



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 9, 2023 – 10:09 am BST

PDB ID : 8OXV  
Title : Transglutaminase 3 zymogen in complex with DH patient-derived Fab DH63-B02  
Authors : Heggelund, J.E.; Sollid, L.M.  
Deposited on : 2023-05-02  
Resolution : 1.80 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](mailto: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>.

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

MolProbity : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35.1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.35.1

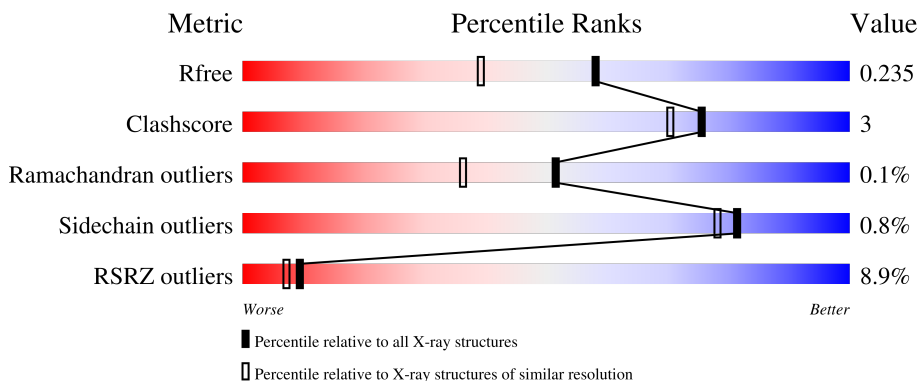
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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  $\geq 3$ , 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	693	 8% (red), 87% (green), 11% (yellow), .. (grey)
2	B	225	 17% (red), 91% (green), 8% (yellow), . (grey)
3	C	216	 3% (red), 95% (green), 5% (yellow)

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 18710 atoms, of which 8599 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 Protein-glutamine gamma-glutamyltransferase E 27 kDa non-catalytic chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	681	10666	3382	5305	926	1026	27	137	7	0

- Molecule 2 is a protein called Antibody Fab fragment Heavy chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
2	B	225	3431	1085	1691	299	348	8	73	5	0

- Molecule 3 is a protein called Antibody Fab fragment light chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
3	C	216	3233	1021	1585	275	345	7	74	3	0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total	Ca	0	0
			3	3		

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Cl	0	0
			1	1		

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	H	O	1	0
			10	2	6	2		
6	B	1	Total	C	H	O	1	0
			10	2	6	2		
6	C	1	Total	C	H	O	1	0
			10	2	6	2		

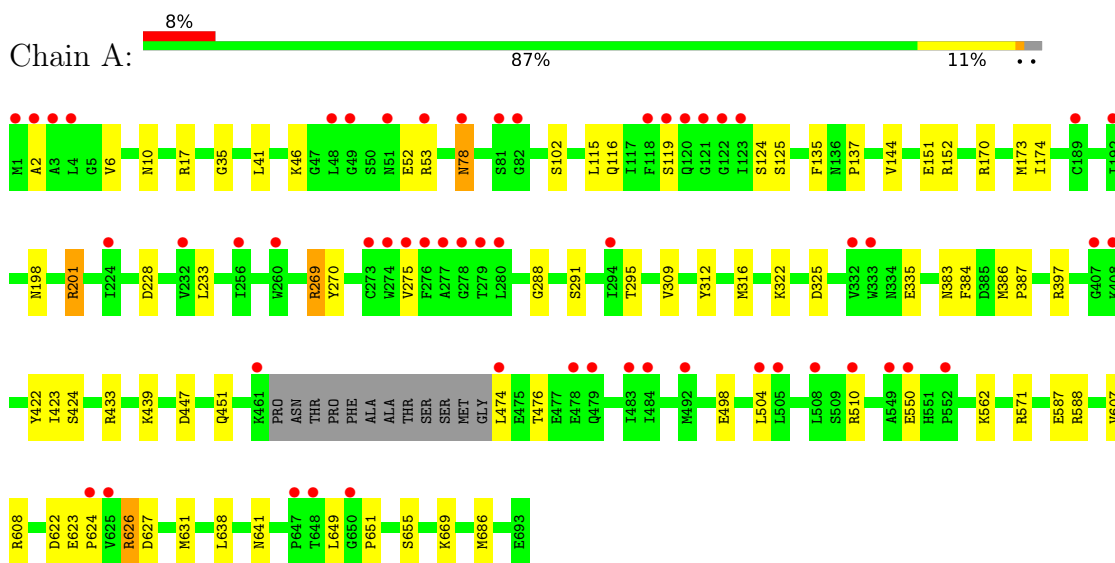
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	808	Total	O	0	0
			808	808		
7	B	199	Total	O	0	0
			199	199		
7	C	339	Total	O	0	0
			339	339		

