



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 03:19 AM UTC

PDB ID : 7TZ2 / pdb_00007tz2
Title : Structure of human Fibrinogen-like protein 1
Authors : Ming, Q.; Tran, T.H.; Luca, V.C.
Deposited on : 2022-02-15
Resolution : 2.55 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

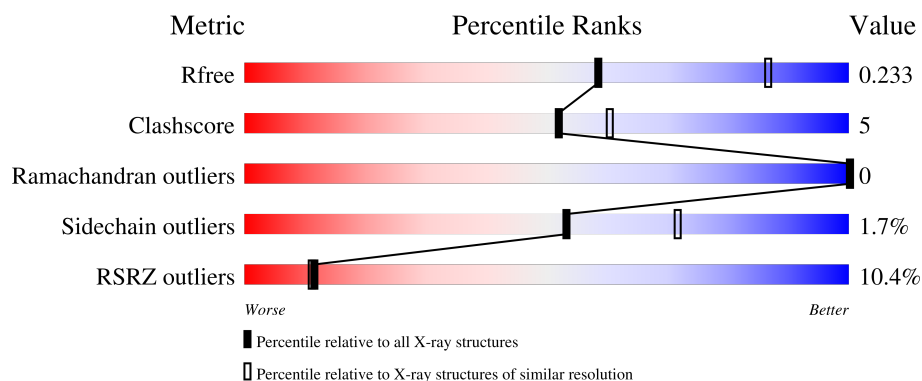
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1091 (2.54-2.54)
Clashscore	190562	1120 (2.54-2.54)
Ramachandran outliers	187476	1106 (2.54-2.54)
Sidechain outliers	187428	1106 (2.54-2.54)
RSRZ outliers	180081	1091 (2.54-2.54)

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	233	7% 82% 12% 6%
1	B	233	13% 79% 20% .
1	C	233	10% 89% 9% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5755 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 Fibrinogen-like protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	220	Total	C	N	O	S	0	0	0
			1811	1148	308	348	7			
1	B	231	Total	C	N	O	S	0	0	0
			1896	1207	324	358	7			
1	C	231	Total	C	N	O	S	0	0	0
			1918	1220	327	364	7			

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

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

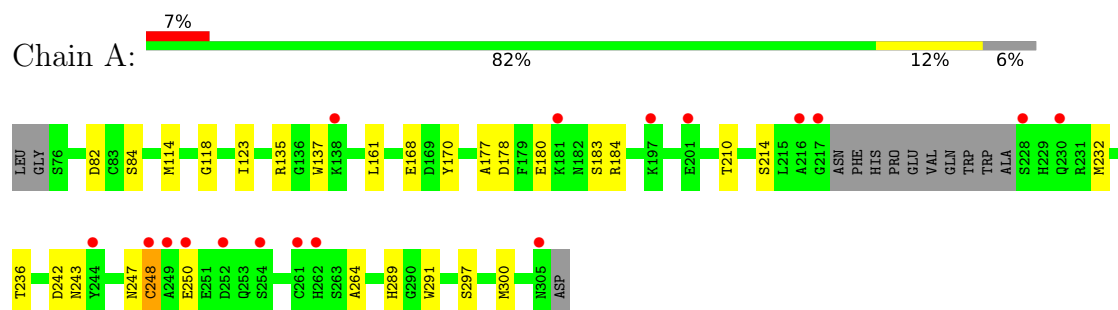
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	37	Total	O	0	0
			37	37		
3	B	44	Total	O	0	0
			44	44		
3	C	48	Total	O	0	0
			48	48		

