



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 05:00 AM UTC

PDB ID : 4NTW / pdb_00004ntw
Title : Structure of acid-sensing ion channel in complex with snake toxin
Authors : Bacongus, I.; Bohlen, C.J.; Goehring, A.; Julius, D.; Gouaux, E.
Deposited on : 2013-12-02
Resolution : 2.07 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

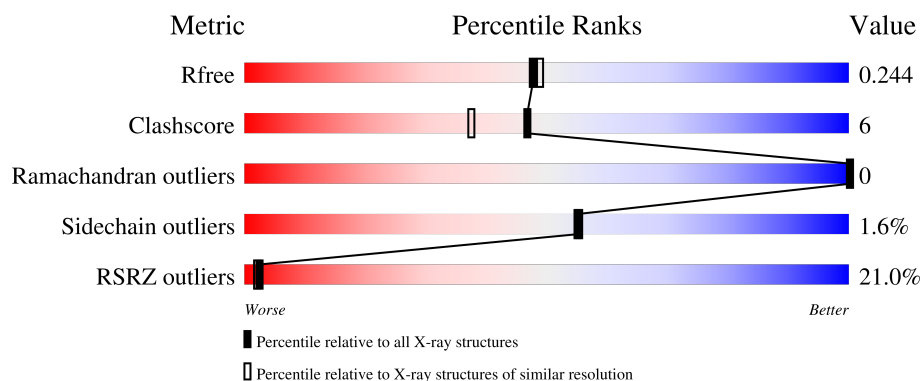
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.07 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	3774 (2.08-2.04)
Clashscore	190562	3883 (2.08-2.04)
Ramachandran outliers	187476	3860 (2.08-2.04)
Sidechain outliers	187428	3860 (2.08-2.04)
RSRZ outliers	180081	3775 (2.08-2.04)

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	450	17% 81% 9% 9%
2	B	60	5% 88% 12%
3	C	119	37% 79% 18% ..

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 5011 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 Acid-sensing ion channel 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	410	Total	C	N	O	S	0	0	0
			3238	2077	526	608	27			

- Molecule 2 is a protein called Neurotoxin MitTx-alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	60	Total	C	N	O	S	0	0	0
			493	314	83	89	7			

- Molecule 3 is a protein called Basic phospholipase A2 homolog Tx-beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	118	Total	C	N	O	S	0	0	0
			906	558	162	170	16			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O 14 8 1 5	0	0
4	A	1	Total C N O 14 8 1 5	0	0

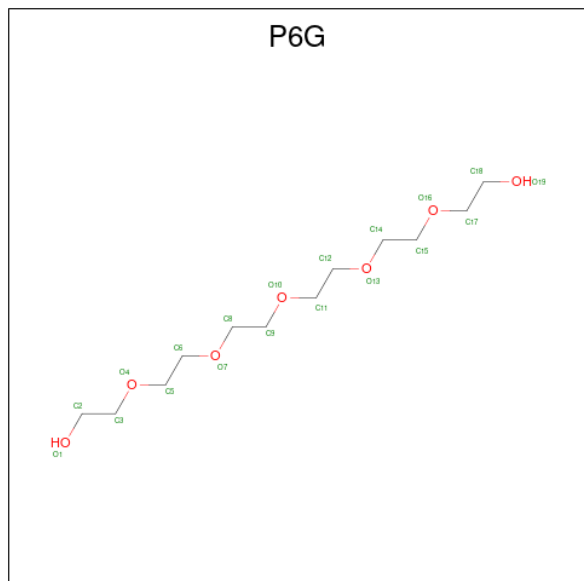
- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

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

- Molecule 6 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	2	Total Na 2 2	0	0
6	C	1	Total Na 1 1	0	0

- Molecule 7 is HEXAETHYLENE GLYCOL (CCD ID: P6G) (formula: C₁₂H₂₆O₇).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C O 19 12 7	0	0

