



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:38 PM UTC

PDB ID : 3PBB / pdb_00003pbb
Title : Crystal structure of human secretory glutaminyl cyclase in complex with PBD150
Authors : Huang, K.F.; Liaw, S.S.; Huang, W.L.; Chia, C.Y.; Lo, Y.C.; Chen, Y.L.; Wang, A.H.J.
Deposited on : 2010-10-20
Resolution : 1.95 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

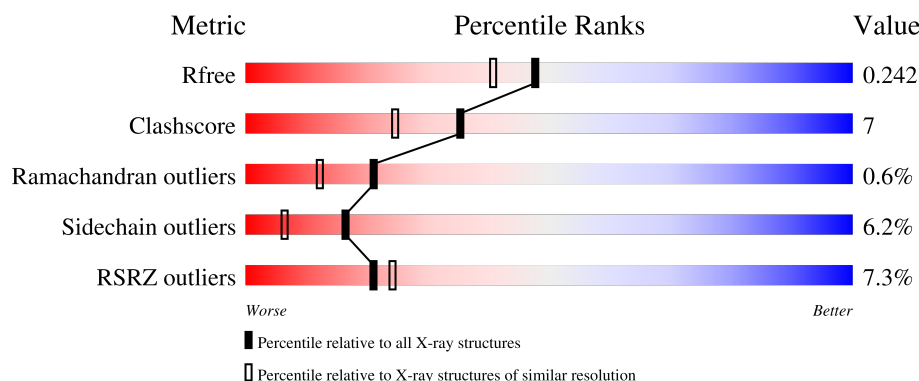
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	329	9% 80% 16% ...
1	B	329	5% 78% 16% 5% .

2 Entry composition [i](#)

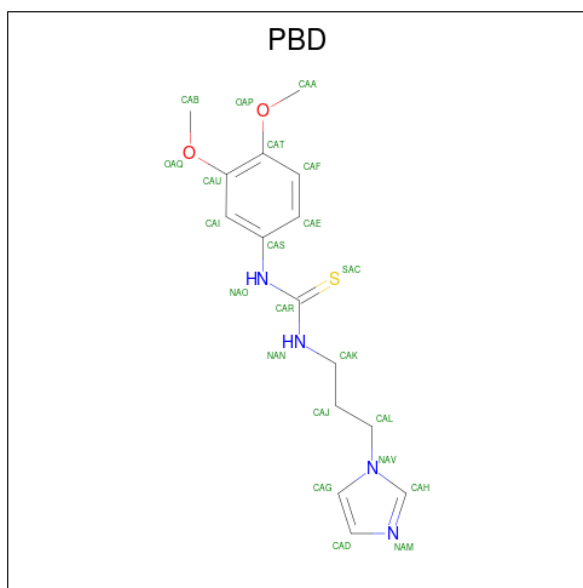
There are 4 unique types of molecules in this entry. The entry contains 5550 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Glutaminyl-peptide cyclotransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	323	Total	C	N	O	S	5	0	0
			2610	1673	450	478	9			
1	B	323	Total	C	N	O	S	5	0	0
			2610	1673	450	478	9			

- Molecule 2 is 1-(3,4-dimethoxyphenyl)-3-[3-(1H-imidazol-1-yl)propyl]thiourea (CCD ID: PBD) (formula: C₁₅H₂₀N₄O₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			22	15	4	2	1		
2	B	1	Total	C	N	O	S	0	0
			22	15	4	2	1		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	Zn 1	0	0
3	B	1	Total 1	Zn 1	0	0

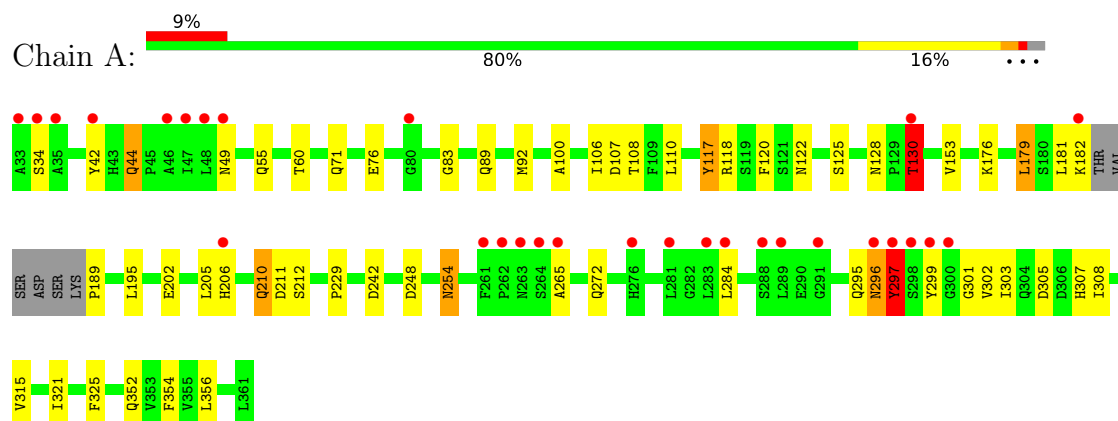
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	142	Total 142	O 142	0	0
4	B	142	Total 142	O 142	0	0