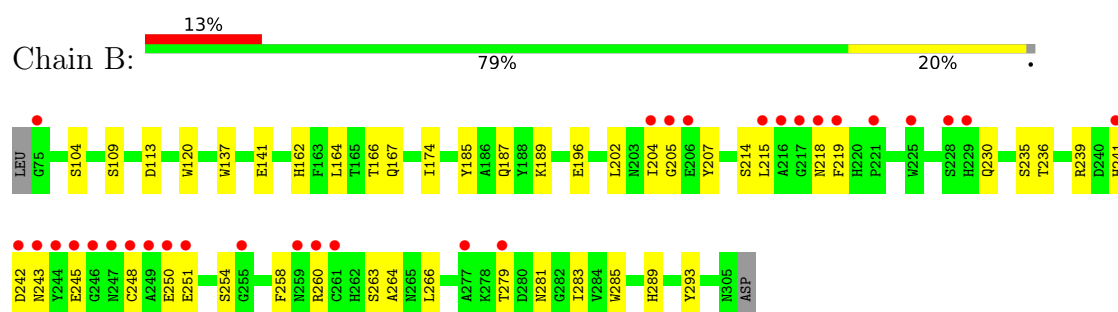
3 Residue-property plots [i](#)

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.

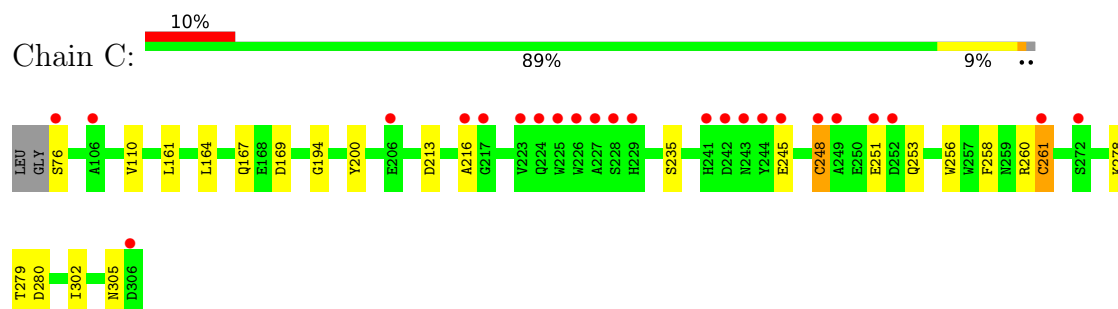
• Molecule 1: Fibrinogen-like protein 1



• Molecule 1: Fibrinogen-like protein 1



• Molecule 1: Fibrinogen-like protein 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	45.28Å 110.89Å 148.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.30 – 2.55 45.30 – 2.55	Depositor EDS
% Data completeness (in resolution range)	99.4 (45.30-2.55) 93.3 (45.30-2.55)	Depositor EDS
R_{merge}	0.35	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.74 (at 2.54Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.185 , 0.234 0.188 , 0.233	Depositor DCC
R_{free} test set	1288 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	26.4	Xtriage
Anisotropy	0.217	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 37.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5755	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.76% 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: 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	0.43	0/1867	0.70	1/2523 (0.0%)
1	B	0.57	0/1959	0.84	5/2652 (0.2%)
1	C	0.46	0/1983	0.70	1/2685 (0.0%)
All	All	0.49	0/5809	0.75	7/7860 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	291	TRP	N-CA-C	-7.22	103.63	113.30
1	B	254	SER	CA-C-N	-7.20	112.80	120.43
1	B	254	SER	C-N-CA	-7.20	112.80	120.43
1	B	258	PHE	CA-C-N	-6.16	112.01	122.11
1	B	258	PHE	C-N-CA	-6.16	112.01	122.11
1	B	243	ASN	N-CA-C	-5.95	105.68	113.12
1	C	76	SER	CA-CB-OG	-5.28	100.55	111.10

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	1811	0	1629	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1896	0	1702	23	0
1	C	1918	0	1721	16	0
2	A	1	0	0	0	0
3	A	37	0	0	1	0
3	B	44	0	0	0	0
3	C	48	0	0	0	0
All	All	5755	0	5052	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 5.