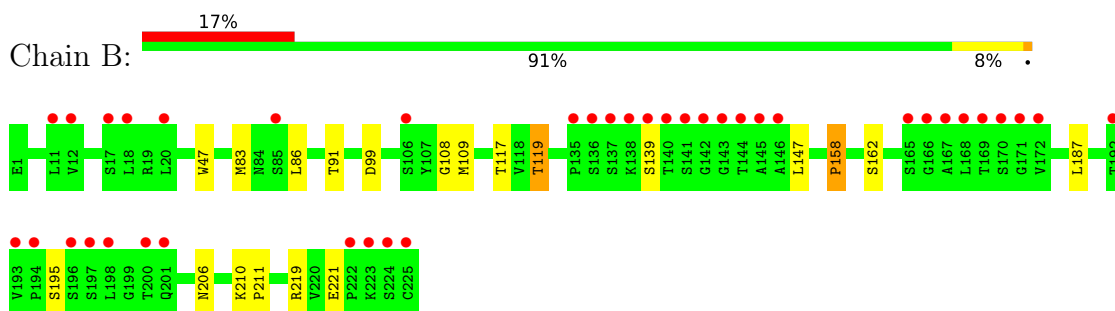
### 3 Residue-property plots [i](#)

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.

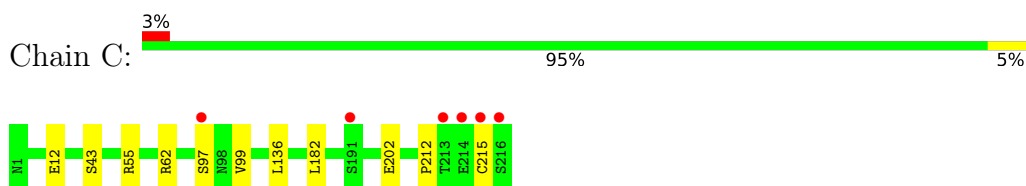
- Molecule 1: Protein-glutamine gamma-glutamyltransferase E 27 kDa non-catalytic chain



- Molecule 2: Antibody Fab fragment Heavy chain



- Molecule 3: Antibody Fab fragment light chain



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.66Å 94.04Å 91.14Å 90.00° 93.46° 90.00°	Depositor
Resolution (Å)	41.81 – 1.80 41.77 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (41.81-1.80) 97.4 (41.77-1.80)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.15 (at 1.79Å)	Xtrriage
Refinement program	REFMAC 5.8.0405	Depositor
R, $R_{free}$	0.185 , 0.229 0.193 , 0.235	Depositor DCC
$R_{free}$ test set	6180 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	27.5	Xtrriage
Anisotropy	0.112	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 47.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	18710	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.80% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: EDO, 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	0.59	1/5481 (0.0%)	0.90	6/7430 (0.1%)
2	B	0.59	0/1780	0.89	1/2421 (0.0%)
3	C	0.65	1/1690 (0.1%)	0.94	2/2305 (0.1%)
All	All	0.60	2/8951 (0.0%)	0.90	9/12156 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	151	GLU	CD-OE2	-6.09	1.19	1.25
3	C	202	GLU	CD-OE2	5.14	1.31	1.25

