



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 13, 2023 – 03:55 PM EST

PDB ID : 8TRT
Title : Structure of the EphA2 CRD bound to FabS1CE_C1, monoclinic form
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Deposited on : 2023-08-10
Resolution : 3.00 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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

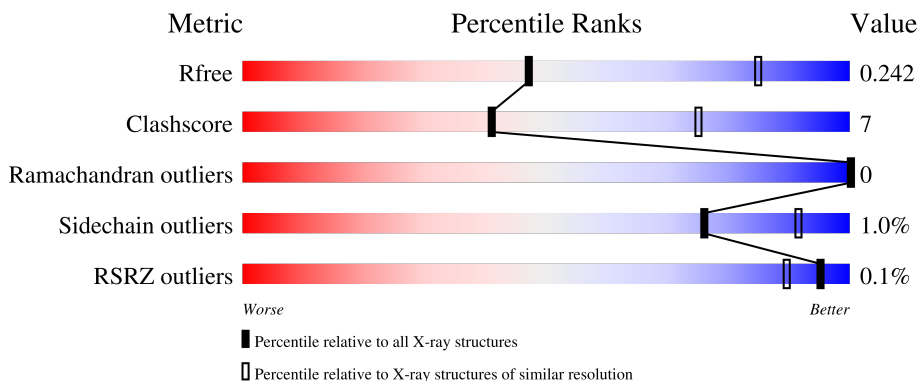
1 Overall quality at a glance

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 $\leq 5\%$. 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	222	82% 14% .
1	B	222	77% 21% .
2	C	215	83% 16%
2	G	215	80% 20%
3	D	132	81% 13% 6%

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Mol	Chain	Length	Quality of chain
3	E	132	 84% 10% 6%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 8225 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 S1CE variant of Fab C1 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	213	Total	C	N	O	S	0	0	0
			1596	1020	260	309	7			
1	B	216	Total	C	N	O	S	0	1	0
			1622	1033	263	319	7			

- Molecule 2 is a protein called S1CE variant of Fab C1 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	G	214	Total	C	N	O	S	0	0	0
			1618	1019	261	333	5			
2	C	214	Total	C	N	O	S	0	1	0
			1629	1020	268	336	5			

- Molecule 3 is a protein called Ephrin type-A receptor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	E	124	Total	C	N	O	S	0	0	0
			874	546	142	172	14			
3	D	124	Total	C	N	O	S	0	0	0
			878	552	143	169	14			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	327	LEU	-	expression tag	UNP P29317
E	328	VAL	-	expression tag	UNP P29317
E	329	PRO	-	expression tag	UNP P29317
E	330	ARG	-	expression tag	UNP P29317
D	327	LEU	-	expression tag	UNP P29317
D	328	VAL	-	expression tag	UNP P29317
D	329	PRO	-	expression tag	UNP P29317
D	330	ARG	-	expression tag	UNP P29317

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	G	2	Total Cl 2 2	0	0
4	B	1	Total Cl 1 1	0	0
4	C	1	Total Cl 1 1	0	0

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	2	Total Na 2 2	0	0

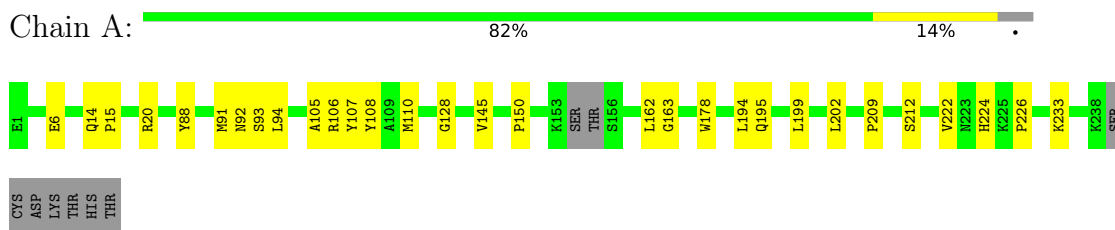
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	G	2	Total O 2 2	0	0

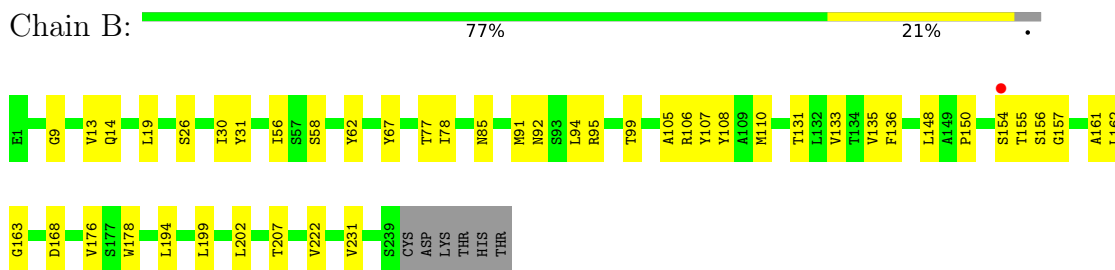
3 Residue-property plots

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.