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)
1:C:253:GLN:HB3	1:C:258:PHE:CZ	2.27	0.70
1:A:178:ASP:HB3	1:A:180:GLU:H	1.62	0.65
1:C:245:GLU:HG3	1:C:248:CYS:HB2	1.79	0.64
1:B:248:CYS:SG	1:B:250:GLU:HB3	2.37	0.64
1:A:232:MET:HE1	1:A:243:ASN:HD21	1.63	0.62
1:C:245:GLU:HG3	1:C:248:CYS:CB	2.32	0.60
1:C:278:LYS:HG2	1:C:279:THR:HG23	1.86	0.57
1:C:164:LEU:HD13	1:C:302:ILE:HD11	1.88	0.55
1:B:279:THR:HG22	1:B:281:ASN:HB3	1.89	0.55
1:A:247:ASN:HB2	1:A:250:GLU:HB3	1.89	0.55
1:C:253:GLN:HB3	1:C:258:PHE:CE1	2.41	0.54
1:B:202:LEU:HD11	1:B:204:ILE:HG23	1.91	0.52
1:A:184:ARG:NH1	1:A:210:THR:O	2.43	0.52
1:A:214:SER:HB3	1:A:264:ALA:HB2	1.90	0.52
1:C:169:ASP:OD1	1:C:305:ASN:ND2	2.44	0.50
1:B:137:TRP:HA	1:B:236:THR:HG21	1.93	0.49
1:B:214:SER:HB2	1:B:285:TRP:CE2	2.47	0.49
1:C:256:TRP:HB3	1:C:258:PHE:CZ	2.48	0.49
1:B:266:LEU:HA	1:B:283:ILE:HG23	1.94	0.48
1:B:164:LEU:O	1:B:167:GLN:HG2	2.13	0.48
1:B:289:HIS:HB3	1:B:293:TYR:HB3	1.96	0.48
1:A:178:ASP:OD1	1:A:289:HIS:NE2	2.48	0.47
1:B:214:SER:HB3	1:B:264:ALA:HB2	1.96	0.47
1:B:218:ASN:O	1:B:219:PHE:C	2.58	0.46
1:B:239:ARG:HG2	1:B:241:HIS:CE1	2.49	0.46
1:A:168:GLU:HB3	1:A:170:TYR:CE1	2.51	0.46
1:B:162:HIS:CE1	1:B:166:THR:HG21	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:141:GLU:OE2	1:B:196:GLU:HG3	2.15	0.46
1:B:251:GLU:H	1:B:279:THR:HG21	1.81	0.45
1:C:194:GLY:O	1:C:200:TYR:HA	2.16	0.45
1:B:187:GLN:O	1:B:207:TYR:HA	2.16	0.45
1:A:114:MET:HA	1:A:118:GLY:HA2	1.98	0.45
1:C:213:ASP:OD2	1:C:216:ALA:HB3	2.17	0.45
1:B:215:LEU:HG	1:B:285:TRP:CH2	2.52	0.45
1:C:164:LEU:O	1:C:167:GLN:HG2	2.17	0.44
1:B:248:CYS:SG	1:B:248:CYS:O	2.75	0.44
1:B:242:ASP:HB3	1:B:245:GLU:HA	2.00	0.43
1:A:177:ALA:HB3	1:A:297:SER:OG	2.18	0.43
1:C:251:GLU:HG2	1:C:253:GLN:HG3	2.01	0.43
1:A:82:ASP:OD1	1:A:84:SER:OG	2.35	0.43
1:A:137:TRP:HA	1:A:236:THR:HG21	1.99	0.43
1:B:113:ASP:HB3	1:B:120:TRP:HB2	2.01	0.42
1:B:260:ARG:HG3	1:B:263:SER:HA	2.01	0.42
1:A:161:LEU:HD23	1:A:161:LEU:HA	1.70	0.42
1:B:174:ILE:O	1:B:185:TYR:HA	2.20	0.42
1:A:123:ILE:HD11	1:A:300:MET:HE2	2.01	0.42
1:B:189:LYS:O	1:B:205:GLY:HA3	2.20	0.42
1:A:135:ARG:NH2	3:A:502:HOH:O	2.53	0.41
1:C:161:LEU:HD23	1:C:161:LEU:HA	1.82	0.41
1:C:260:ARG:HG3	1:C:261:CYS:O	2.19	0.41
1:A:242:ASP:OD2	1:A:248:CYS:HB2	2.21	0.41
1:C:245:GLU:HG2	1:C:245:GLU:O	2.22	0.40
1:C:280:ASP:OD1	1:C:280:ASP:N	2.54	0.40
1:B:260:ARG:HG3	1:B:263:SER:CA	2.52	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	216/233 (93%)	211 (98%)	5 (2%)	0	100	100
1	B	229/233 (98%)	220 (96%)	9 (4%)	0	100	100
1	C	229/233 (98%)	223 (97%)	6 (3%)	0	100	100
All	All	674/699 (96%)	654 (97%)	20 (3%)	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	187/200 (94%)	185 (99%)	2 (1%)	65	79
1	B	193/200 (96%)	189 (98%)	4 (2%)	47	66
1	C	198/200 (99%)	194 (98%)	4 (2%)	48	67
All	All	578/600 (96%)	568 (98%)	10 (2%)	53	72