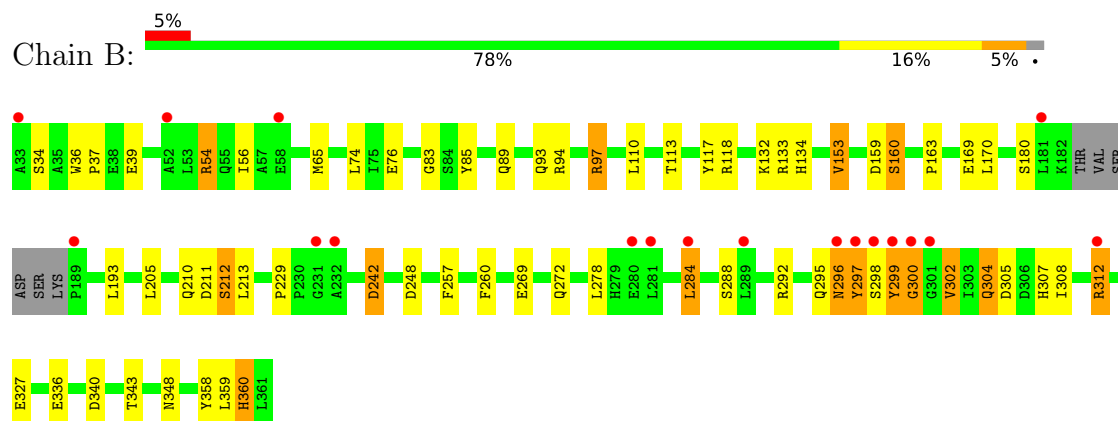
3 Residue-property plots [i](#)

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: Glutaminyl-peptide cyclotransferase



• Molecule 1: Glutaminyl-peptide cyclotransferase



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	155.75Å 155.75Å 80.52Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	30.00 – 1.95 30.00 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.2 (30.00-1.95) 99.1 (30.00-1.95)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.11 (at 1.93Å)	Xtriage
Refinement program	CNS, REFMAC 5.5.0102	Depositor
R, R_{free}	0.181 , 0.239 0.204 , 0.242	Depositor DCC
R_{free} test set	2704 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	29.8	Xtriage
Anisotropy	0.635	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 47.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.018 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5550	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.94% 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: PBD, ZN

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	1.16	4/2687 (0.1%)	1.23	21/3656 (0.6%)
1	B	1.18	5/2687 (0.2%)	1.13	6/3656 (0.2%)
All	All	1.17	9/5374 (0.2%)	1.18	27/7312 (0.4%)

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	1
1	B	0	1
All	All	0	2

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	308	ILE	CA-CB	7.97	1.59	1.53
1	B	308	ILE	CA-CB	7.43	1.58	1.54
1	B	308	ILE	CA-C	6.70	1.58	1.52
1	A	321	ILE	CA-CB	6.66	1.59	1.54
1	B	312	ARG	CG-CD	5.84	1.70	1.52
1	A	321	ILE	CA-C	5.83	1.56	1.52
1	B	213	LEU	C-O	5.49	1.30	1.23
1	A	303	ILE	N-CA	-5.30	1.39	1.46
1	B	348	ASN	C-O	5.30	1.30	1.24

