



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2026 – 09:01 PM UTC

PDB ID : 2HA4 / pdb_00002ha4
Title : Crystal structure of mutant S203A of mouse acetylcholinesterase complexed with acetylcholine
Authors : Bourne, Y.; Radic, Z.; Sulzenbacher, G.; Kim, E.; Taylor, P.; Marchot, P.
Deposited on : 2006-06-12
Resolution : 2.56 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

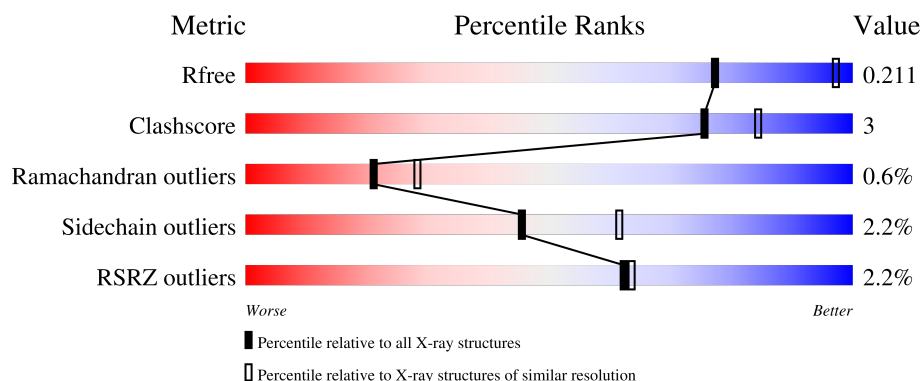
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.56 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	1853 (2.58-2.54)
Clashscore	190562	1897 (2.58-2.54)
Ramachandran outliers	187476	1875 (2.58-2.54)
Sidechain outliers	187428	1875 (2.58-2.54)
RSRZ outliers	180081	1853 (2.58-2.54)

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	543	2% 92% 7% .
1	B	543	3% 90% 8% ..

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8887 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.

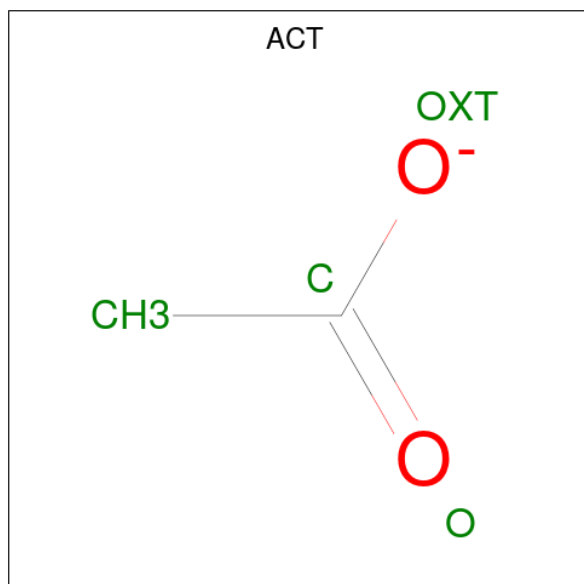
- Molecule 1 is a protein called Acetylcholinesterase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	537	Total	C	N	O	S	0	7	0
			4220	2707	732	767	14			
1	B	535	Total	C	N	O	S	0	1	0
			4179	2683	724	758	14			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	203	ALA	SER	engineered mutation	UNP P21836
B	203	ALA	SER	engineered mutation	UNP P21836

- Molecule 2 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



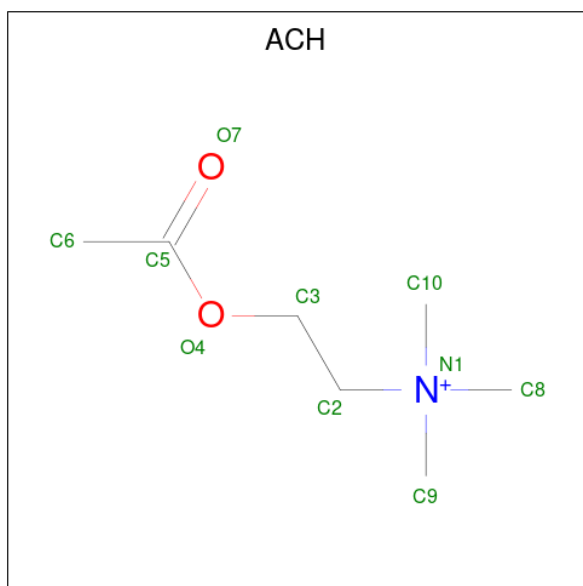
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		