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	269	ARG	NE-CZ-NH2	-8.18	116.21	120.30
1	A	201	ARG	NE-CZ-NH1	7.47	124.04	120.30
3	C	62	ARG	NE-CZ-NH1	-7.41	116.59	120.30
1	A	571	ARG	NE-CZ-NH1	-6.75	116.92	120.30
2	B	158	PRO	N-CA-CB	-6.01	95.99	102.60
1	A	201	ARG	NE-CZ-NH2	-5.74	117.43	120.30
1	A	433	ARG	NE-CZ-NH1	5.60	123.10	120.30
3	C	55	ARG	NE-CZ-NH2	-5.53	117.53	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	152	ARG	NE-CZ-NH1	-5.14	117.73	120.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	17	ARG	Sidechain
1	A	510	ARG	Sidechain
1	A	53	ARG	Sidechain
1	A	588	ARG	Sidechain
1	A	626	ARG	Sidechain

## 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	5361	5305	5295	41	0
2	B	1740	1691	1684	11	0
3	C	1648	1585	1580	3	0
4	A	3	0	0	0	0
5	A	1	0	0	0	0
6	B	8	12	12	0	0
6	C	4	6	6	0	0
7	A	808	0	0	9	0
7	B	199	0	0	1	0
7	C	339	0	0	0	0
All	All	10111	8599	8577	54	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 3.

All (54) 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:B:117:THR:OG1	7:B:401:HOH:O	2.05	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:631[B]:MET:SD	7:A:1283:HOH:O	2.50	0.70
1:A:78:ASN:OD1	7:A:801:HOH:O	2.14	0.66
1:A:649:LEU:HD11	1:A:655:SER:HB2	1.77	0.66
2:B:139:SER:O	2:B:195:SER:HB3	1.98	0.62
1:A:198[A]:ASN:OD1	1:A:201:ARG:NH2	2.33	0.61
2:B:187:LEU:HD12	2:B:187:LEU:C	2.22	0.59
3:C:136:LEU:HD12	3:C:182:LEU:HD23	1.86	0.57
1:A:233:LEU:HD11	1:A:275:VAL:HG12	1.87	0.56
1:A:170:ARG:HD2	7:A:1110:HOH:O	2.06	0.55
2:B:147:LEU:C	2:B:147:LEU:HD12	2.28	0.55
1:A:447:ASP:O	1:A:451:GLN:HG3	2.09	0.52
1:A:439:LYS:HE2	7:A:802:HOH:O	2.10	0.50
1:A:386:MET:N	1:A:387:PRO:CD	2.75	0.50
1:A:562:LYS:HG2	1:A:562:LYS:O	2.11	0.49
1:A:638:LEU:HD23	1:A:638:LEU:N	2.27	0.49
1:A:607:VAL:HG12	1:A:608:ARG:HG3	1.94	0.49
2:B:47:TRP:CG	3:C:99:VAL:HB	2.47	0.49
1:A:6:VAL:CG2	1:A:115:LEU:HD23	2.43	0.48
1:A:309:VAL:HG12	1:A:325:ASP:HB3	1.96	0.47
1:A:35:GLY:HA2	1:A:102:SER:O	2.16	0.46
1:A:52:GLU:OE2	1:A:119:SER:OG	2.29	0.46
1:A:115:LEU:O	1:A:125:SER:HA	2.16	0.46
1:A:173:MET:HE3	1:A:686[B]:MET:SD	2.56	0.46
3:C:212:PRO:O	3:C:215:CYS:SG	2.74	0.46
1:A:312:TYR:CD2	1:A:322:LYS:HD3	2.52	0.45
1:A:135:PHE:HB3	1:A:144:VAL:HG21	1.98	0.44
2:B:162:SER:OG	2:B:206:ASN:OD1	2.34	0.44
2:B:210:LYS:N	2:B:211:PRO:CD	2.80	0.44
1:A:622:ASP:C	1:A:651:PRO:HB3	2.38	0.43
1:A:476:THR:HG21	7:A:1521:HOH:O	2.17	0.43
2:B:99:ASP:HA	2:B:108:GLY:O	2.18	0.43
1:A:669:LYS:NZ	7:A:803:HOH:O	2.24	0.43
2:B:83:MET:HE2	2:B:86:LEU:HD21	2.00	0.43
1:A:291:SER:HA	1:A:335:GLU:O	2.17	0.43
1:A:116:GLN:HA	1:A:124:SER:O	2.19	0.43
2:B:219:ARG:HG2	2:B:221[B]:GLU:HG2	2.01	0.42
2:B:91:THR:HG23	2:B:119:THR:HA	2.00	0.42
1:A:626:ARG:HG3	1:A:627:ASP:OD2	2.19	0.42
1:A:295:THR:O	1:A:423:ILE:HA	2.19	0.42
1:A:174:ILE:HD12	7:A:1226:HOH:O	2.19	0.42
1:A:623:GLU:HB2	1:A:624:PRO:CD	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:ALA:O	1:A:46:LYS:HD2	2.20	0.41
1:A:316:MET:HE1	7:A:1297:HOH:O	2.19	0.41
1:A:474:LEU:HD23	1:A:474:LEU:O	2.21	0.41
1:A:10:ASN:HB3	1:A:41:LEU:HB2	2.02	0.41
1:A:422:TYR:O	1:A:424:SER:OG	2.35	0.41
1:A:504:LEU:CD2	1:A:550:GLU:HG2	2.51	0.41
1:A:137:PRO:HG3	1:A:288:GLY:O	2.21	0.40
1:A:397:ARG:NH2	1:A:587:GLU:OE2	2.55	0.40
1:A:498:GLU:HG2	7:A:1218:HOH:O	2.21	0.40
1:A:607:VAL:O	1:A:608:ARG:HB2	2.21	0.40
1:A:269:ARG:HA	1:A:270:TYR:HA	1.80	0.40
1:A:383:ASN:HA	1:A:384:PHE:HA	1.78	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	684/693 (99%)	658 (96%)	25 (4%)	1 (0%)	51	36
2	B	228/225 (101%)	217 (95%)	11 (5%)	0	100	100
3	C	217/216 (100%)	209 (96%)	8 (4%)	0	100	100
All	All	1129/1134 (100%)	1084 (96%)	44 (4%)	1 (0%)	51	36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	228	ASP