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	229	PRO	CA-C-N	-9.07	111.05	120.03
1	A	229	PRO	C-N-CA	-9.07	111.05	120.03
1	A	71	GLN	CA-C-N	-8.48	110.99	119.56
1	A	71	GLN	C-N-CA	-8.48	110.99	119.56
1	A	130	THR	O-C-N	-6.86	112.91	122.37
1	B	260	PHE	N-CA-C	6.00	117.82	111.28
1	A	265	ALA	N-CA-C	5.99	118.77	111.82
1	B	113	THR	CA-C-N	-5.90	113.73	119.87
1	B	113	THR	C-N-CA	-5.90	113.73	119.87
1	B	302	VAL	CB-CA-C	-5.88	103.51	111.63
1	A	308	ILE	CA-C-N	-5.84	113.66	119.56
1	A	308	ILE	C-N-CA	-5.84	113.66	119.56
1	A	130	THR	N-CA-C	-5.76	106.02	113.16
1	A	297	TYR	CB-CA-C	5.72	119.18	109.80
1	A	325	PHE	N-CA-C	-5.65	101.91	110.39
1	A	254	ASN	CA-C-N	-5.60	114.20	119.85
1	A	254	ASN	C-N-CA	-5.60	114.20	119.85
1	A	202	GLU	N-CA-C	5.50	118.25	110.50
1	A	297	TYR	CA-CB-CG	5.18	123.22	113.90
1	A	100	ALA	CA-C-N	-5.14	114.45	122.16
1	A	100	ALA	C-N-CA	-5.14	114.45	122.16
1	A	128	ASN	CA-C-N	5.12	124.79	119.56
1	A	128	ASN	C-N-CA	5.12	124.79	119.56
1	B	257	PHE	CB-CA-C	-5.11	104.28	110.15
1	A	315	VAL	CA-C-N	5.06	124.82	119.76
1	A	315	VAL	C-N-CA	5.06	124.82	119.76
1	B	159	ASP	N-CA-CB	-5.02	103.56	111.23

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	130	THR	Mainchain
1	B	297	TYR	Peptide

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	2610	0	2529	32	1
1	B	2610	0	2529	44	1
2	A	22	0	20	0	0
2	B	22	0	20	2	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	142	0	0	7	1
4	B	142	0	0	5	1
All	All	5550	0	5098	76	2