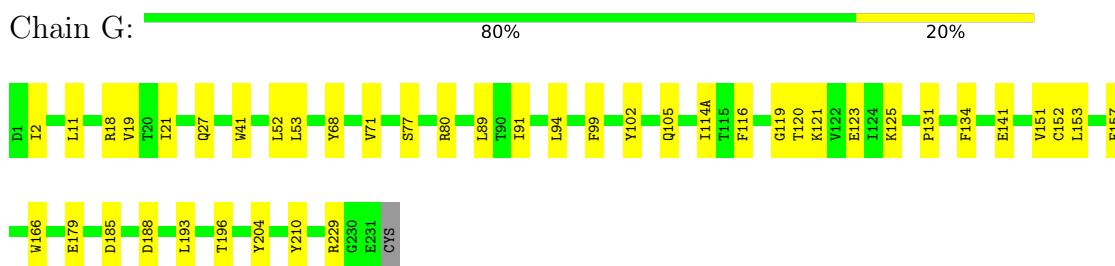
- Molecule 1: S1CE variant of Fab C1 heavy chain



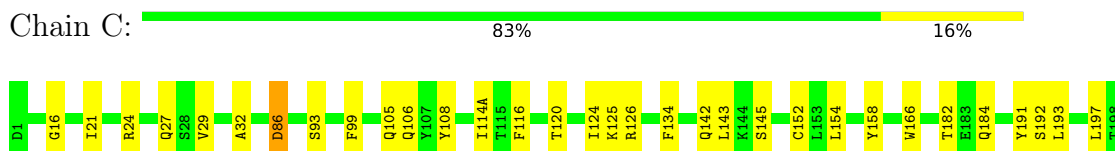
- Molecule 1: S1CE variant of Fab C1 heavy chain



- Molecule 2: S1CE variant of Fab C1 light chain



- Molecule 2: S1CE variant of Fab C1 light chain





- Molecule 3: Ephrin type-A receptor 2

Chain E: 84% 10% 6%



- Molecule 3: Ephrin type-A receptor 2

Chain D: 81% 13% 6%



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	57.71Å 182.13Å 74.38Å 90.00° 92.93° 90.00°	Depositor
Resolution (Å)	68.78 – 3.00 68.78 – 2.90	Depositor EDS
% Data completeness (in resolution range)	96.0 (68.78-3.00) 95.6 (68.78-2.90)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 2.91Å)	Xtrriage
Refinement program	PHENIX 1.19.2_4158, PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.194 , 0.244 0.192 , 0.242	Depositor DCC
R_{free} test set	1998 reflections (6.17%)	wwPDB-VP
Wilson B-factor (Å ²)	59.3	Xtrriage
Anisotropy	0.599	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 29.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	0.055 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8225	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.66% 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: NA, 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	0.51	0/1638	0.71	2/2236 (0.1%)
1	B	0.60	0/1665	0.76	1/2275 (0.0%)
2	C	0.67	0/1665	0.77	0/2268
2	G	0.56	0/1654	0.70	0/2251
3	D	0.43	0/904	0.59	0/1237
3	E	0.41	0/899	0.59	0/1229
All	All	0.56	0/8425	0.71	3/11496 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	202	LEU	CA-CB-CG	5.91	128.88	115.30
1	B	202	LEU	CA-CB-CG	5.48	127.90	115.30
1	A	194	LEU	CB-CG-CD1	-5.00	102.49	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	1596	0	1531	22	0
1	B	1622	0	1548	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	1629	0	1537	24	0
2	G	1618	0	1540	27	0
3	D	878	0	786	9	0
3	E	874	0	774	9	0
4	B	1	0	0	1	0
4	C	1	0	0	0	0
4	G	2	0	0	0	0
5	B	2	0	0	0	0
6	G	2	0	0	0	0
All	All	8225	0	7716	113	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 7.

