



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 03:57 AM UTC

PDB ID : 4WV9 / pdb_00004wv9
Title : Crystal structure of acetylcholine binding protein (AChBP) from Aplysia Californica in complex with click chemistry compound (3-exo)-8,8-dimethyl-3-[4-(pyridin-4-yl)-1H-1,2,3-triazol-1-yl]-8-azoniabicyclo[3.2.1]octane
Authors : Talley, T.T.; Bobango, J.; Wu, J.M.; Sankaran, B.
Deposited on : 2014-11-04
Resolution : 2.00 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:

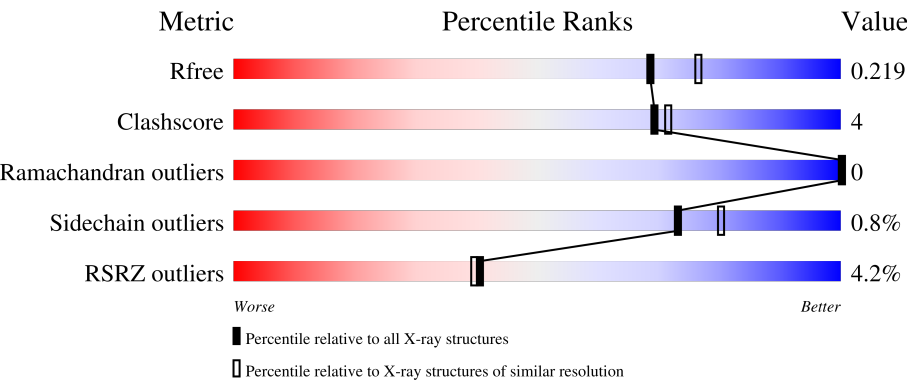
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	216	6% 88% 7% 5%
1	B	216	6% 91% 7% .
1	C	216	4% 85% 10% 5%
1	D	216	3% 87% 7% 6%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	E	216	2% 89% 8%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9042 atoms, of which 44 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 Soluble acetylcholine receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	206	Total	C	N	O	S	0	2	0
			1618	1025	265	320	8			
1	B	213	Total	C	N	O	S	0	2	0
			1704	1077	276	343	8			
1	C	205	Total	C	N	O	S	0	2	0
			1630	1031	268	323	8			
1	D	203	Total	C	N	O	S	0	2	0
			1597	1013	259	317	8			
1	E	210	Total	C	N	O	S	0	2	0
			1663	1051	273	331	8			

There are 45 discrepancies between the modelled and reference sequences:

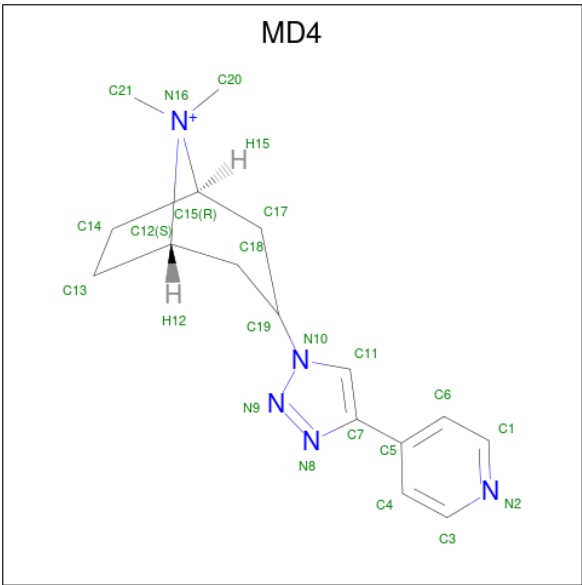
Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	ASP	-	expression tag	UNP Q8WSF8
A	-7	TYR	-	expression tag	UNP Q8WSF8
A	-6	LYS	-	expression tag	UNP Q8WSF8
A	-5	ASP	-	expression tag	UNP Q8WSF8
A	-4	ASP	-	expression tag	UNP Q8WSF8
A	-3	ASP	-	expression tag	UNP Q8WSF8
A	-2	ASP	-	expression tag	UNP Q8WSF8
A	-1	LYS	-	expression tag	UNP Q8WSF8
A	0	LEU	-	expression tag	UNP Q8WSF8
B	-8	ASP	-	expression tag	UNP Q8WSF8
B	-7	TYR	-	expression tag	UNP Q8WSF8
B	-6	LYS	-	expression tag	UNP Q8WSF8
B	-5	ASP	-	expression tag	UNP Q8WSF8
B	-4	ASP	-	expression tag	UNP Q8WSF8
B	-3	ASP	-	expression tag	UNP Q8WSF8
B	-2	ASP	-	expression tag	UNP Q8WSF8
B	-1	LYS	-	expression tag	UNP Q8WSF8
B	0	LEU	-	expression tag	UNP Q8WSF8
C	-8	ASP	-	expression tag	UNP Q8WSF8