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 (76) 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:312:ARG:HD3	4:B:616:HOH:O	1.67	0.92
1:B:304:GLN:HG2	2:B:381:PBD:SAC	2.17	0.84
1:B:76:GLU:HG3	1:B:153:VAL:HG13	1.60	0.83
1:B:54:ARG:HD2	4:B:603:HOH:O	1.80	0.82
1:A:210:GLN:HG2	4:A:428:HOH:O	1.80	0.81
1:A:302:VAL:HB	4:A:542:HOH:O	1.83	0.79
1:B:292:ARG:NH2	1:B:296:ASN:HD21	1.82	0.77
1:B:292:ARG:NH2	1:B:296:ASN:ND2	2.34	0.75
1:B:292:ARG:HH21	1:B:296:ASN:ND2	1.89	0.69
1:B:34:SER:O	1:B:37:PRO:HD2	1.93	0.68
1:A:295:GLN:C	1:A:297:TYR:H	2.06	0.63
1:B:134:HIS:ND1	4:B:635:HOH:O	2.30	0.63
1:A:60:THR:HB	1:A:352:GLN:OE1	1.99	0.61
1:B:304:GLN:CG	2:B:381:PBD:SAC	2.88	0.61
1:B:292:ARG:HH22	1:B:296:ASN:HD21	1.49	0.61
1:B:118:ARG:NH1	4:B:669:HOH:O	2.32	0.61
1:A:254:ASN:ND2	4:A:664:HOH:O	2.34	0.60
1:B:85:TYR:CE2	1:B:89:GLN:OE1	2.55	0.59
1:B:132:LYS:HG2	1:B:229:PRO:HG3	1.85	0.59
1:B:296:ASN:ND2	1:B:296:ASN:H	1.99	0.59
1:B:359:LEU:O	1:B:360:HIS:HB2	2.04	0.58
1:A:42:TYR:O	1:A:44:GLN:NE2	2.39	0.55
1:B:170:LEU:C	1:B:170:LEU:HD23	2.32	0.55
1:B:296:ASN:ND2	1:B:296:ASN:N	2.56	0.53
1:A:305:ASP:HB3	1:A:307:HIS:HD2	1.73	0.52
1:B:307:HIS:H	1:B:307:HIS:CD2	2.28	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:340:ASP:OD1	1:B:343:THR:OG1	2.22	0.51
1:B:305:ASP:HB3	1:B:307:HIS:HD2	1.76	0.51
1:A:307:HIS:CD2	1:A:307:HIS:H	2.29	0.50
1:B:299:TYR:O	1:B:300:GLY:C	2.55	0.50
1:A:302:VAL:CA	4:A:542:HOH:O	2.60	0.49
1:B:65:MET:HG3	1:B:169:GLU:HB2	1.94	0.49
1:A:107:ASP:HB3	1:A:122:ASN:HB2	1.94	0.49
1:B:295:GLN:HB3	1:B:297:TYR:HD2	1.78	0.49
1:A:49:ASN:HB2	4:A:644:HOH:O	2.12	0.49
1:A:299:TYR:CD1	1:A:301:GLY:O	2.66	0.48
1:B:305:ASP:HB3	1:B:307:HIS:CD2	2.48	0.48
1:B:296:ASN:N	1:B:296:ASN:HD22	2.10	0.48
1:A:189:PRO:N	4:A:627:HOH:O	2.47	0.47
1:A:305:ASP:HB3	1:A:307:HIS:CD2	2.49	0.47
1:A:92:MET:CE	1:A:106:ILE:HD11	2.44	0.47
1:A:295:GLN:C	1:A:297:TYR:N	2.72	0.46
1:B:76:GLU:HG3	1:B:153:VAL:CG1	2.38	0.46
1:B:242:ASP:OD2	1:B:358:TYR:OH	2.30	0.46
1:A:125:SER:HB3	1:A:195:LEU:HB2	1.97	0.46
1:B:97:ARG:HD2	4:B:537:HOH:O	2.15	0.46
1:A:302:VAL:C	4:A:542:HOH:O	2.60	0.45
1:A:248:ASP:OD2	1:A:305:ASP:OD2	2.34	0.45
1:B:160:SER:C	1:B:163:PRO:HD2	2.42	0.44
1:A:92:MET:SD	1:A:106:ILE:HD11	2.56	0.44
1:A:176:LYS:O	1:A:179:LEU:HB2	2.17	0.44
1:A:299:TYR:HD1	1:A:301:GLY:O	2.00	0.44
1:A:354:PHE:CD2	1:A:354:PHE:C	2.96	0.43
1:B:36:TRP:CG	1:B:37:PRO:HD3	2.53	0.43
1:B:278:LEU:HB3	1:B:284:LEU:HD13	2.01	0.43
1:B:94:ARG:HD2	1:B:94:ARG:HA	1.84	0.43
1:A:181:LEU:C	1:A:182:LYS:HG2	2.43	0.43
1:B:269:GLU:HA	1:B:272:GLN:HE21	1.84	0.42
1:A:76:GLU:O	1:A:83:GLY:HA3	2.19	0.42
1:A:356:LEU:HD23	1:A:356:LEU:HA	1.91	0.42
1:A:205:LEU:HD23	1:A:205:LEU:HA	1.67	0.42
1:B:292:ARG:HH21	1:B:296:ASN:CG	2.28	0.41
1:A:179:LEU:HD12	1:A:179:LEU:HA	1.76	0.41
1:A:211:ASP:O	1:A:212:SER:HB3	2.20	0.41
1:B:211:ASP:O	1:B:212:SER:HB3	2.21	0.41
1:A:108:THR:HA	1:A:120:PHE:O	2.20	0.41
1:B:304:GLN:HG2	1:B:304:GLN:H	1.52	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:76:GLU:O	1:B:83:GLY:HA3	2.21	0.41
1:A:92:MET:HE3	1:A:106:ILE:HD11	2.03	0.41
1:B:248:ASP:OD2	1:B:305:ASP:OD2	2.39	0.41
1:B:74:LEU:HD13	1:B:336:GLU:HB2	2.03	0.41
1:A:118:ARG:HH11	1:A:118:ARG:HD2	1.65	0.40
1:B:56:ILE:N	1:B:56:ILE:HD13	2.36	0.40
1:B:292:ARG:NH2	1:B:296:ASN:CG	2.80	0.40
1:B:39:GLU:OE1	1:B:133:ARG:NH1	2.51	0.40
1:B:193:LEU:HB2	1:B:359:LEU:HD11	2.03	0.40

All (2) 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)
1:B:312:ARG:NH1	4:A:500:HOH:O[9_454]	1.86	0.34
1:A:117:TYR:OH	4:B:475:HOH:O[5_565]	2.10	0.10

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	319/329 (97%)	298 (93%)	20 (6%)	1 (0%)	36	28
1	B	319/329 (97%)	300 (94%)	16 (5%)	3 (1%)	14	6
All	All	638/658 (97%)	598 (94%)	36 (6%)	4 (1%)	21	12

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	300	GLY
1	A	296	ASN
1	B	212	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	360	HIS