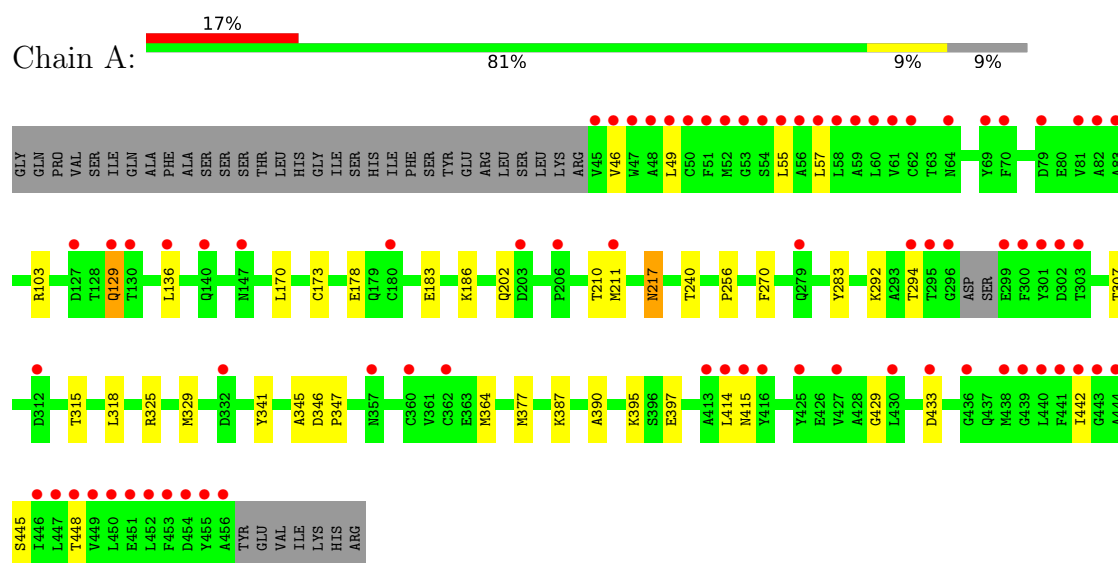
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	258	Total 258	O 258	0	0
8	B	31	Total 31	O 31	0	0
8	C	34	Total 34	O 34	0	0

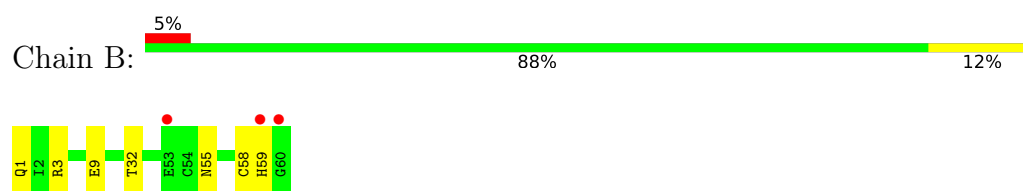
3 Residue-property plots [i](#)

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.

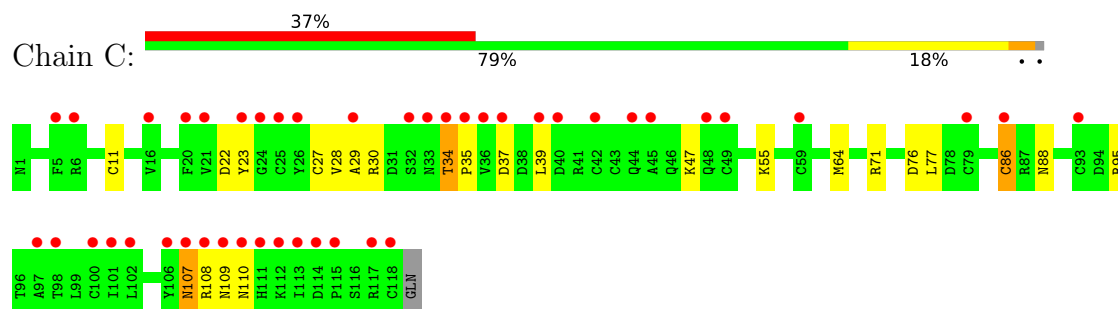
• Molecule 1: Acid-sensing ion channel 1



• Molecule 2: Neurotoxin MitTx-alpha



• Molecule 3: Basic phospholipase A2 homolog Tx-beta



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	151.93Å 151.93Å 123.79Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	28.00 – 2.07 28.00 – 2.07	Depositor EDS
% Data completeness (in resolution range)	94.2 (28.00-2.07) 93.6 (28.00-2.07)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.04 (at 1.96Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1402)	Depositor
R, R_{free}	0.206 , 0.246 0.206 , 0.244	Depositor DCC
R_{free} test set	3271 reflections (4.61%)	wwPDB-VP
Wilson B-factor (Å ²)	39.4	Xtriage
Anisotropy	0.117	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.019 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5011	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.16% 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: PCA, NA, CL, NAG, P6G