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	-7	TYR	-	expression tag	UNP Q8WSF8
C	-6	LYS	-	expression tag	UNP Q8WSF8
C	-5	ASP	-	expression tag	UNP Q8WSF8
C	-4	ASP	-	expression tag	UNP Q8WSF8
C	-3	ASP	-	expression tag	UNP Q8WSF8
C	-2	ASP	-	expression tag	UNP Q8WSF8
C	-1	LYS	-	expression tag	UNP Q8WSF8
C	0	LEU	-	expression tag	UNP Q8WSF8
D	-8	ASP	-	expression tag	UNP Q8WSF8
D	-7	TYR	-	expression tag	UNP Q8WSF8
D	-6	LYS	-	expression tag	UNP Q8WSF8
D	-5	ASP	-	expression tag	UNP Q8WSF8
D	-4	ASP	-	expression tag	UNP Q8WSF8
D	-3	ASP	-	expression tag	UNP Q8WSF8
D	-2	ASP	-	expression tag	UNP Q8WSF8
D	-1	LYS	-	expression tag	UNP Q8WSF8
D	0	LEU	-	expression tag	UNP Q8WSF8
E	-8	ASP	-	expression tag	UNP Q8WSF8
E	-7	TYR	-	expression tag	UNP Q8WSF8
E	-6	LYS	-	expression tag	UNP Q8WSF8
E	-5	ASP	-	expression tag	UNP Q8WSF8
E	-4	ASP	-	expression tag	UNP Q8WSF8
E	-3	ASP	-	expression tag	UNP Q8WSF8
E	-2	ASP	-	expression tag	UNP Q8WSF8
E	-1	LYS	-	expression tag	UNP Q8WSF8
E	0	LEU	-	expression tag	UNP Q8WSF8

- Molecule 2 is (3-exo)-8,8-dimethyl-3-[4-(pyridin-4-yl)-1H-1,2,3-triazol-1-yl]-8-azoniabicyclo[3.2.1]octane (CCD ID: MD4) (formula: C₁₆H₂₂N₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	N	0	0
			43	16	22	5		
2	D	1	Total	C	H	N	0	0
			43	16	22	5		

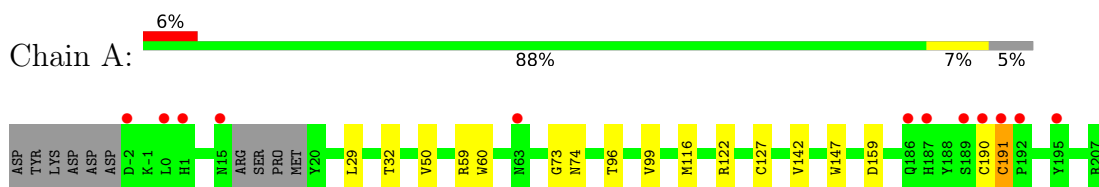
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	144	Total	O	0	0
			144	144		
3	B	150	Total	O	0	0
			150	150		
3	C	154	Total	O	0	0
			154	154		
3	D	149	Total	O	0	0
			149	149		
3	E	147	Total	O	0	0
			147	147		

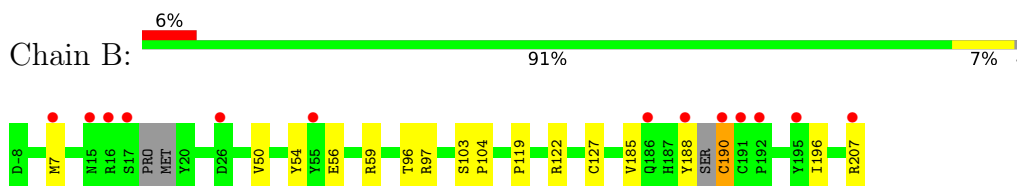
3 Residue-property plots [i](#)

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.