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	183	SER
1	A	248	CYS
1	B	104	SER
1	B	109	SER
1	B	230	GLN
1	B	235	SER
1	C	110	VAL
1	C	235	SER
1	C	248	CYS
1	C	261	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	182	ASN
1	A	203	ASN
1	A	243	ASN
1	B	134	ASN
1	B	149	GLN
1	B	151	HIS
1	B	230	GLN
1	C	190	ASN
1	C	203	ASN
1	C	241	HIS
1	C	253	GLN
1	C	289	HIS

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 1 ligands modelled in this entry, 1 is 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 ⓘ

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	220/233 (94%)	0.38	17 (7%) 19 18	22, 31, 71, 118	0
1	B	231/233 (99%)	0.63	30 (12%) 7 6	22, 31, 97, 163	0
1	C	231/233 (99%)	0.46	24 (10%) 11 11	23, 32, 87, 201	0
All	All	682/699 (97%)	0.49	71 (10%) 11 11	22, 31, 85, 201	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	244	TYR	6.6
1	C	225	TRP	6.1
1	A	252	ASP	5.9
1	B	251	GLU	5.9
1	B	260	ARG	5.9
1	B	247	ASN	5.6
1	B	219	PHE	5.6
1	B	244	TYR	5.4
1	C	242	ASP	5.4
1	C	226	TRP	5.4
1	B	217	GLY	5.4
1	C	223	VAL	5.1
1	A	305	ASN	5.0
1	B	218	ASN	4.9
1	B	216	ALA	4.1
1	C	216	ALA	4.0
1	C	227	ALA	4.0
1	B	206	GLU	3.8
1	B	243	ASN	3.7
1	B	261	CYS	3.6
1	C	217	GLY	3.6
1	C	243	ASN	3.5
1	B	241	HIS	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	245	GLU	3.4
1	B	248	CYS	3.4
1	B	229	HIS	3.3
1	C	261	CYS	3.2
1	C	229	HIS	3.2
1	B	255	GLY	3.2
1	B	204	ILE	3.2
1	A	216	ALA	3.1
1	B	249	ALA	3.1
1	A	250	GLU	3.1
1	C	251	GLU	3.1
1	B	242	ASP	3.0
1	C	76	SER	3.0
1	A	244	TYR	2.9
1	A	261	CYS	2.9
1	B	250	GLU	2.9
1	B	259	ASN	2.9
1	B	75	GLY	2.9
1	B	205	GLY	2.9
1	A	230	GLN	2.8
1	C	241	HIS	2.6
1	B	246	GLY	2.6
1	A	228	SER	2.5
1	B	225	TRP	2.5
1	B	279	THR	2.5
1	C	306	ASP	2.5
1	A	201	GLU	2.4
1	B	228	SER	2.4
1	C	224	GLN	2.3
1	C	248	CYS	2.3
1	B	277	ALA	2.3
1	A	248	CYS	2.3
1	A	249	ALA	2.3
1	A	217	GLY	2.3
1	A	197	LYS	2.3
1	C	245	GLU	2.3
1	A	262	HIS	2.2
1	C	106	ALA	2.2
1	A	138	LYS	2.2
1	C	272	SER	2.2
1	A	254	SER	2.1
1	C	252	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	215	LEU	2.1
1	B	221	PRO	2.1
1	A	181	LYS	2.1
1	C	228	SER	2.1
1	C	249	ALA	2.0
1	C	206	GLU	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](#)