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	0/3314	0.77	0/4491
2	B	0.48	0/503	0.76	0/681
3	C	0.44	0/923	0.88	2/1253 (0.2%)
All	All	0.50	0/4740	0.79	2/6425 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	34	THR	CA-C-N	5.07	124.83	119.76
3	C	34	THR	C-N-CA	5.07	124.83	119.76

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	3238	0	3103	28	0
2	B	493	0	428	6	0
3	C	906	0	815	19	0
4	A	28	0	26	0	0
5	A	1	0	0	0	0
6	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	C	1	0	0	0	0
7	A	19	0	26	0	0
8	A	258	0	0	5	0
8	B	31	0	0	0	0
8	C	34	0	0	1	0
All	All	5011	0	4398	52	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 6.

All (52) 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)
3:C:107:ASN:OD1	3:C:109:ASN:N	2.19	0.74
1:A:325:ARG:HB2	1:A:329:MET:HE2	1.73	0.70
2:B:55:ASN:O	2:B:59:HIS:HB2	1.93	0.69
1:A:315:THR:HG23	1:A:329:MET:HE3	1.77	0.66
1:A:129:GLN:OE1	1:A:136:LEU:HD13	1.96	0.66
3:C:107:ASN:OD1	3:C:108:ARG:N	2.31	0.63
1:A:445:SER:H	1:A:448:THR:HB	1.63	0.62
1:A:210:THR:HG23	1:A:217:ASN:HB3	1.80	0.61
3:C:107:ASN:HD21	3:C:110:ASN:HB2	1.65	0.61
1:A:170:LEU:HD11	1:A:173:CYS:HB2	1.82	0.60
3:C:29:ALA:O	3:C:47:LYS:NZ	2.34	0.60
1:A:211:MET:O	1:A:414:LEU:HD11	2.02	0.60
3:C:107:ASN:HD21	3:C:110:ASN:CB	2.14	0.59
3:C:88:ASN:ND2	8:C:316:HOH:O	2.35	0.59
1:A:240:THR:OG1	8:A:812:HOH:O	2.17	0.58
1:A:256:PRO:HG2	1:A:307:THR:HG22	1.86	0.57
1:A:55:LEU:HD13	1:A:442:ILE:HD11	1.86	0.56
1:A:103:ARG:NH2	8:A:851:HOH:O	2.38	0.56
2:B:3:ARG:HD3	2:B:58:CYS:O	2.05	0.56
1:A:387:LYS:NZ	8:A:764:HOH:O	2.13	0.54
1:A:315:THR:HA	1:A:329:MET:CE	2.39	0.53
1:A:270:PHE:CD2	1:A:377:MET:HE2	2.43	0.53
1:A:292:LYS:NZ	1:A:294:THR:O	2.42	0.53
1:A:186:LYS:HE2	1:A:202:GLN:OE1	2.08	0.52
1:A:283:TYR:CE1	1:A:364:MET:HE2	2.45	0.52
1:A:325:ARG:CB	1:A:329:MET:HE2	2.39	0.51
2:B:32:THR:HA	2:B:59:HIS:HD2	1.76	0.50
3:C:23:TYR:OH	3:C:37:ASP:OD2	2.28	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:GLU:OE2	8:A:853:HOH:O	2.19	0.49
1:A:387:LYS:HG2	1:A:397:GLU:OE1	2.12	0.49
2:B:32:THR:HA	2:B:59:HIS:CD2	2.48	0.49
3:C:22:ASP:OD1	3:C:30:ARG:NH1	2.47	0.48
1:A:341:TYR:HA	1:A:345:ALA:HB3	1.95	0.47
1:A:429:GLY:O	1:A:433:ASP:HB2	2.16	0.46
3:C:77:LEU:HD22	3:C:95:ARG:HG3	1.99	0.44
2:B:3:ARG:NH1	2:B:59:HIS:O	2.51	0.43
3:C:22:ASP:HA	3:C:30:ARG:NH1	2.33	0.43
3:C:34:THR:HA	3:C:35:PRO:HD2	1.86	0.43
3:C:107:ASN:OD1	3:C:107:ASN:C	2.61	0.43
2:B:3:ARG:NH2	3:C:11:CYS:O	2.51	0.43
3:C:27:CYS:HA	3:C:28:VAL:HA	1.53	0.43
3:C:23:TYR:CZ	3:C:39:LEU:HD23	2.53	0.42
3:C:55:LYS:HE2	3:C:55:LYS:HB2	1.76	0.42
3:C:71:ARG:HB2	3:C:76:ASP:HB3	2.01	0.42
1:A:390:ALA:HB1	1:A:395:LYS:O	2.18	0.42
1:A:57:LEU:HD23	1:A:57:LEU:HA	1.87	0.42
3:C:64:MET:HE1	3:C:86:CYS:HB3	2.03	0.41
1:A:315:THR:HA	1:A:329:MET:HE3	2.03	0.41
1:A:318:LEU:HD12	1:A:329:MET:SD	2.61	0.41
1:A:346:ASP:HB2	1:A:347:PRO:HD3	2.02	0.40
1:A:415:ASN:N	8:A:801:HOH:O	2.55	0.40
3:C:107:ASN:ND2	3:C:110:ASN:HB2	2.34	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	406/450 (90%)	394 (97%)	12 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	58/60 (97%)	55 (95%)	3 (5%)	0	100	100
3	C	116/119 (98%)	110 (95%)	6 (5%)	0	100	100
All	All	580/629 (92%)	559 (96%)	21 (4%)	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	344/392 (88%)	339 (98%)	5 (2%)	57	58
2	B	53/54 (98%)	52 (98%)	1 (2%)	50	49
3	C	97/109 (89%)	95 (98%)	2 (2%)	47	45
All	All	494/555 (89%)	486 (98%)	8 (2%)	55	55