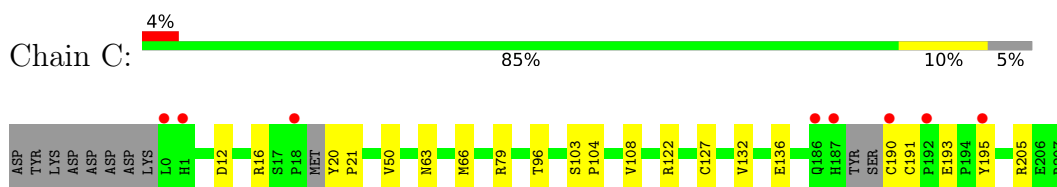
- Molecule 1: Soluble acetylcholine receptor



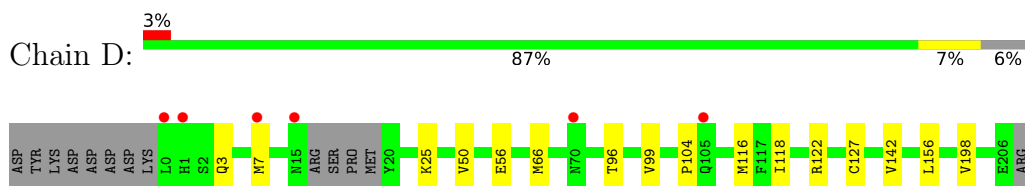
- Molecule 1: Soluble acetylcholine receptor



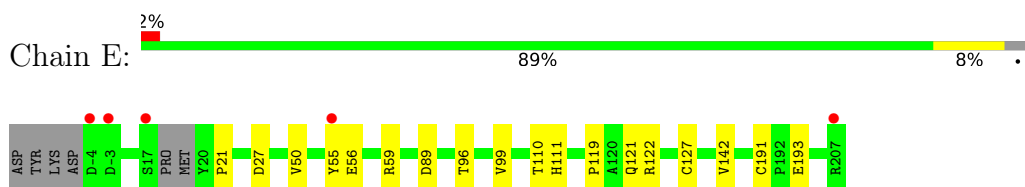
- Molecule 1: Soluble acetylcholine receptor



- Molecule 1: Soluble acetylcholine receptor



- Molecule 1: Soluble acetylcholine receptor



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	87.01Å 115.39Å 130.26Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.09 – 2.00 48.09 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.09-2.00) 96.1 (48.09-2.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.23 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.182 , 0.220 (Not available) , 0.219	Depositor DCC
R_{free} test set	4452 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	25.8	Xtriage
Anisotropy	0.338	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 42.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9042	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% 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: MD4

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	0.46	0/1662	0.67	0/2272
1	B	0.43	0/1749	0.73	2/2384 (0.1%)
1	C	0.47	0/1673	0.71	2/2281 (0.1%)
1	D	0.46	0/1641	0.72	0/2244
1	E	0.43	0/1708	0.71	0/2331
All	All	0.45	0/8433	0.71	4/11512 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	20	TYR	CA-C-N	5.28	126.44	119.84
1	C	20	TYR	C-N-CA	5.28	126.44	119.84
1	B	54	TYR	CA-C-N	-5.17	114.70	122.81
1	B	54	TYR	C-N-CA	-5.17	114.70	122.81

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	1618	0	1530	13	0
1	B	1704	0	1615	12	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	1630	0	1564	13	0
1	D	1597	0	1513	16	0
1	E	1663	0	1578	15	0
2	A	21	22	22	1	0
2	D	21	22	22	1	0
3	A	144	0	0	2	0
3	B	150	0	0	1	0
3	C	154	0	0	1	0
3	D	149	0	0	1	0
3	E	147	0	0	0	0
All	All	8998	44	7844	57	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 4.