All (113) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:13:VAL:HB	1:B:19:LEU:HD13	1.67	0.75
1:B:150:PRO:HB3	1:B:162:LEU:HB3	1.68	0.74
1:A:14:GLN:HG3	1:A:15:PRO:HD2	1.73	0.70
1:A:108:TYR:HE1	2:G:114(A):ILE:HD11	1.58	0.68
3:D:314:PHE:HB3	3:D:328:VAL:HG22	1.76	0.68
3:D:267:GLU:HB3	3:D:290:CYS:SG	2.35	0.67
3:E:293:CYS:HB3	3:E:297:THR:HG21	1.78	0.66
3:E:205:LEU:HD22	3:E:271:ASP:HB3	1.77	0.66
2:C:143:LEU:HB3	2:C:201:LYS:HE2	1.77	0.65
1:B:176:VAL:HG22	1:B:222:VAL:HG12	1.78	0.65
2:C:29:VAL:HG13	2:C:108:TYR:HB2	1.80	0.64
1:B:154:SER:HB3	1:B:161:ALA:O	1.98	0.63
1:A:20:ARG:HD3	1:A:88:TYR:HD2	1.64	0.62
2:G:179:GLU:HG2	2:G:193:LEU:HD21	1.83	0.60
3:E:293:CYS:HB3	3:E:297:THR:CG2	2.32	0.60
1:B:9:GLY:H	1:B:131:THR:HG21	1.66	0.60
1:B:56:ILE:HB	1:B:78:ILE:HG12	1.82	0.60
1:A:195:GLN:HG3	1:A:199:LEU:O	2.01	0.59
1:B:222:VAL:HG22	1:B:231:VAL:HB	1.86	0.58
1:A:105:ALA:HB1	1:A:110:MET:HB3	1.85	0.58
1:B:108:TYR:CD1	2:C:114(A):ILE:HD11	2.39	0.57
1:B:155:THR:HG22	1:B:157:GLY:H	1.69	0.57
2:G:68:TYR:O	2:G:71:VAL:HG22	2.05	0.57
1:B:156:SER:HA	4:B:301:CL:CL	2.41	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:91:MET:HB3	1:A:94:LEU:HD21	1.87	0.56
1:B:91:MET:HB3	1:B:94:LEU:HD21	1.88	0.56
1:A:92:ASN:OD1	1:A:93:SER:N	2.37	0.56
1:A:224:HIS:CD2	1:A:226:PRO:HD2	2.42	0.55
1:B:105:ALA:HB1	1:B:110:MET:HB3	1.88	0.55
1:B:161:ALA:HB2	1:B:207:THR:HG22	1.88	0.54
3:D:282:LYS:NZ	3:D:284:GLU:O	2.42	0.53
1:A:163:GLY:HA2	1:A:178:TRP:CH2	2.43	0.53
1:B:108:TYR:HD1	2:C:114(A):ILE:HD11	1.74	0.52
1:A:145:VAL:HG21	1:A:222:VAL:HG21	1.91	0.52
1:B:31:TYR:HA	1:B:58:SER:HB2	1.92	0.52
1:A:14:GLN:HG3	1:A:15:PRO:CD	2.40	0.52
1:B:95:ARG:O	1:B:135:VAL:HG11	2.11	0.51
2:C:21:ILE:HG12	2:C:120:THR:HG21	1.92	0.51
1:B:9:GLY:HA3	1:B:131:THR:HG22	1.92	0.51
1:B:222:VAL:CG2	1:B:231:VAL:HB	2.41	0.51
2:G:94:LEU:HD21	2:G:99:PHE:CZ	2.46	0.50
2:G:2:ILE:HG23	2:G:27:GLN:HG3	1.93	0.50
3:E:227:ALA:HB2	3:E:244:ARG:NH2	2.26	0.50
2:C:105:GLN:HB2	2:C:116:PHE:CE1	2.46	0.50
2:C:16:GLY:HA2	2:C:93:SER:HB2	1.92	0.50
3:E:257:ILE:HG13	3:E:257:ILE:O	2.11	0.50
2:C:29:VAL:O	2:C:29:VAL:HG12	2.12	0.50
2:C:184:GLN:HG3	2:C:191:TYR:CZ	2.46	0.50
3:D:204:LEU:HD23	3:D:245:MET:HE1	1.93	0.50
1:A:233:LYS:HE3	2:G:141:GLU:OE1	2.12	0.49
2:C:29:VAL:HG11	2:C:106:GLN:HB2	1.95	0.49
2:G:152:CYS:HB2	2:G:166:TRP:CZ2	2.48	0.49
1:A:20:ARG:HD3	1:A:88:TYR:CD2	2.48	0.49
1:A:150:PRO:HB3	1:A:162:LEU:HB3	1.95	0.48
1:B:168:ASP:HB3	1:B:199:LEU:HD13	1.96	0.48
3:E:245:MET:HE2	3:E:245:MET:HB3	1.67	0.48
2:G:102:TYR:O	2:G:119:GLY:HA2	2.14	0.48
2:G:204:TYR:HA	2:G:210:TYR:OH	2.14	0.48
1:B:13:VAL:HB	1:B:19:LEU:CD1	2.41	0.47
3:D:282:LYS:NZ	3:D:286:SER:H	2.12	0.47
2:C:154:LEU:HD22	2:C:193:LEU:HD22	1.96	0.47
2:C:142:GLN:O	2:C:145:SER:HB3	2.14	0.47
2:G:21:ILE:HG12	2:G:120:THR:HG21	1.97	0.46
2:G:121:LYS:HD2	2:G:123:GLU:OE2	2.15	0.46
2:G:11:LEU:HD21	2:G:19:VAL:HG13	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:41:TRP:O	2:G:53:LEU:HB2	2.16	0.46
2:G:151:VAL:HG22	2:G:196:THR:HG23	1.98	0.45
2:G:185:ASP:HB3	2:G:188:ASP:OD1	2.17	0.45
3:D:298:LEU:HD13	3:D:310:GLU:HA	1.99	0.45
1:B:14:GLN:HG2	1:B:136:PHE:CZ	2.51	0.44
2:C:152:CYS:HB2	2:C:166:TRP:CZ2	2.51	0.44
2:C:32:ALA:O	2:C:106:GLN:HA	2.18	0.44
3:D:270:GLU:HB3	3:D:271:ASP:H	1.58	0.44
2:G:105:GLN:HB2	2:G:116:PHE:CD1	2.52	0.44
1:A:106:ARG:O	1:A:110:MET:HA	2.17	0.44
1:B:67:TYR:CE1	1:B:77:THR:HA	2.53	0.44
1:A:94:LEU:HA	1:A:94:LEU:HD23	1.79	0.43
1:B:99:THR:HA	1:B:133:VAL:O	2.18	0.43
2:C:197:LEU:HG	2:C:199:LEU:HD13	2.00	0.43
2:G:134:PHE:CD2	2:G:153:LEU:HD23	2.54	0.43
3:E:283:PHE:HB3	3:E:305:THR:O	2.18	0.43
3:E:234:ALA:HB2	3:E:273:CYS:SG	2.57	0.43
1:B:163:GLY:HA2	1:B:178:TRP:CZ2	2.54	0.43
1:A:145:VAL:CG2	1:A:222:VAL:HG21	2.48	0.43
1:A:163:GLY:HA2	1:A:178:TRP:CZ2	2.54	0.43
1:A:209:PRO:HG2	1:A:212:SER:OG	2.20	0.42
2:C:184:GLN:HG3	2:C:191:TYR:CE1	2.53	0.42
2:G:18:ARG:HA	2:G:91:ILE:O	2.20	0.42
2:G:229:ARG:HG2	2:G:229:ARG:HH11	1.84	0.42
1:A:108:TYR:CE1	2:G:114(A):ILE:HD11	2.45	0.42
2:G:114(A):ILE:H	2:G:114(A):ILE:HD12	1.84	0.42
1:B:148:LEU:HD23	1:B:148:LEU:HA	1.87	0.42
1:B:154:SER:HA	2:C:134:PHE:HD2	1.83	0.42
2:G:2:ILE:H	2:G:2:ILE:HD12	1.84	0.42
2:C:24[A]:ARG:CZ	2:C:86:ASP:OD1	2.68	0.42
1:B:106:ARG:O	1:B:107:TYR:HB2	2.20	0.41
1:A:106:ARG:O	1:A:107:TYR:HB2	2.21	0.41
2:G:52:LEU:HD23	2:G:68:TYR:CG	2.55	0.41
2:C:204:TYR:HA	2:C:210:TYR:OH	2.21	0.41
2:C:126:ARG:HG2	2:C:158:TYR:CG	2.56	0.41
2:C:99:PHE:CZ	2:C:124:ILE:HG12	2.55	0.41
2:G:53:LEU:HA	2:G:71:VAL:HG11	2.03	0.41
2:G:131:PRO:HB3	2:G:157:PHE:HB3	2.02	0.41
1:A:6:GLU:OE2	1:A:128:GLY:HA3	2.20	0.41
2:G:19:VAL:HG21	2:G:94:LEU:HD12	2.03	0.41
2:C:27:GLN:O	2:C:29:VAL:HG23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:205:LEU:HD23	3:D:205:LEU:HA	1.92	0.41
2:G:77:SER:O	2:G:89:LEU:HD12	2.22	0.40
3:D:263:GLN:HA	3:D:285:ALA:HB2	2.03	0.40
1:B:30:ILE:HD12	1:B:85:ASN:C	2.41	0.40
3:E:294:PRO:O	3:E:297:THR:HG22	2.20	0.40
2:C:24[B]:ARG:NE	2:C:86:ASP:OD2	2.53	0.40
2:C:182:THR:HG23	2:C:192:SER:O	2.22	0.40