### 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	593/595 (100%)	591 (100%)	2 (0%)	92	91
2	B	196/191 (103%)	193 (98%)	3 (2%)	65	56
3	C	192/189 (102%)	189 (98%)	3 (2%)	62	54
All	All	981/975 (101%)	973 (99%)	8 (1%)	81	78

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	78	ASN
1	A	641	ASN
2	B	109	MET
2	B	119	THR
2	B	158	PRO
3	C	12	GLU
3	C	43	SER
3	C	97	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	78	ASN

### 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 7 ligands modelled in this entry, 4 are monoatomic - leaving 3 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	EDO	C	301	-	3,3,3	0.39	0	2,2,2	0.46	0
6	EDO	B	301	-	3,3,3	0.62	0	2,2,2	0.69	0
6	EDO	B	302	-	3,3,3	0.12	0	2,2,2	0.12	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	EDO	C	301	-	-	1/1/1/1	-
6	EDO	B	301	-	-	1/1/1/1	-
6	EDO	B	302	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	B	301	EDO	O1-C1-C2-O2
6	C	301	EDO	O1-C1-C2-O2
6	B	302	EDO	O1-C1-C2-O2

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

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	681/693 (98%)	0.39	55 (8%) 12 9	17, 34, 65, 119	0
2	B	225/225 (100%)	0.94	39 (17%) 1 1	22, 43, 94, 162	0
3	C	216/216 (100%)	0.01	6 (2%) 53 47	21, 30, 50, 144	0
All	All	1122/1134 (98%)	0.43	100 (8%) 9 7	17, 35, 68, 162	0