All (57) 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:A:59:ARG:HD3	1:A:116:MET:HE1	1.60	0.83
1:C:191:CYS:HB3	1:C:193:GLU:OE2	1.89	0.72
1:D:3:GLN:NE2	1:E:27:ASP:OD2	2.27	0.68
1:A:29:LEU:HD11	1:A:60:TRP:HB2	1.78	0.66
1:D:7:MET:CE	1:E:21:PRO:HD3	2.30	0.62
1:A:59:ARG:HD3	1:A:116:MET:CE	2.29	0.62
1:A:190:CYS:SG	1:A:191:CYS:N	2.72	0.62
1:B:122:ARG:HD2	1:C:96:THR:O	2.02	0.60
1:C:79:ARG:HD2	1:C:108:VAL:HG22	1.83	0.60
1:C:63:ASN:HA	1:C:66:MET:HE2	1.86	0.58
1:B:50:VAL:HG21	1:B:127:CYS:SG	2.45	0.56
1:E:191:CYS:HB3	1:E:193:GLU:OE2	2.05	0.56
1:A:122:ARG:HD2	1:B:96:THR:O	2.06	0.56
1:E:99[B]:VAL:CG1	1:E:121:GLN:HB3	2.36	0.55
1:B:207:ARG:HA	3:B:412:HOH:O	2.06	0.55
1:D:7:MET:HE2	1:E:21:PRO:HD3	1.89	0.53
1:E:50:VAL:HG21	1:E:127:CYS:SG	2.49	0.53
1:C:63:ASN:CA	1:C:66:MET:HE2	2.40	0.52
1:A:96:THR:O	1:E:122:ARG:HD2	2.10	0.51
1:B:185:VAL:HG13	1:B:196:ILE:CD1	2.40	0.51
1:D:122:ARG:HD2	1:E:96:THR:O	2.10	0.50
1:C:122:ARG:HD2	1:D:96:THR:O	2.10	0.50
1:D:104:PRO:HG3	1:E:89:ASP:HB2	1.94	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:56:GLU:O	1:B:119:PRO:HD2	2.13	0.49
1:D:50:VAL:HG21	1:D:127:CYS:SG	2.52	0.49
1:B:59:ARG:HD3	1:B:59:ARG:C	2.38	0.48
1:A:32:THR:HG21	1:A:59:ARG:NH1	2.28	0.48
1:C:50:VAL:HG21	1:C:127:CYS:SG	2.53	0.48
1:D:7:MET:HE3	1:E:21:PRO:HD3	1.95	0.48
1:B:188:TYR:O	1:B:190:CYS:HB3	2.13	0.48
1:A:50:VAL:HG21	1:A:127:CYS:SG	2.53	0.47
1:D:99[B]:VAL:HG22	3:D:470:HOH:O	2.14	0.47
1:A:116:MET:HE3	2:A:301:MD4:N2	2.31	0.46
1:E:56:GLU:O	1:E:119:PRO:HD2	2.15	0.46
1:E:193:GLU:H	1:E:193:GLU:CD	2.24	0.46
1:D:156:LEU:HD13	1:D:198:VAL:HG23	1.98	0.45
1:A:147:TRP:HH2	1:E:55:TYR:CE1	2.34	0.45
3:A:424:HOH:O	1:B:97[B]:ARG:HD3	2.17	0.45
1:C:79:ARG:NH1	3:C:306:HOH:O	2.49	0.45
1:A:59:ARG:NH1	1:A:159:ASP:OD2	2.46	0.44
1:B:103:SER:HB2	1:B:104:PRO:HD2	1.98	0.44
1:C:132:VAL:HG23	1:C:205:ARG:HA	1.99	0.44
1:D:66:MET:HE2	1:D:66:MET:HB3	1.89	0.44
1:C:103:SER:HB2	1:C:104:PRO:HD2	2.00	0.44
1:D:116:MET:HE2	1:D:116:MET:HB2	1.82	0.44
1:D:25:LYS:HE2	1:D:25:LYS:HB3	1.86	0.43
1:D:118:ILE:HG22	1:D:118:ILE:O	2.18	0.43
1:B:7:MET:SD	1:C:21:PRO:HB3	2.59	0.42
1:B:50:VAL:CG2	1:B:127:CYS:SG	3.08	0.42
1:A:73:GLY:O	1:A:74:ASN:HB2	2.19	0.42
1:C:12:ASP:HA	1:C:16:ARG:HB2	2.01	0.42
1:D:118:ILE:HD13	2:D:301:MD4:C7	2.50	0.41
1:E:59:ARG:HD3	1:E:59:ARG:C	2.45	0.41
1:C:193:GLU:HG2	1:C:195:TYR:CE1	2.56	0.40
1:E:110:THR:HG22	1:E:111:HIS:N	2.36	0.40
1:A:99[B]:VAL:HG22	3:A:482:HOH:O	2.21	0.40
1:D:56:GLU:O	1:D:118:ILE:HA	2.21	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	204/216 (94%)	204 (100%)	0	0	100	100
1	B	167/216 (77%)	162 (97%)	5 (3%)	0	100	100
1	C	201/216 (93%)	197 (98%)	4 (2%)	0	100	100
1	D	201/216 (93%)	200 (100%)	1 (0%)	0	100	100
1	E	208/216 (96%)	206 (99%)	2 (1%)	0	100	100
All	All	981/1080 (91%)	969 (99%)	12 (1%)	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	180/197 (91%)	178 (99%)	2 (1%)	65	73
1	B	193/197 (98%)	192 (100%)	1 (0%)	81	87
1	C	185/197 (94%)	183 (99%)	2 (1%)	65	73
1	D	179/197 (91%)	178 (99%)	1 (1%)	78	85
1	E	187/197 (95%)	186 (100%)	1 (0%)	81	87
All	All	924/985 (94%)	917 (99%)	7 (1%)	73	80

