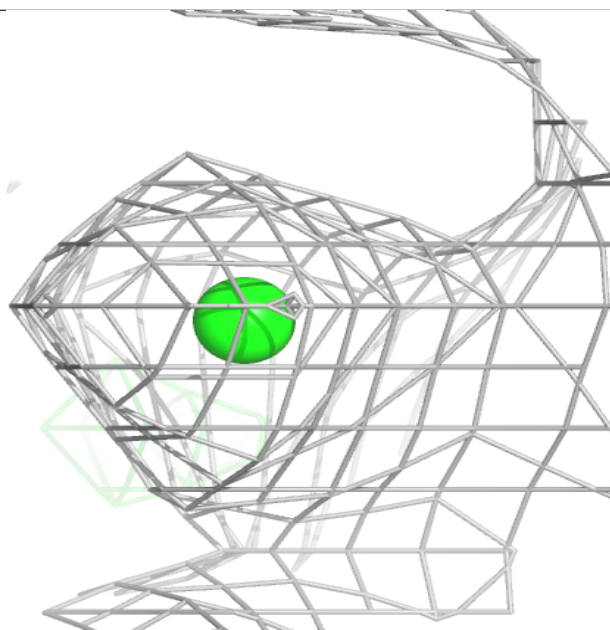
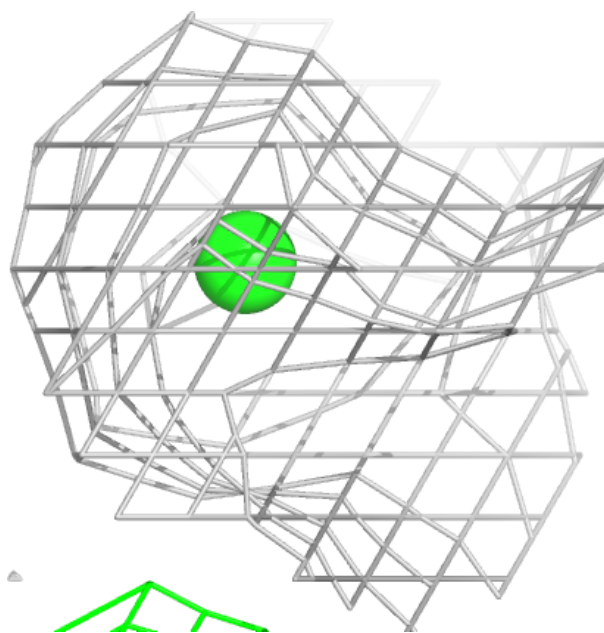
Electron density around CL A 301:

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



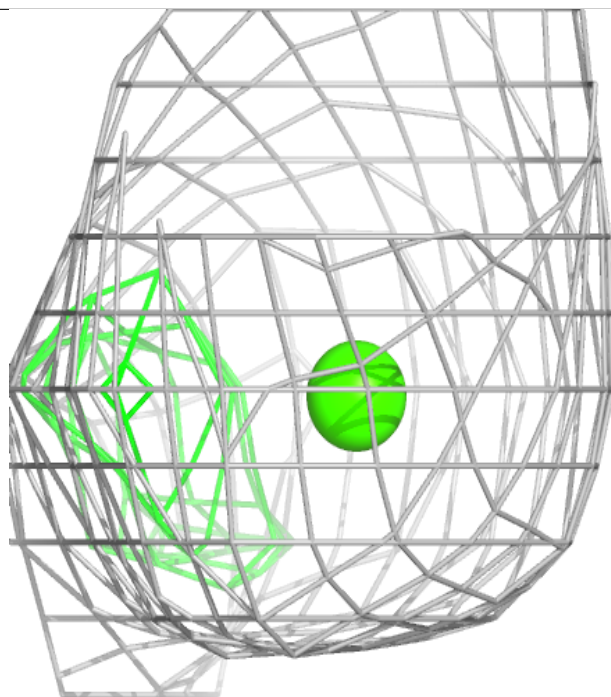
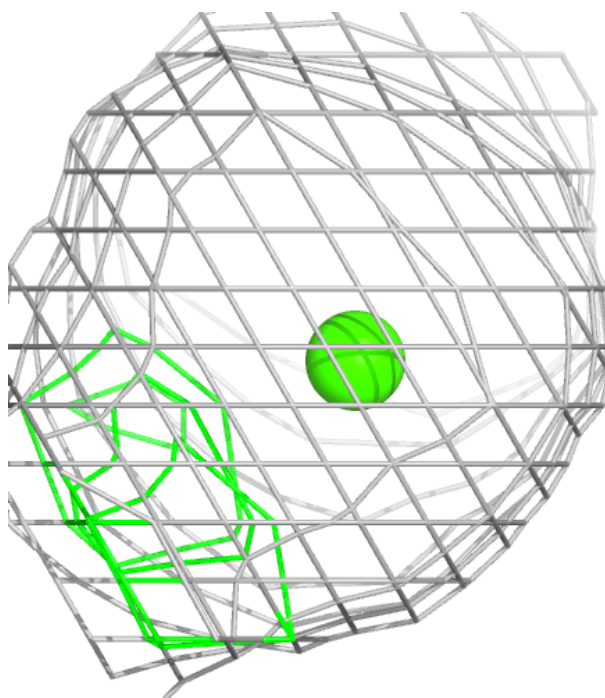
Electron density around CL C 301:

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



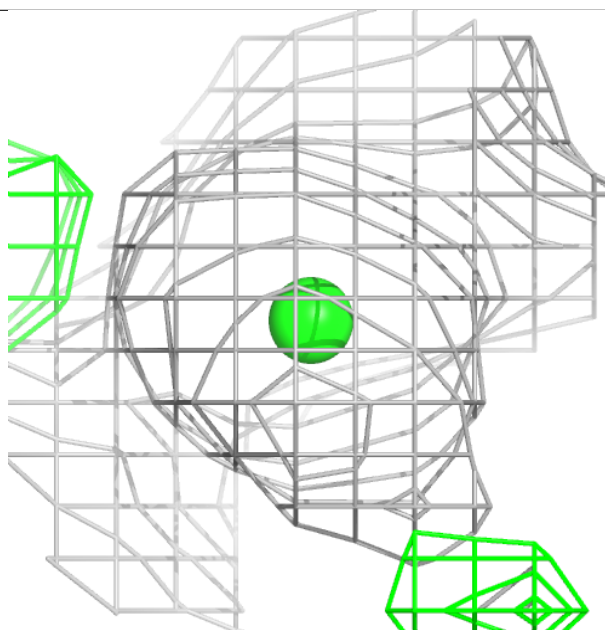
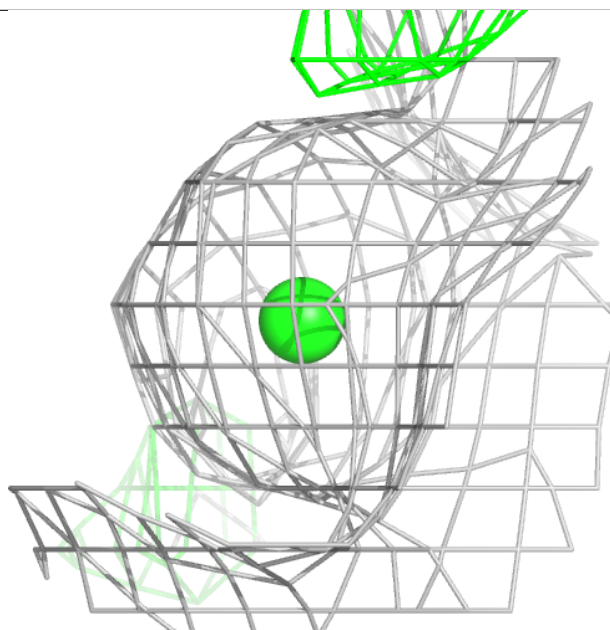
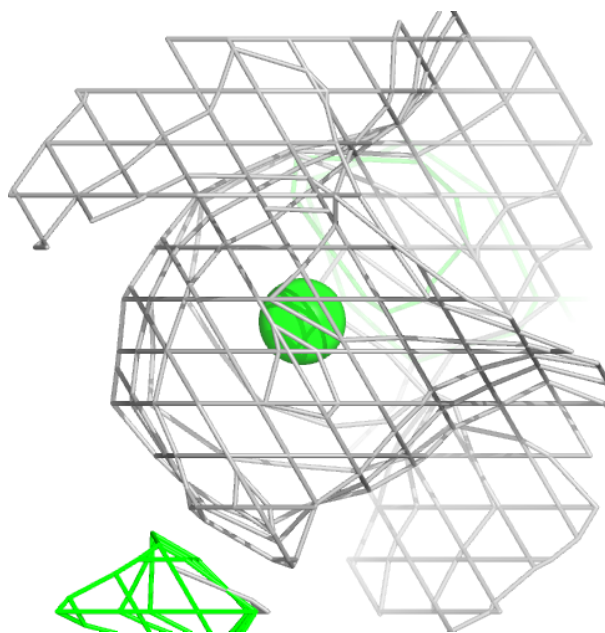
Electron density around CA C 302:

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and green (positive)



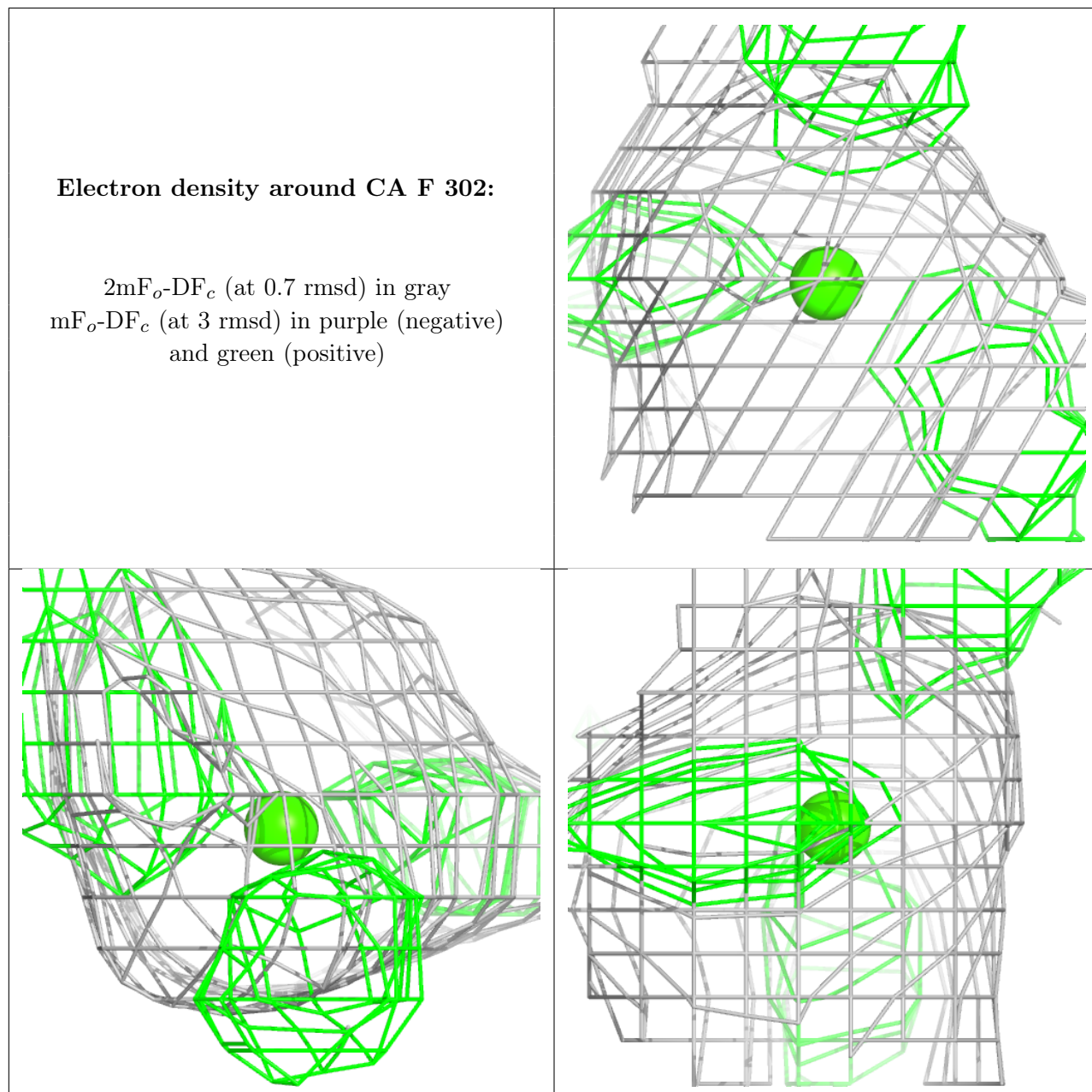
Electron density around CL F 301:

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



Electron density around CA F 302:

$2mF_o-DF_c$ (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.