All (100) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	140	THR	12.8
2	B	142	GLY	11.6
2	B	139	SER	10.0
2	B	141	SER	9.7
3	C	216	SER	8.9
1	A	1	MET	8.1
3	C	215	CYS	6.8
2	B	200	THR	6.7
2	B	136	SER	6.4
1	A	3	ALA	6.2
2	B	225	CYS	6.0
1	A	2	ALA	5.5
2	B	138	LYS	5.5
1	A	82	GLY	5.3
2	B	167	ALA	5.2
2	B	198	LEU	5.1
2	B	137	SER	5.1
1	A	478	GLU	4.9
2	B	145	ALA	4.8
2	B	143	GLY	4.6
2	B	169	THR	4.6
1	A	78	ASN	4.6
1	A	118	PHE	4.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
3	C	213	THR	4.5
1	A	479	GLN	4.3
1	A	474	LEU	4.2
1	A	51	ASN	4.2
2	B	194	PRO	4.1
2	B	197	SER	4.1
2	B	196	SER	4.0
2	B	172	VAL	4.0
1	A	4	LEU	4.0
1	A	461	LYS	3.7
1	A	549	ALA	3.6
2	B	11	LEU	3.6
2	B	224	SER	3.5
1	A	81	SER	3.5
3	C	214	GLU	3.5
2	B	223	LYS	3.5
2	B	18	LEU	3.4
1	A	552	PRO	3.3
2	B	12	VAL	3.2
1	A	332	VAL	3.2
1	A	273	CYS	3.2
1	A	504	LEU	3.1
1	A	333	TRP	3.0
1	A	280	LEU	3.0
1	A	508	LEU	2.9
3	C	97	SER	2.9
2	B	146	ALA	2.9
1	A	492	MET	2.9
1	A	48	LEU	2.8
1	A	120	GLN	2.8
2	B	168	LEU	2.7
1	A	119	SER	2.7
1	A	408	LYS	2.7
1	A	123	ILE	2.7
1	A	510	ARG	2.7
2	B	192	THR	2.6
1	A	625	VAL	2.6
2	B	17	SER	2.6
1	A	49	GLY	2.6
2	B	166	GLY	2.6
1	A	278	GLY	2.5
1	A	407	GLY	2.4

*Continued on next page...*

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Mol	Chain	Res	Type	RSRZ
1	A	256	ILE	2.4
1	A	276	PHE	2.4
2	B	201	GLN	2.4
1	A	277	ALA	2.4
2	B	171	GLY	2.3
2	B	193	VAL	2.3
1	A	483	ILE	2.3
1	A	53	ARG	2.3
1	A	624	PRO	2.2
1	A	122	GLY	2.2
2	B	135	PRO	2.2
2	B	170	SER	2.2
1	A	647	PRO	2.2
2	B	165	SER	2.2
2	B	144	THR	2.2
1	A	484	ILE	2.2
1	A	121	GLY	2.1
1	A	648	THR	2.1
2	B	106	SER	2.1
1	A	550	GLU	2.1
2	B	85	SER	2.1
1	A	224	ILE	2.1
1	A	294	ILE	2.1
2	B	20	LEU	2.1
2	B	222	PRO	2.1
1	A	274	TRP	2.1
1	A	189	CYS	2.1
1	A	279	THR	2.0
1	A	192	ILE	2.0
1	A	232	VAL	2.0
1	A	275	VAL	2.0
1	A	650	GLY	2.0
1	A	260	TRP	2.0
1	A	505	LEU	2.0
3	C	191	SER	2.0