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	142	VAL
1	A	191	CYS
1	B	190	CYS
1	C	136	GLU
1	C	190	CYS
1	D	142	VAL
1	E	142	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	GLN
1	A	74	ASN
1	A	187	HIS
1	B	57	GLN
1	B	162	GLN
1	C	15	ASN
1	C	162	GLN
1	D	15	ASN
1	D	38	GLN
1	D	70	ASN
1	E	111	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](#)

2 ligands are 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	MD4	A	301	-	24,24,24	2.23	4 (16%)	31,36,36	2.56	13 (41%)
2	MD4	D	301	-	24,24,24	2.15	4 (16%)	31,36,36	2.15	10 (32%)

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	MD4	A	301	-	-	0/8/33/33	0/5/4/4
2	MD4	D	301	-	-	0/8/33/33	0/5/4/4

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	MD4	C12-N16	-6.12	1.47	1.53
2	D	301	MD4	C12-N16	-5.83	1.47	1.53
2	D	301	MD4	N8-N9	5.42	1.40	1.32
2	A	301	MD4	C15-N16	-5.41	1.48	1.53
2	A	301	MD4	N8-N9	5.29	1.40	1.32
2	D	301	MD4	C15-N16	-5.04	1.48	1.53
2	A	301	MD4	N10-N9	3.93	1.40	1.35
2	D	301	MD4	N10-N9	3.50	1.39	1.35

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	MD4	C17-C15-C14	-7.15	106.58	113.14
2	D	301	MD4	C17-C15-C14	-6.10	107.54	113.14
2	A	301	MD4	C14-C15-N16	4.88	105.87	102.31
2	A	301	MD4	C18-C12-C13	-4.62	108.90	113.14
2	A	301	MD4	C19-N10-N9	-3.93	115.60	120.94
2	D	301	MD4	C18-C12-C13	-3.80	109.65	113.14
2	D	301	MD4	C17-C19-N10	-3.51	106.64	111.06