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

Mol	Chain	Res	Type
1	A	46	VAL
1	A	49	LEU
1	A	129	GLN
1	A	178	GLU
1	A	217	ASN
2	B	9	GLU
3	C	86	CYS
3	C	107	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	323	ASN
1	A	415	ASN
3	C	3	ASN

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Mol	Chain	Res	Type
3	C	57	HIS
3	C	110	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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	PCA	B	1	2	7,8,9	1.81	1 (14%)	9,10,12	1.85	4 (44%)

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	PCA	B	1	2	-	0/0/11/13	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	PCA	CD-N	4.60	1.45	1.34

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	PCA	CB-CA-N	2.63	110.49	103.24
2	B	1	PCA	CA-N-CD	-2.53	104.92	113.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	PCA	OE-CD-CG	-2.53	122.20	126.72
2	B	1	PCA	CG-CD-N	2.44	114.36	108.39

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	$\# Z > 2$
7	P6G	A	506	-	18,18,18	0.54	0	17,17,17	0.92	1 (5%)
4	NAG	A	501	1	14,14,15	0.33	0	17,19,21	0.42	0
4	NAG	A	502	1	14,14,15	0.26	0	17,19,21	0.83	1 (5%)

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
7	P6G	A	506	-	-	6/16/16/16	-
4	NAG	A	501	1	-	0/6/23/26	0/1/1/1
4	NAG	A	502	1	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	502	NAG	C1-O5-C5	2.90	116.08	112.19
7	A	506	P6G	C5-O4-C3	2.00	122.01	113.26

There are no chirality outliers.

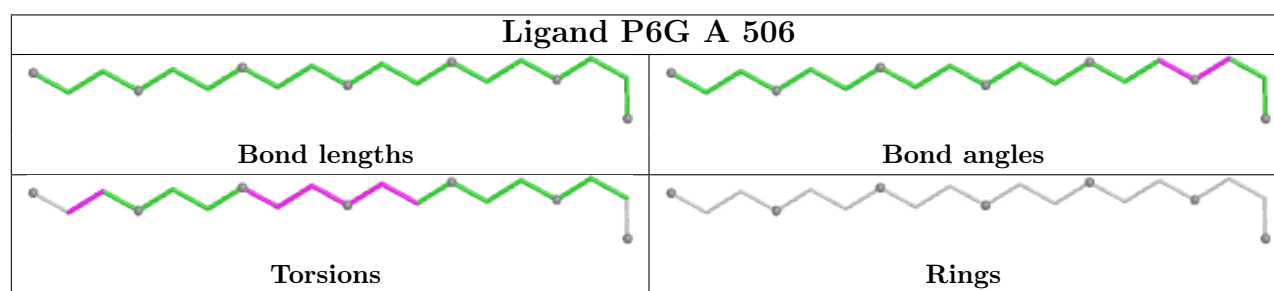
All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	506	P6G	O10-C11-C12-O13
7	A	506	P6G	O7-C8-C9-O10
7	A	506	P6G	O16-C17-C18-O19
4	A	502	NAG	O5-C5-C6-O6
7	A	506	P6G	C11-C12-O13-C14
7	A	506	P6G	C8-C9-O10-C11
7	A	506	P6G	C12-C11-O10-C9

There are no ring outliers.