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	209/222 (94%)	205 (98%)	4 (2%)	0	100	100
1	B	215/222 (97%)	208 (97%)	7 (3%)	0	100	100
2	C	213/215 (99%)	205 (96%)	8 (4%)	0	100	100
2	G	212/215 (99%)	204 (96%)	8 (4%)	0	100	100
3	D	120/132 (91%)	113 (94%)	7 (6%)	0	100	100
3	E	120/132 (91%)	114 (95%)	6 (5%)	0	100	100
All	All	1089/1138 (96%)	1049 (96%)	40 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	171/186 (92%)	171 (100%)	0	100	100
1	B	175/186 (94%)	171 (98%)	4 (2%)	50	80
2	C	180/187 (96%)	178 (99%)	2 (1%)	73	90
2	G	179/187 (96%)	177 (99%)	2 (1%)	73	90
3	D	92/107 (86%)	91 (99%)	1 (1%)	73	90
3	E	91/107 (85%)	91 (100%)	0	100	100
All	All	888/960 (92%)	879 (99%)	9 (1%)	76	91

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	G	80	ARG
2	G	125	LYS
1	B	26	SER
1	B	62	TYR
1	B	92	ASN
1	B	194	LEU
2	C	86	ASP
2	C	125	LYS
3	D	206	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

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	213/222 (95%)	-0.36	0 100 100	36, 60, 78, 89	0
1	B	216/222 (97%)	-0.36	1 (0%) 91 75	30, 48, 70, 82	0
2	C	214/215 (99%)	-0.45	0 100 100	34, 46, 62, 68	0
2	G	214/215 (99%)	-0.38	0 100 100	35, 64, 92, 103	0
3	D	124/132 (93%)	-0.25	0 100 100	51, 91, 116, 136	0
3	E	124/132 (93%)	-0.24	0 100 100	71, 89, 116, 126	0
All	All	1105/1138 (97%)	-0.36	1 (0%) 95 89	30, 58, 100, 136	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	154	SER	2.7

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](#)