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	284/290 (98%)	268 (94%)	16 (6%)	19	8
1	B	284/290 (98%)	265 (93%)	19 (7%)	15	5
All	All	568/580 (98%)	533 (94%)	35 (6%)	16	6

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	SER
1	A	44	GLN
1	A	55	GLN
1	A	89	GLN
1	A	110	LEU
1	A	117	TYR
1	A	130	THR
1	A	153	VAL
1	A	179	LEU
1	A	206	HIS
1	A	210	GLN
1	A	242	ASP
1	A	272	GLN
1	A	284	LEU
1	A	296	ASN
1	A	297	TYR
1	B	54	ARG
1	B	93	GLN
1	B	97	ARG
1	B	110	LEU
1	B	117	TYR
1	B	153	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	160	SER
1	B	180	SER
1	B	205	LEU
1	B	210	GLN
1	B	242	ASP
1	B	284	LEU
1	B	288	SER
1	B	296	ASN
1	B	298	SER
1	B	299	TYR
1	B	302	VAL
1	B	304	GLN
1	B	327	GLU

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	44	GLN
1	A	89	GLN
1	A	210	GLN
1	A	228	HIS
1	A	259	ASN
1	A	295	GLN
1	A	296	ASN
1	B	89	GLN
1	B	276	HIS
1	B	279	HIS
1	B	296	ASN
1	B	307	HIS

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 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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
2	PBD	B	381	3	23,23,23	1.64	3 (13%)	29,29,29	1.71	8 (27%)
2	PBD	A	380	3	23,23,23	1.58	4 (17%)	29,29,29	1.99	12 (41%)

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
2	PBD	B	381	3	-	0/15/15/15	0/2/2/2
2	PBD	A	380	3	-	0/15/15/15	0/2/2/2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	380	PBD	CAS-NAO	-4.62	1.32	1.41
2	B	381	PBD	CAR-SAC	3.83	1.76	1.68
2	B	381	PBD	OAQ-CAU	3.49	1.42	1.37
2	A	380	PBD	CAR-SAC	3.40	1.75	1.68
2	B	381	PBD	CAS-NAO	-3.14	1.35	1.41
2	A	380	PBD	OAQ-CAB	2.61	1.50	1.42
2	A	380	PBD	CAR-NAN	2.16	1.37	1.33

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	381	PBD	CAG-NAV-CAH	4.77	112.66	106.71
2	A	380	PBD	CAG-NAV-CAH	4.34	112.12	106.71
2	A	380	PBD	CAB-OAQ-CAU	-3.63	112.19	117.51
2	A	380	PBD	NAO-CAR-NAN	3.04	121.23	114.19
2	A	380	PBD	CAF-CAT-CAU	2.98	123.66	119.71
2	A	380	PBD	NAV-CAH-NAM	-2.98	104.36	111.45
2	B	381	PBD	NAV-CAH-NAM	-2.94	104.44	111.45
2	A	380	PBD	CAJ-CAK-NAN	-2.91	104.03	112.20
2	A	380	PBD	CAD-NAM-CAH	2.89	111.01	105.47
2	B	381	PBD	CAD-NAM-CAH	2.65	110.56	105.47
2	B	381	PBD	CAS-NAO-CAR	-2.63	121.22	128.54
2	A	380	PBD	CAA-OAP-CAT	-2.62	113.67	117.51
2	A	380	PBD	OAP-CAT-CAU	-2.47	112.05	115.40
2	B	381	PBD	NAO-CAR-NAN	2.41	119.77	114.19
2	B	381	PBD	SAC-CAR-NAO	-2.34	117.53	124.33
2	A	380	PBD	SAC-CAR-NAO	-2.32	117.59	124.33
2	B	381	PBD	CAB-OAQ-CAU	-2.25	114.21	117.51
2	A	380	PBD	CAJ-CAL-NAV	-2.22	105.14	112.29
2	B	381	PBD	CAS-CAI-CAU	2.08	121.93	119.27
2	A	380	PBD	CAL-CAJ-CAK	-2.04	106.12	113.70

There are no chirality outliers.