## 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](#)

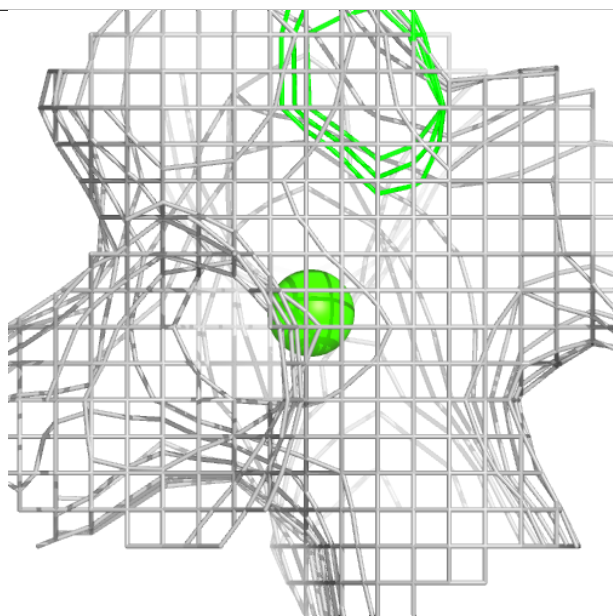
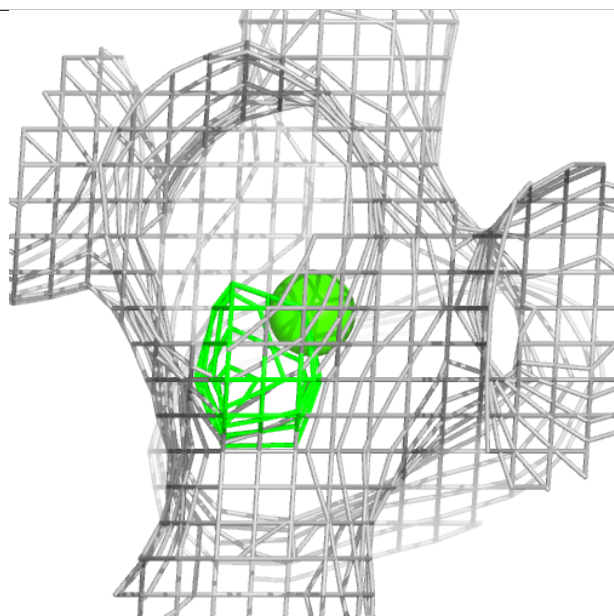
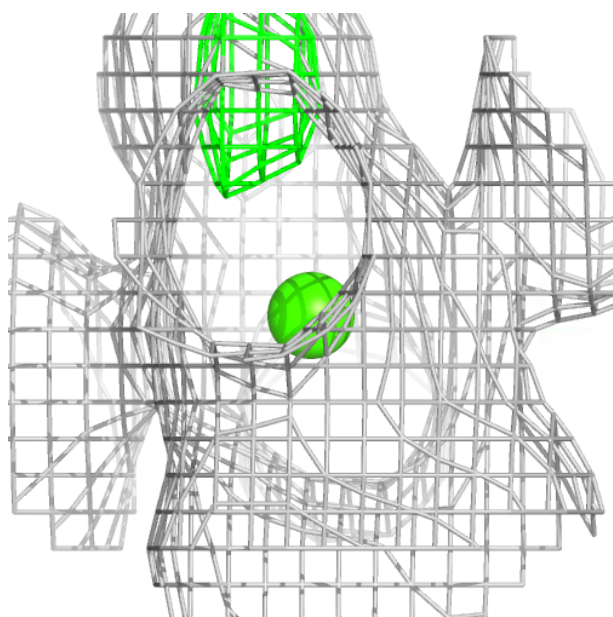
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
6	EDO	C	301	4/4	0.80	0.12	53,58,62,64	1
6	EDO	B	301	4/4	0.81	0.16	54,60,66,66	1
6	EDO	B	302	4/4	0.90	0.20	68,71,74,75	1
4	CA	A	702	1/1	0.97	0.09	37,37,37,37	0
5	CL	A	704	1/1	0.98	0.07	45,45,45,45	0
4	CA	A	701	1/1	0.99	0.14	20,20,20,20	0
4	CA	A	703	1/1	0.99	0.06	35,35,35,35	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.