No monomer is involved in short contacts.

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	410/450 (91%)	0.76	76 (18%) 3 3	24, 43, 107, 123	0
2	B	59/60 (98%)	0.78	3 (5%) 33 33	39, 49, 59, 60	0
3	C	118/119 (99%)	1.79	44 (37%) 1 0	38, 59, 85, 97	0
All	All	587/629 (93%)	0.97	123 (20%) 2 2	24, 48, 100, 123	0

All (123) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	442	ILE	7.0
1	A	47	TRP	6.6
1	A	46	VAL	5.7
1	A	300	PHE	5.6
3	C	118	CYS	5.3
1	A	54	SER	5.1
1	A	455	TYR	5.0
3	C	107	ASN	5.0
1	A	50	CYS	4.7
1	A	51	PHE	4.6
1	A	447	LEU	4.6
1	A	440	LEU	4.6
1	A	452	LEU	4.6
1	A	439	GLY	4.5
1	A	443	GLY	4.5
3	C	25	CYS	4.5
1	A	57	LEU	4.4
1	A	45	VAL	4.3
3	C	23	TYR	4.0
1	A	48	ALA	3.9
1	A	295	THR	3.9
3	C	113	ILE	3.8
1	A	451	GLU	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	81	VAL	3.8
1	A	441	PHE	3.8
1	A	49	LEU	3.7
3	C	36	VAL	3.7
1	A	444	ALA	3.7
3	C	49	CYS	3.7
1	A	52	MET	3.7
3	C	26	TYR	3.6
1	A	433	ASP	3.6
3	C	33	ASN	3.6
3	C	108	ARG	3.6
1	A	299	GLU	3.5
2	B	59	HIS	3.5
1	A	414	LEU	3.5
1	A	360	CYS	3.5
3	C	114	ASP	3.5
3	C	100	CYS	3.5
1	A	58	LEU	3.4
3	C	21	VAL	3.4
1	A	454	ASP	3.3
3	C	34	THR	3.3
1	A	450	LEU	3.2
1	A	456	ALA	3.2
1	A	296	GLY	3.2
1	A	453	PHE	3.2
1	A	436	GLY	3.1
1	A	83	ALA	3.1
1	A	294	THR	3.1
1	A	82	ALA	3.1
3	C	29	ALA	3.1
3	C	45	ALA	3.1
1	A	449	VAL	3.1
1	A	438	MET	3.0
1	A	55	LEU	3.0
3	C	106	TYR	3.0
1	A	180	CYS	2.9
3	C	79	CYS	2.9
3	C	101	ILE	2.9
1	A	129	GLN	2.9
3	C	86	CYS	2.9
3	C	32	SER	2.9
1	A	448	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	415	ASN	2.8
1	A	312	ASP	2.8
1	A	61	VAL	2.8
3	C	16	VAL	2.7
1	A	303	THR	2.7
3	C	48	GLN	2.7
3	C	39	LEU	2.7
1	A	427	VAL	2.7
1	A	430	LEU	2.6
1	A	301	TYR	2.6
1	A	425	TYR	2.6
1	A	53	GLY	2.6
3	C	42	CYS	2.6
3	C	35	PRO	2.6
1	A	64	ASN	2.5
3	C	98	THR	2.5
3	C	59	CYS	2.5
3	C	109	ASN	2.5
1	A	56	ALA	2.5
1	A	140	GLN	2.4
1	A	62	CYS	2.4
1	A	70	PHE	2.4
3	C	20	PHE	2.4
1	A	332	ASP	2.4
1	A	206	PRO	2.4
3	C	115	PRO	2.4
1	A	446	ILE	2.4
3	C	112	LYS	2.3
3	C	111	HIS	2.3
1	A	362	CYS	2.3
3	C	44	GLN	2.3
3	C	110	ASN	2.3
1	A	60	LEU	2.3
1	A	357	ASN	2.3
1	A	211	MET	2.3
3	C	40	ASP	2.2
1	A	69	TYR	2.2
3	C	93	CYS	2.2
1	A	136	LEU	2.2
1	A	416	TYR	2.2
1	A	79	ASP	2.2
3	C	5	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
3	C	97	ALA	2.1
3	C	6	ARG	2.1
1	A	127	ASP	2.1
1	A	203	ASP	2.1
1	A	302	ASP	2.1
1	A	59	ALA	2.1
3	C	24	GLY	2.1
1	A	413	ALA	2.1
1	A	279	GLN	2.1
2	B	60	GLY	2.1
1	A	147	ASN	2.0
3	C	117	ARG	2.0
2	B	53	GLU	2.0
3	C	102	LEU	2.0
3	C	37	ASP	2.0
1	A	130	THR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
2	PCA	B	1	8/9	0.91	0.11	45,48,51,53	0

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.