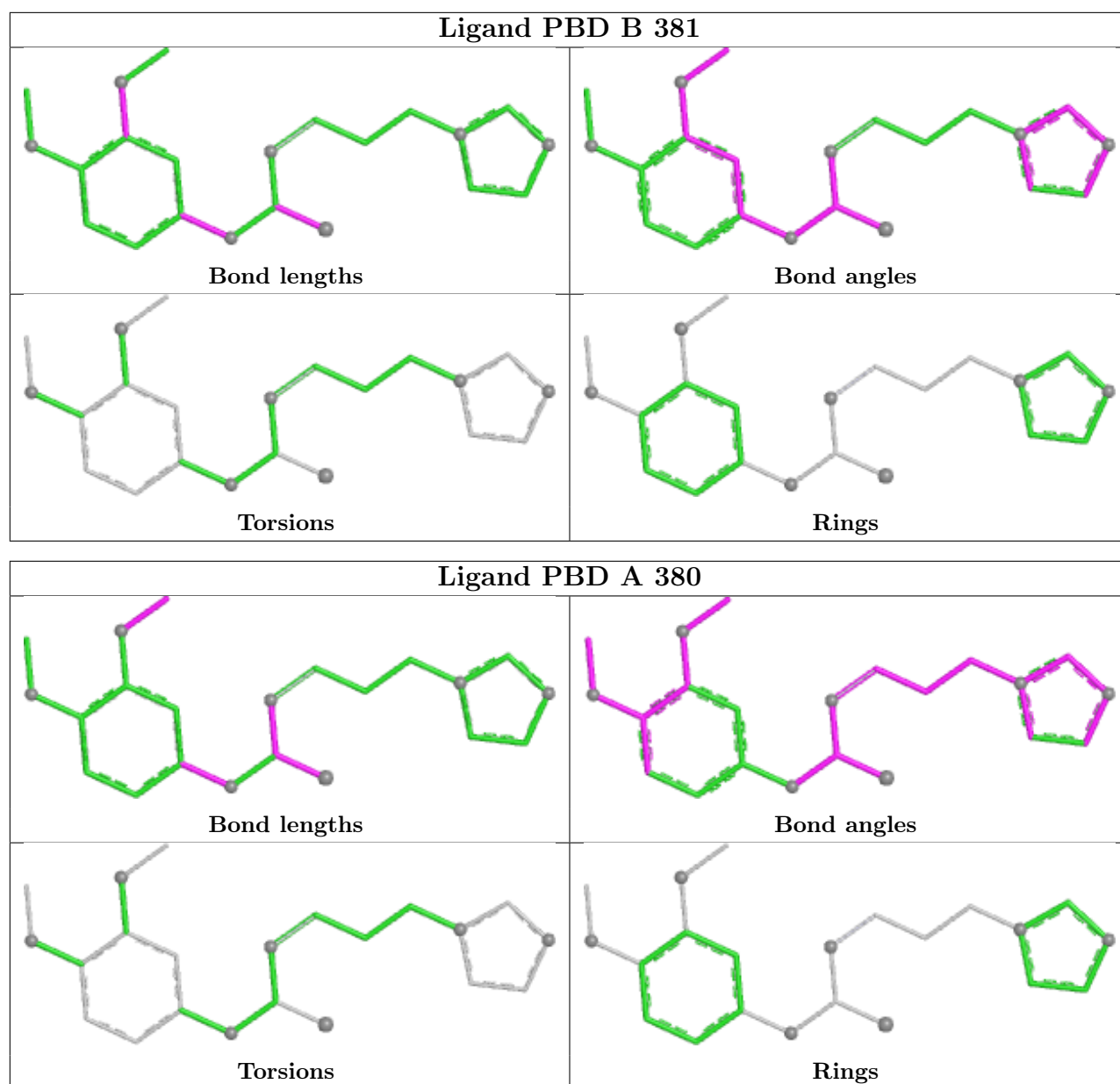
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	381	PBD	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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, 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	322/329 (97%)	0.61	29 (9%) 15 17	22, 38, 63, 77	0
1	B	322/329 (97%)	0.56	18 (5%) 30 35	23, 38, 56, 78	0
All	All	644/658 (97%)	0.58	47 (7%) 21 24	22, 38, 62, 78	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	262	PRO	6.2
1	B	297	TYR	5.7
1	B	300	GLY	5.4
1	B	299	TYR	5.1
1	B	33	ALA	4.6
1	A	300	GLY	4.2
1	A	297	TYR	3.6
1	B	298	SER	3.4
1	A	47	ILE	3.3
1	A	33	ALA	3.2
1	B	280	GLU	3.2
1	B	232	ALA	3.1
1	B	189	PRO	3.1
1	A	264	SER	2.9
1	A	261	PHE	2.8
1	A	48	LEU	2.8
1	A	296	ASN	2.8
1	A	206	HIS	2.8
1	A	182	LYS	2.7
1	A	299	TYR	2.7
1	A	281	LEU	2.7
1	A	289	LEU	2.7
1	B	296	ASN	2.7
1	A	291	GLY	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	283	LEU	2.6
1	A	46	ALA	2.6
1	A	42	TYR	2.5
1	A	265	ALA	2.5
1	B	181	LEU	2.5
1	A	35	ALA	2.4
1	A	34	SER	2.4
1	B	301	GLY	2.3
1	A	284	LEU	2.3
1	B	281	LEU	2.3
1	B	284	LEU	2.2
1	A	263	ASN	2.2
1	A	276	HIS	2.2
1	A	288	SER	2.2
1	A	298	SER	2.2
1	B	231	GLY	2.2
1	B	312	ARG	2.2
1	B	58	GLU	2.1
1	A	80	GLY	2.1
1	B	52	ALA	2.1
1	A	49	ASN	2.1
1	A	130	THR	2.0
1	B	289	LEU	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](#)