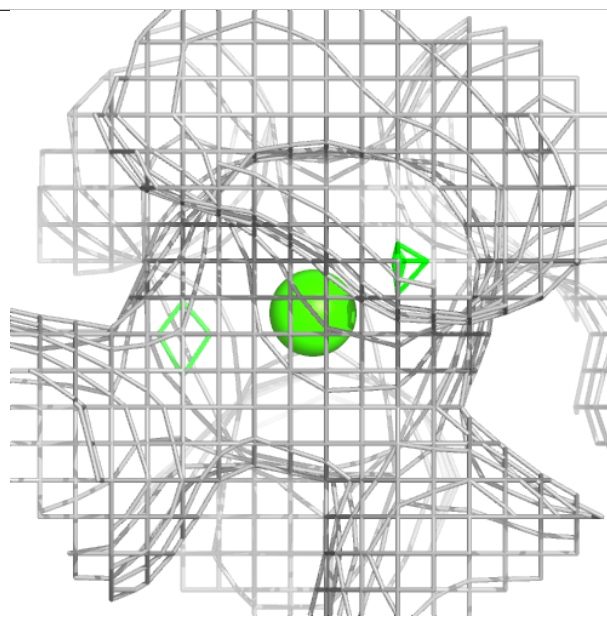
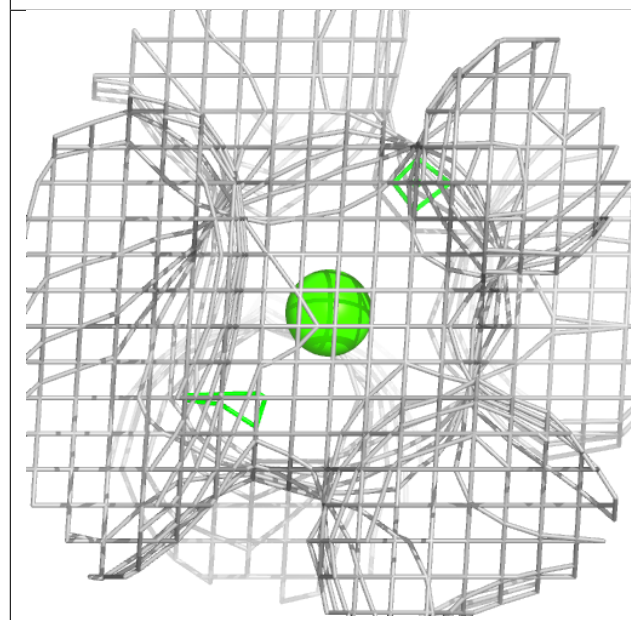
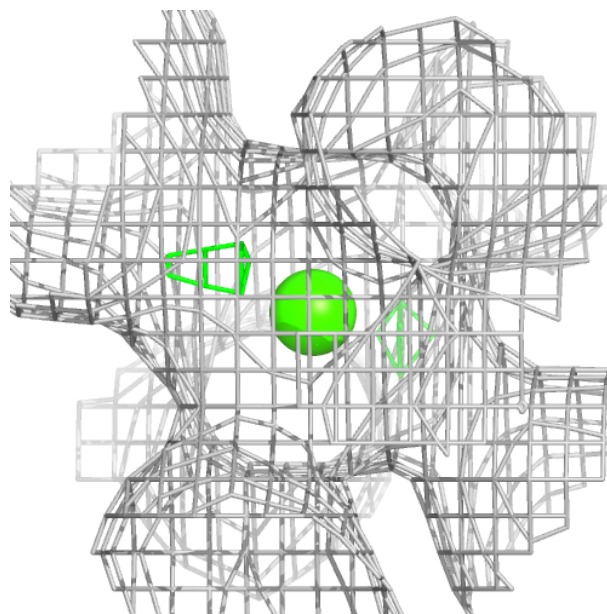
**Electron density around CA A 702:**