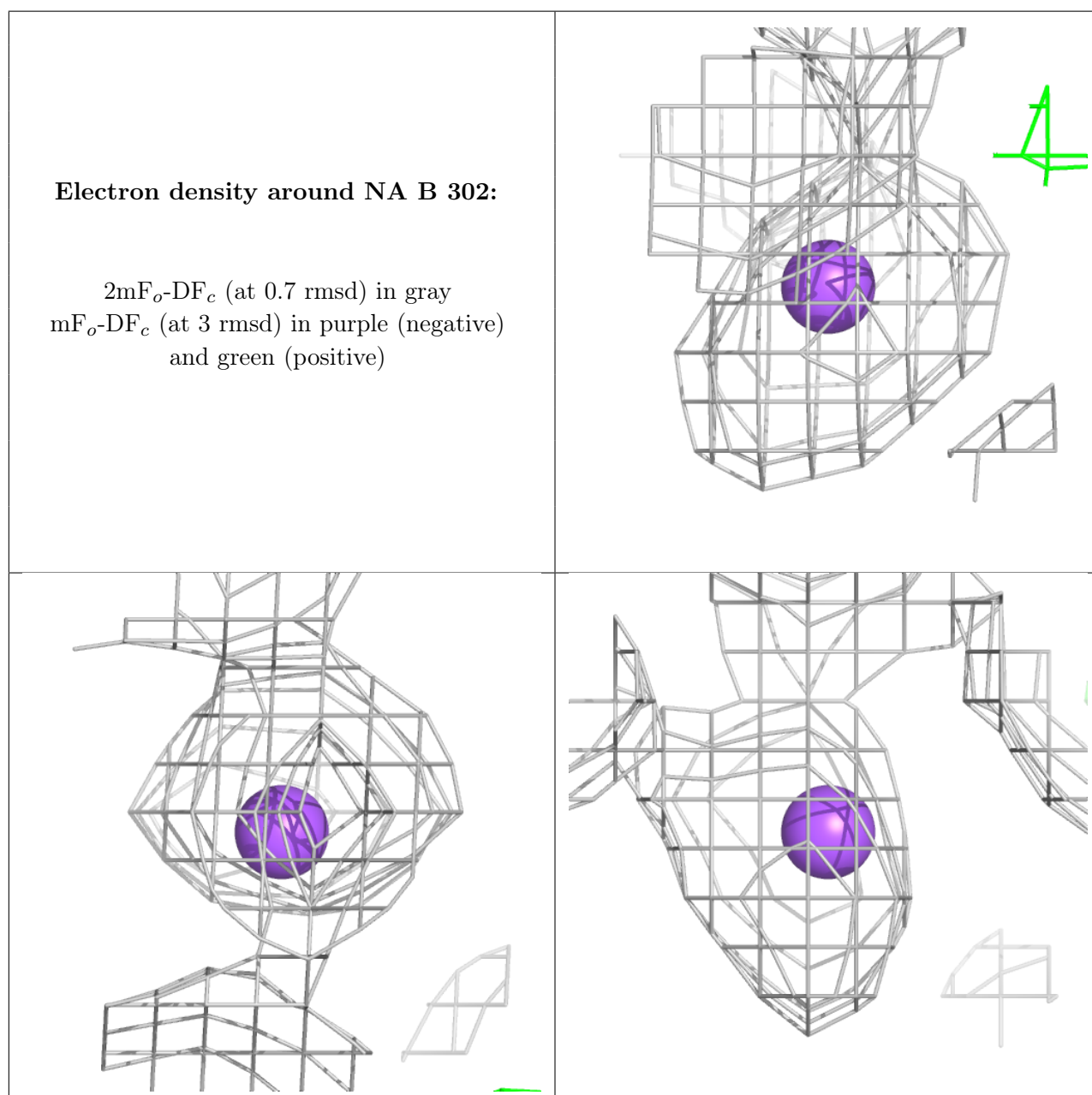
There are no monosaccharides in this entry.

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.

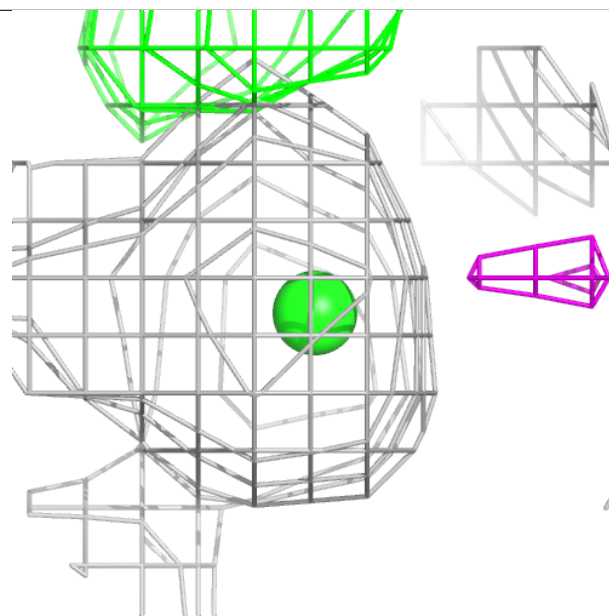
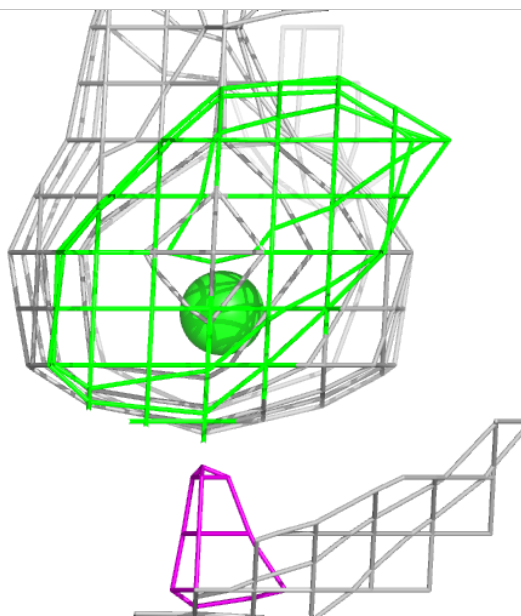
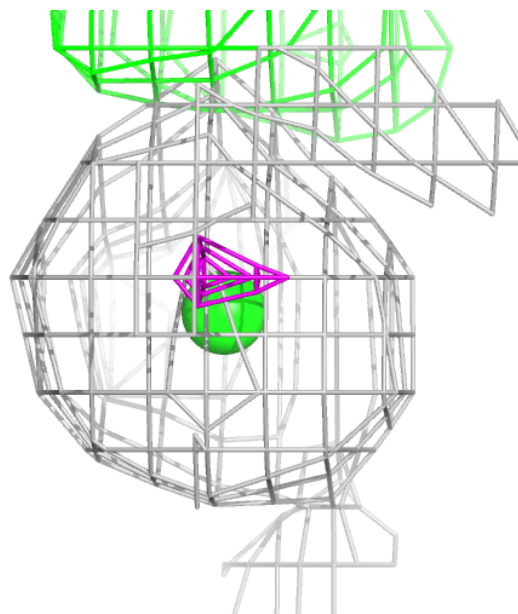
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	NA	B	302	1/1	0.66	0.22	40,40,40,40	0
4	CL	G	301	1/1	0.87	0.24	61,61,61,61	0
4	CL	B	301	1/1	0.89	0.12	65,65,65,65	0
4	CL	C	301	1/1	0.91	0.12	56,56,56,56	0
5	NA	B	303	1/1	0.94	0.23	40,40,40,40	0
4	CL	G	302	1/1	0.96	0.14	52,52,52,52	0