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	MD4	N10-N9-N8	-3.43	104.19	107.09
2	D	301	MD4	N10-N9-N8	-3.33	104.28	107.09
2	A	301	MD4	C17-C19-N10	-3.15	107.10	111.06
2	A	301	MD4	C13-C12-N16	3.15	104.60	102.31
2	D	301	MD4	C14-C15-N16	2.94	104.45	102.31
2	D	301	MD4	C13-C12-N16	2.91	104.43	102.31
2	D	301	MD4	C19-N10-N9	-2.91	116.98	120.94
2	A	301	MD4	C18-C19-C17	2.90	113.81	110.27
2	D	301	MD4	C5-C7-C11	-2.84	125.31	129.65
2	A	301	MD4	C21-N16-C12	-2.61	108.16	112.88
2	A	301	MD4	C4-C5-C7	-2.60	117.96	120.87
2	A	301	MD4	C5-C7-C11	-2.54	125.77	129.65
2	D	301	MD4	C5-C7-N8	2.45	125.99	122.05
2	A	301	MD4	C19-N10-C11	2.14	132.31	128.77
2	A	301	MD4	C3-N2-C1	2.09	121.65	116.86
2	D	301	MD4	C7-C11-N10	2.06	107.28	105.31

There are no chirality outliers.

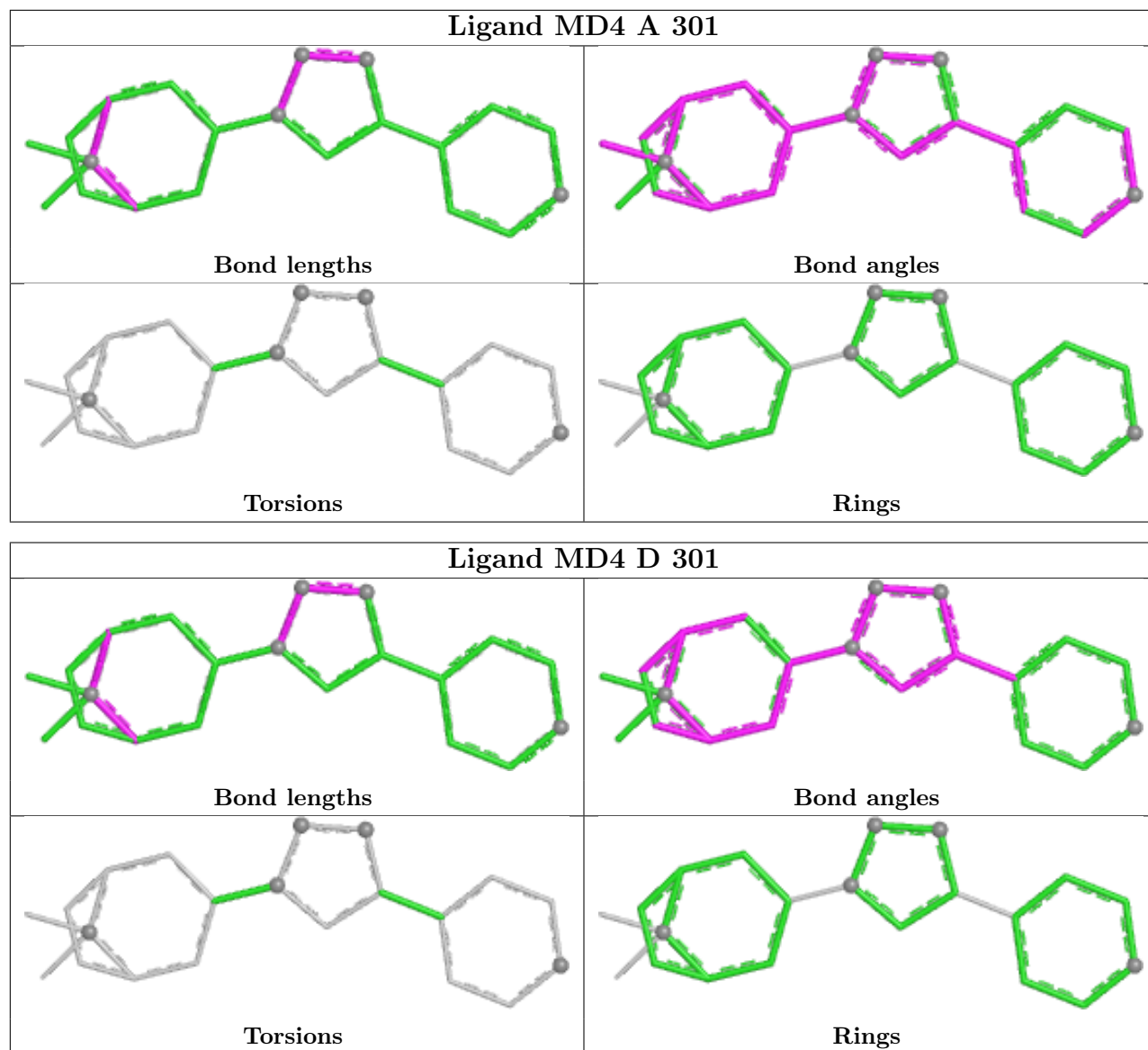
There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	MD4	1	0
2	D	301	MD4	1	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	206/216 (95%)	0.10	12 (5%)	29 27	13, 26, 58, 77	2 (0%)
1	B	213/216 (98%)	0.12	13 (6%)	27 26	13, 28, 52, 81	2 (0%)
1	C	205/216 (94%)	0.15	8 (3%)	43 42	13, 28, 50, 81	2 (0%)
1	D	203/216 (93%)	-0.02	6 (2%)	52 51	13, 27, 48, 66	2 (0%)
1	E	210/216 (97%)	0.01	5 (2%)	59 59	13, 27, 45, 65	2 (0%)
All	All	1037/1080 (96%)	0.07	44 (4%)	40 39	13, 27, 52, 81	10 (0%)