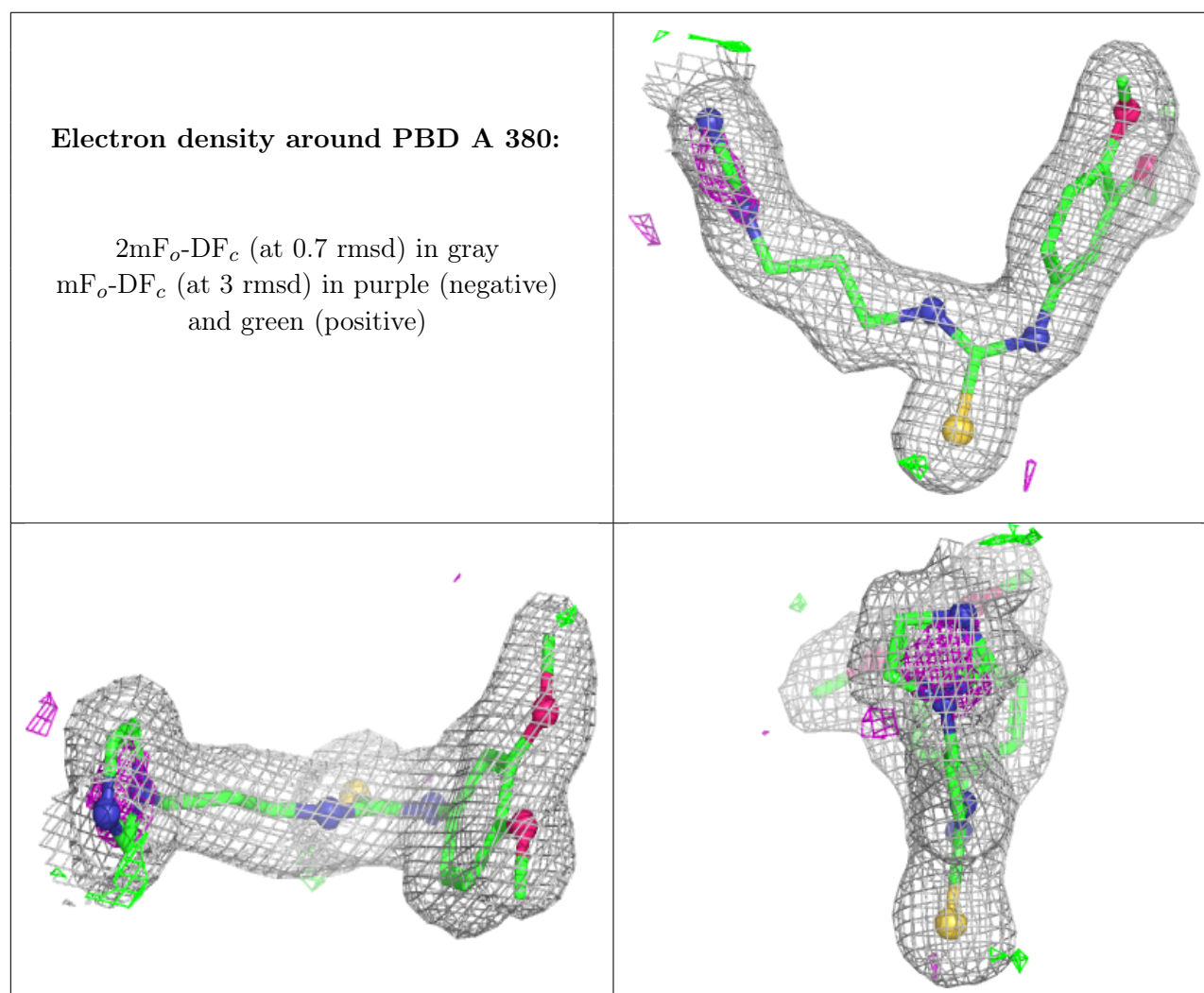
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists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