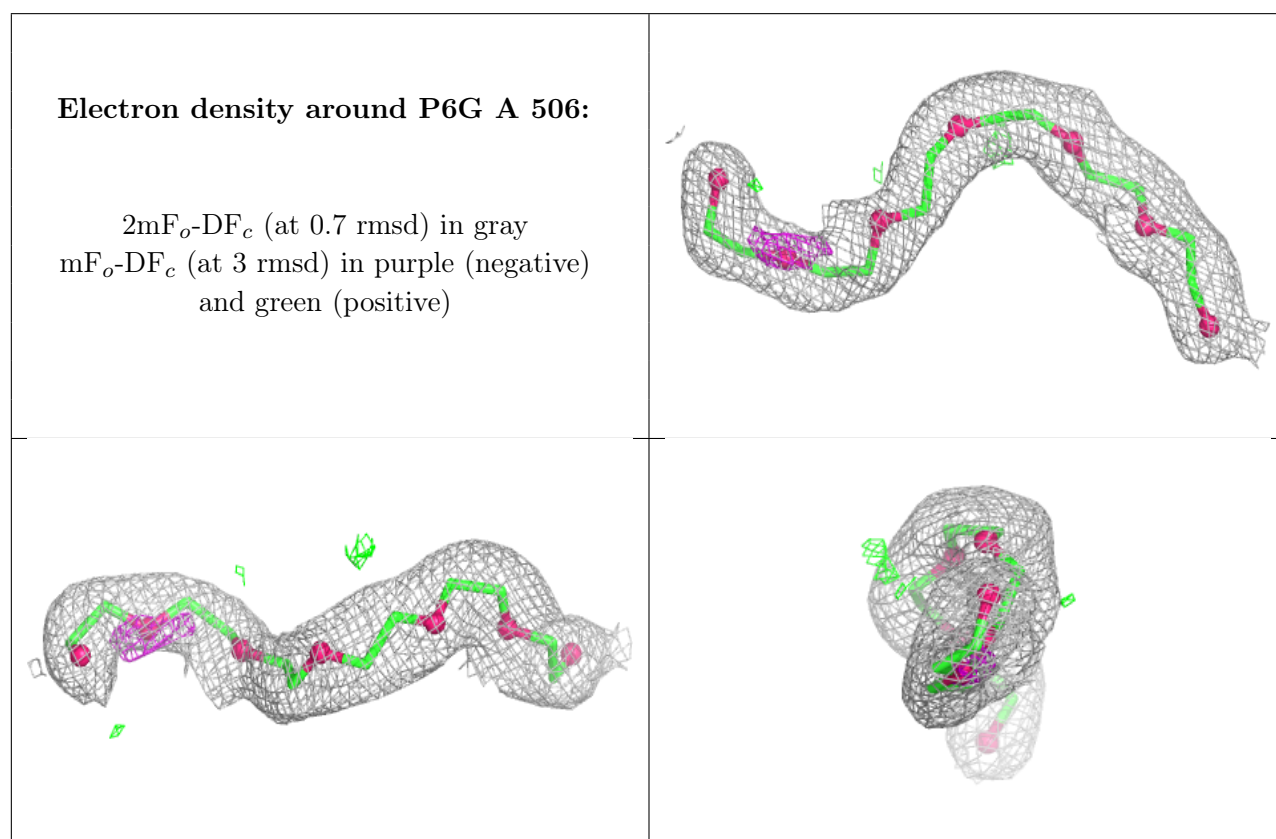
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NAG	A	502	14/15	0.59	0.13	84,87,90,92	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	NAG	A	501	14/15	0.66	0.16	77,81,87,88	0
6	NA	A	504	1/1	0.70	0.25	86,86,86,86	0
6	NA	C	201	1/1	0.90	0.12	54,54,54,54	0
7	P6G	A	506	19/19	0.90	0.13	37,46,61,67	0
5	CL	A	503	1/1	0.94	0.10	54,54,54,54	0
6	NA	A	505	1/1	0.96	0.09	44,44,44,44	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 ⓘ

There are no such residues in this entry.