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.



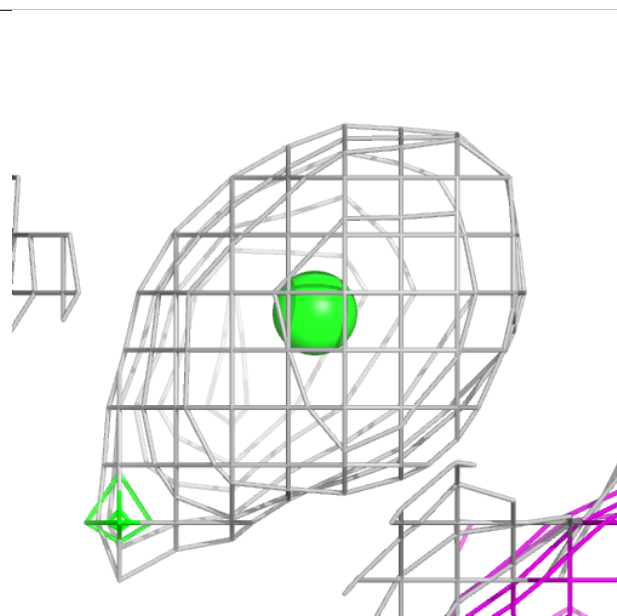
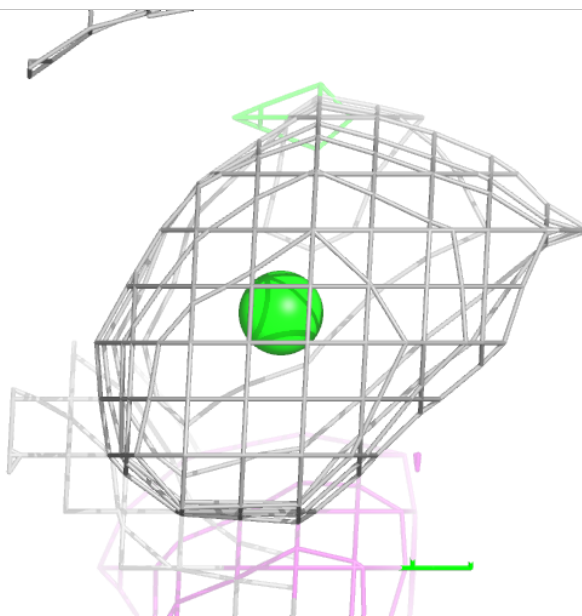
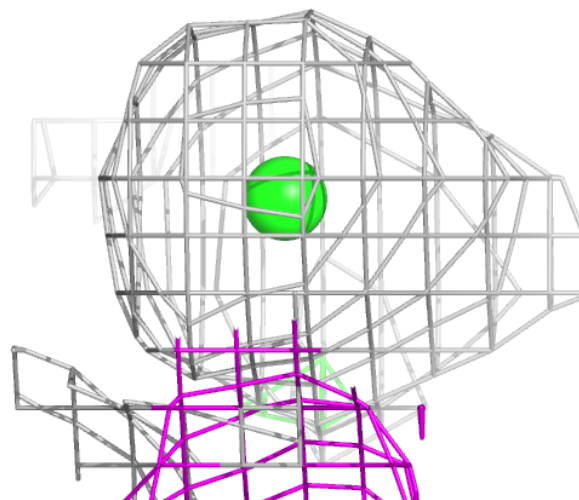
Electron density around CL G 301:

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



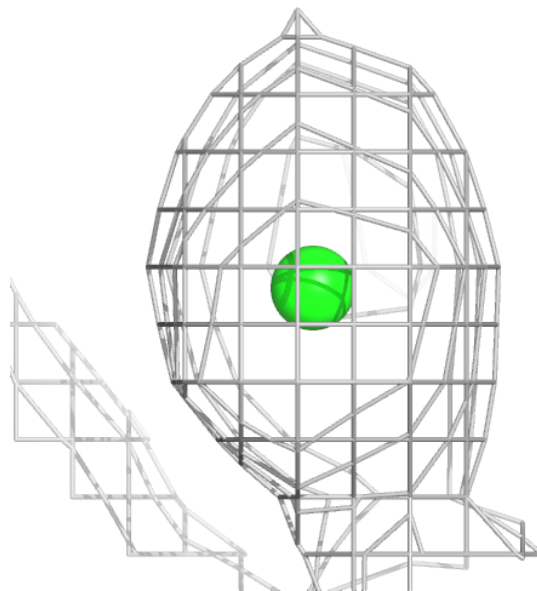
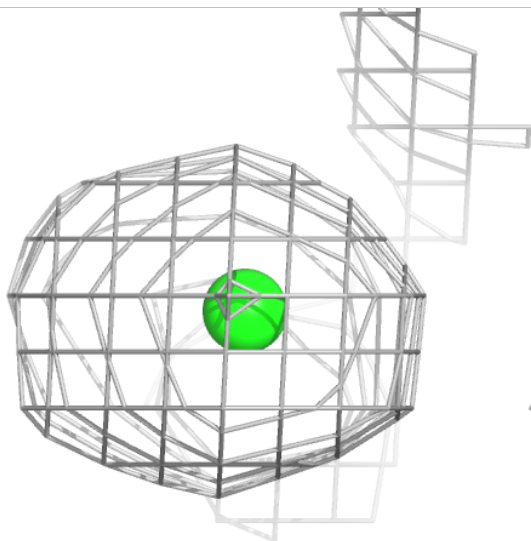
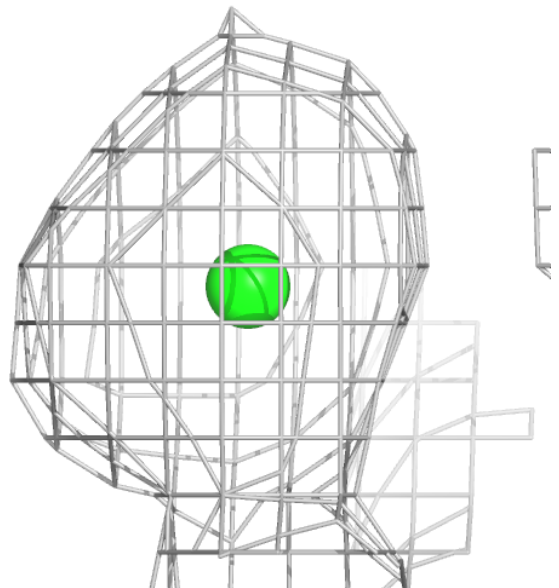
Electron density around CL B 301:

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



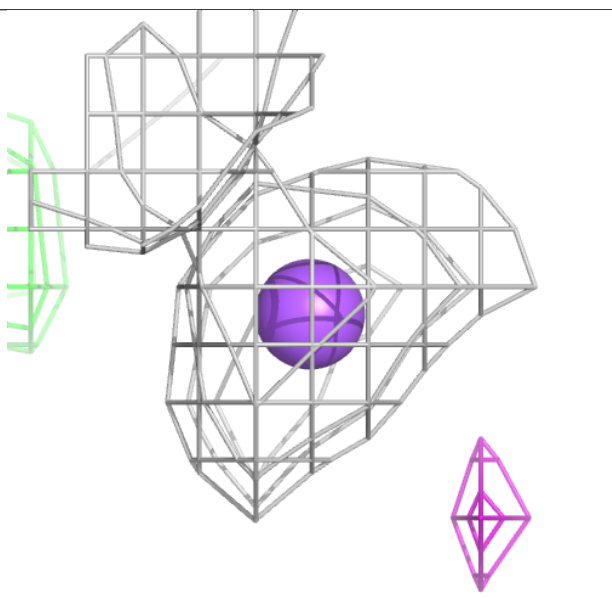
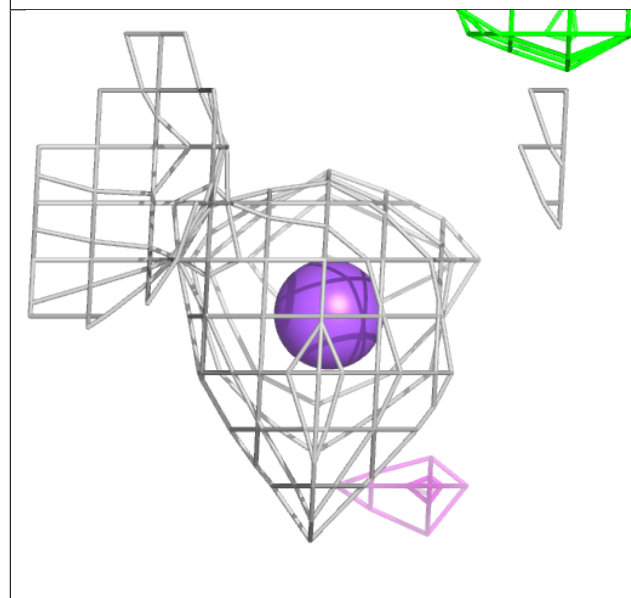
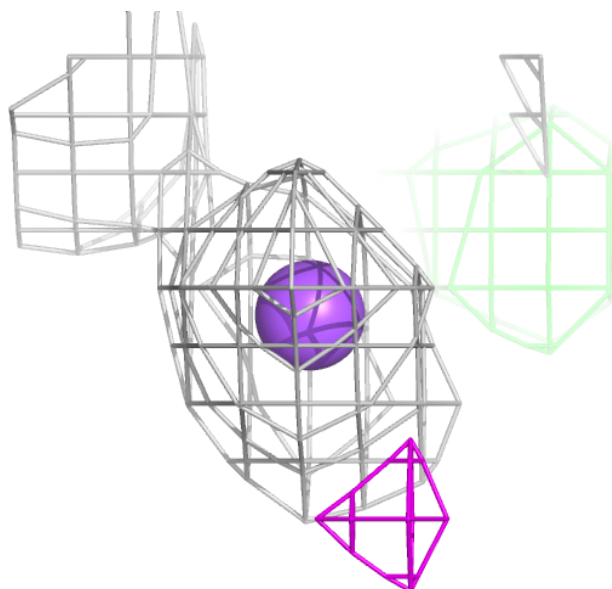
Electron density around CL C 301:

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



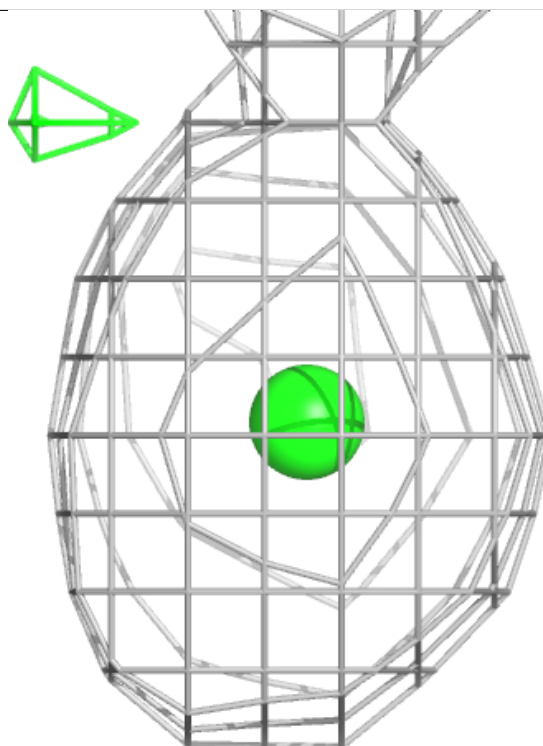
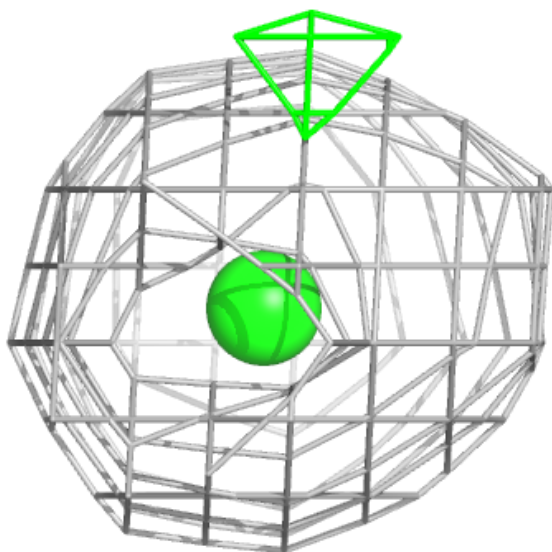
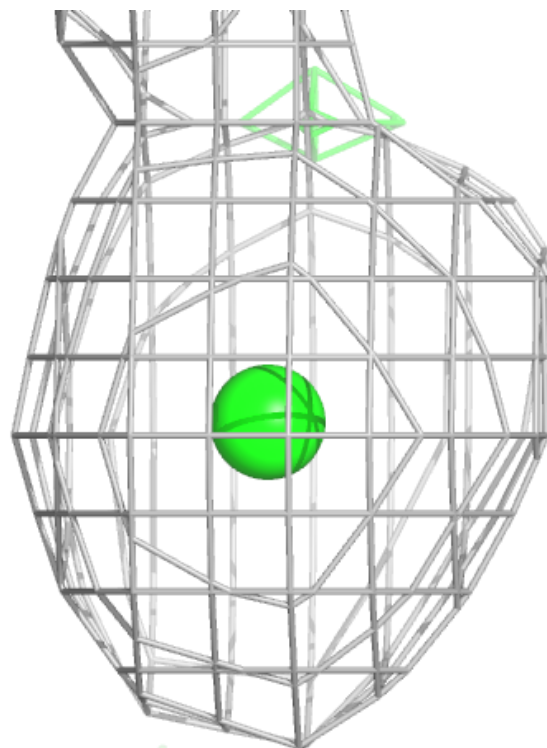
Electron density around NA B 303:

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



Electron density around CL G 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** [i](#)

There are no such residues in this entry.