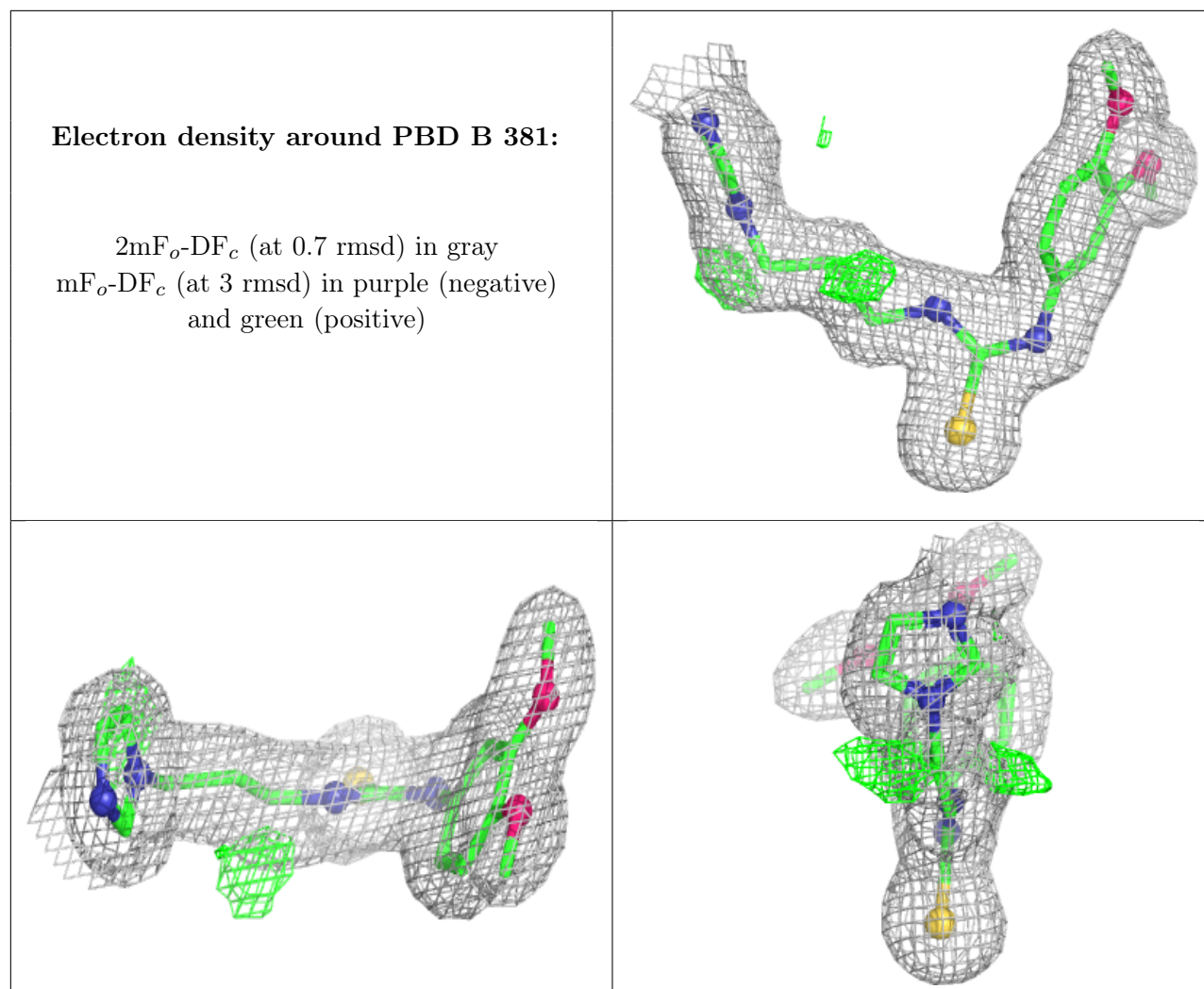
Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	PBD	A	380	22/22	0.95	0.07	19,30,35,38	0
2	PBD	B	381	22/22	0.97	0.06	19,28,35,35	0
3	ZN	A	391	1/1	0.99	0.03	25,25,25,25	0
3	ZN	B	392	1/1	0.99	0.03	26,26,26,26	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.