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	187	HIS	5.0
1	A	-2	ASP	4.7
1	B	190	CYS	4.1
1	C	0	LEU	4.1
1	C	186	GLN	4.0
1	A	189	SER	3.7
1	C	190	CYS	3.6
1	E	-4	ASP	3.6
1	C	18	PRO	3.6
1	D	0	LEU	3.5
1	A	190	CYS	3.3
1	B	191	CYS	3.2
1	C	192	PRO	3.2
1	D	1	HIS	3.2
1	C	1	HIS	3.1
1	B	17	SER	3.1
1	A	192	PRO	3.1
1	B	188	TYR	3.0
1	A	191	CYS	2.9
1	B	15	ASN	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	1	HIS	2.7
1	B	192	PRO	2.7
1	E	55	TYR	2.7
1	A	186	GLN	2.6
1	D	70	ASN	2.5
1	E	207	ARG	2.5
1	E	17	SER	2.5
1	A	187	HIS	2.4
1	A	0	LEU	2.4
1	B	55	TYR	2.3
1	C	195	TYR	2.3
1	A	15	ASN	2.3
1	B	7	MET	2.3
1	B	16	ARG	2.2
1	B	195	TYR	2.2
1	D	7	MET	2.2
1	D	15	ASN	2.1
1	D	105	GLN	2.1
1	B	26	ASP	2.1
1	A	195	TYR	2.1
1	B	207	ARG	2.1
1	B	186	GLN	2.0
1	E	-3	ASP	2.0
1	A	63	ASN	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](#)