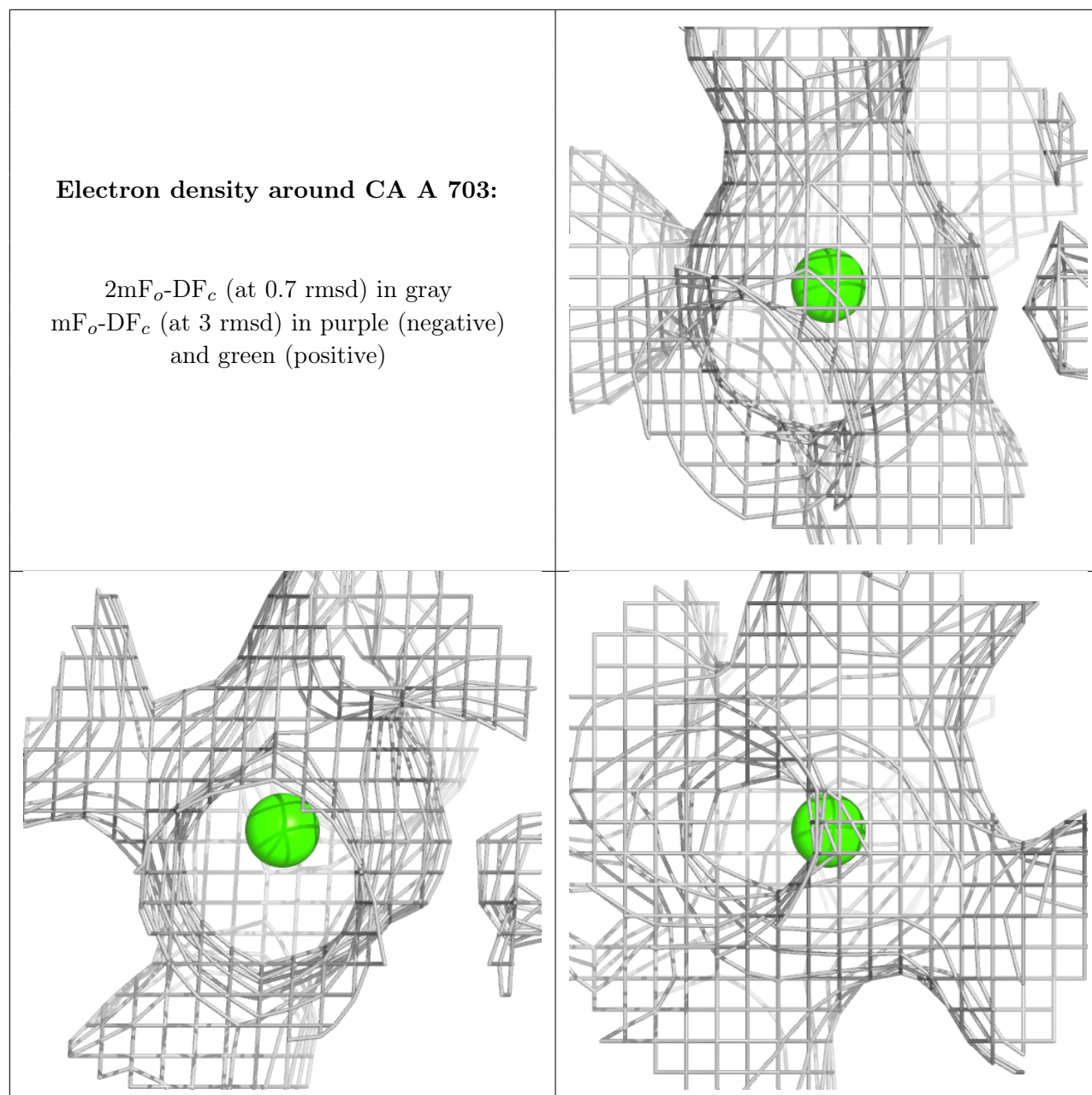
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around CA A 701:**

$2mF_o-DF_c$  (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.