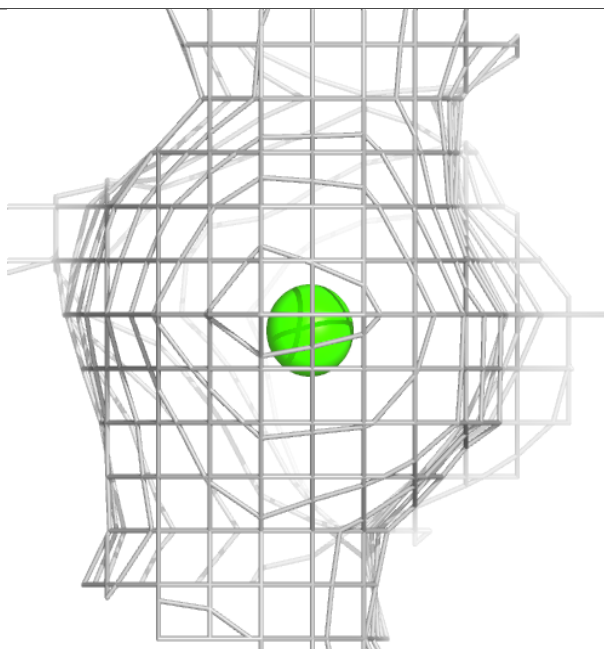
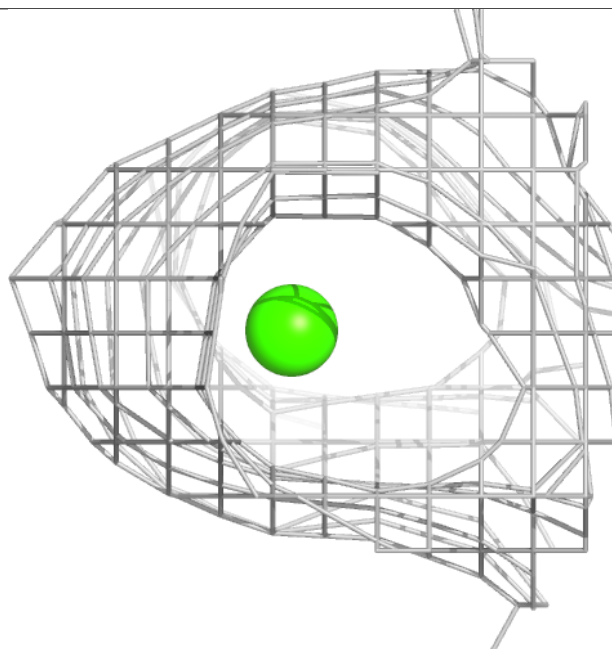
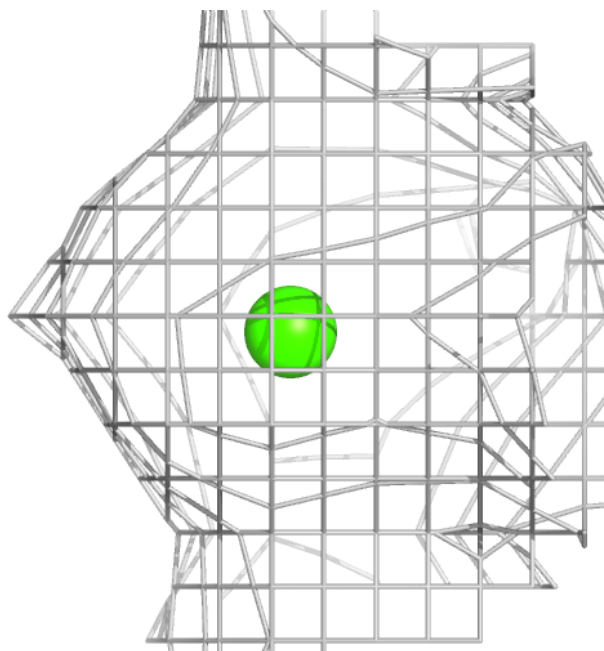
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CA	A	401	1/1	0.95	0.06	68,68,68,68	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 401:

$2mF_o-DF_c$ (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.