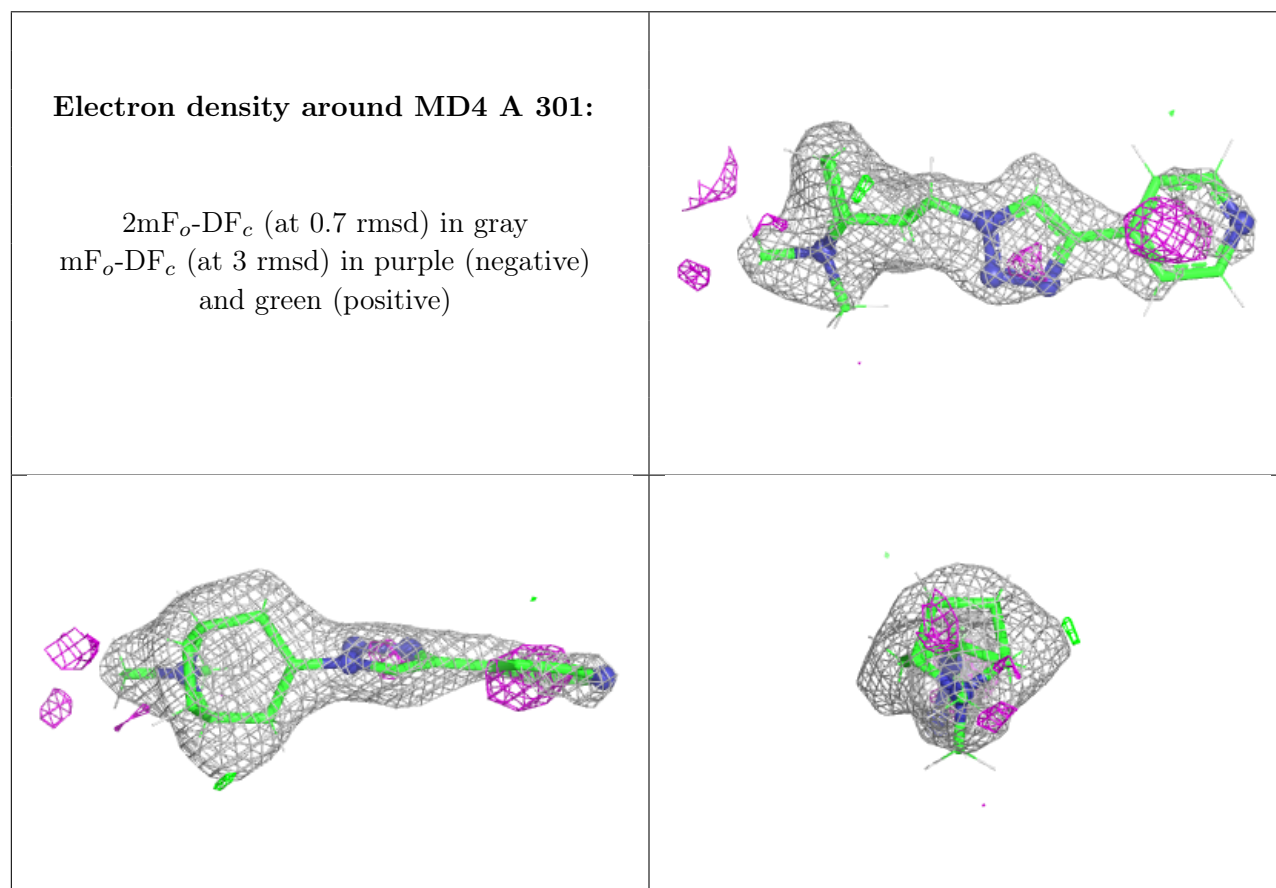
There are no oligosaccharides in this entry.

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.

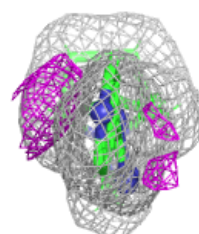
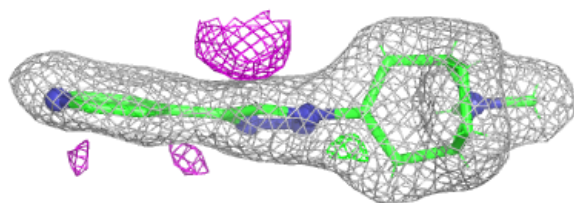
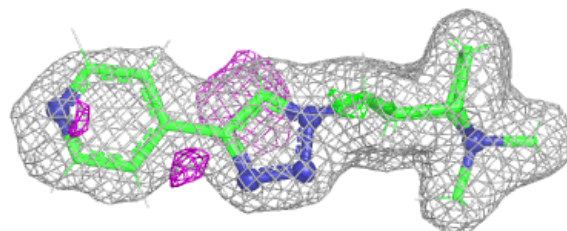
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MD4	A	301	21/21	0.82	0.13	32,47,68,75	0
2	MD4	D	301	21/21	0.94	0.09	21,27,43,49	0

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 MD4 D 301:

$2mF_o-DF_c$ (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.