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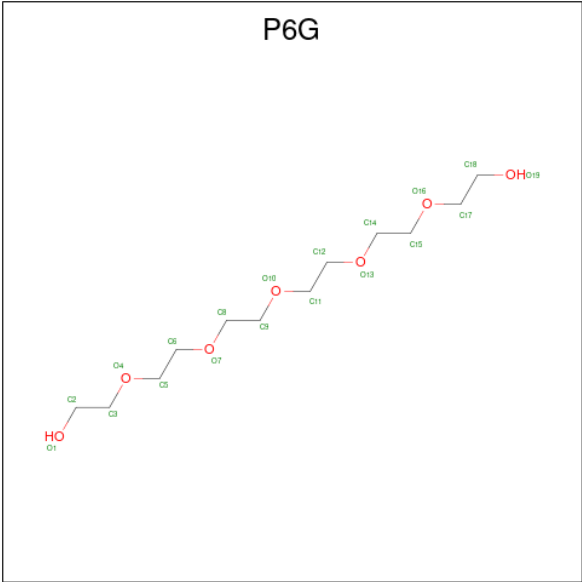
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is ACETYLCHOLINE (CCD ID: ACH) (formula: $C_7H_{16}NO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			10	7	1	2		
3	A	1	Total	C	N	O	0	0
			10	7	1	2		
3	B	1	Total	C	N	O	0	0
			10	7	1	2		
3	B	1	Total	C	N	O	0	0
			10	7	1	2		

- Molecule 4 is HEXAETHYLENE GLYCOL (CCD ID: P6G) (formula: $C_{12}H_{26}O_7$).



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

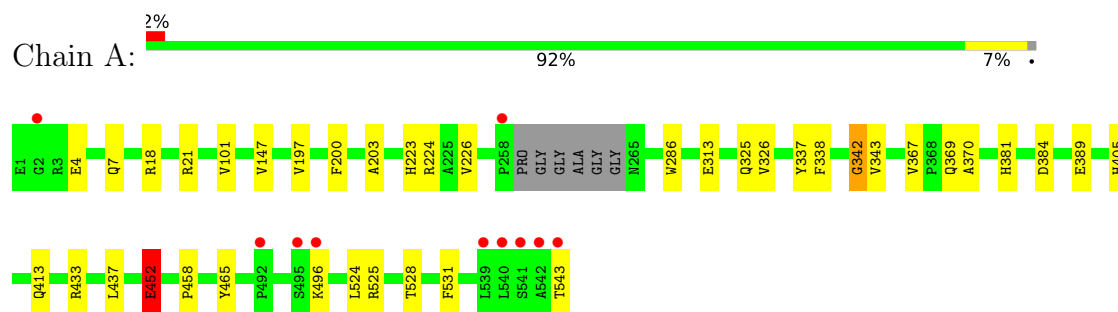
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	241	Total	O	0	0
			241	241		
5	B	180	Total	O	0	0
			180	180		

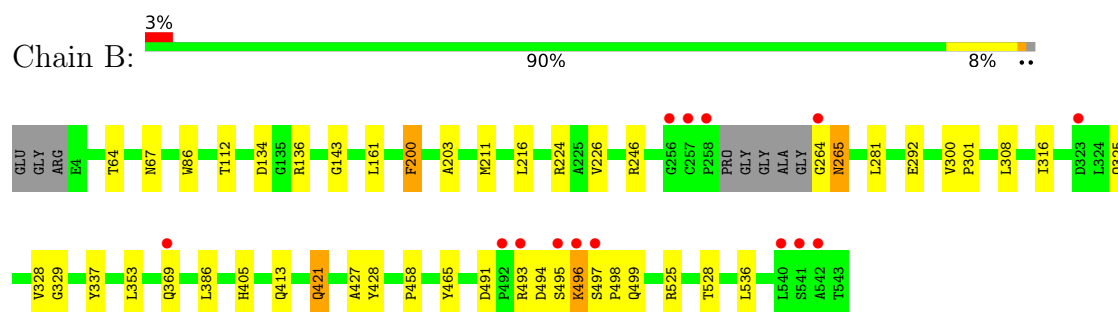
3 Residue-property plots [i](#)

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: Acetylcholinesterase



• Molecule 1: Acetylcholinesterase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	79.67Å 111.73Å 228.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.56 30.00 – 2.56	Depositor EDS
% Data completeness (in resolution range)	99.9 (30.00-2.56) 92.6 (30.00-2.56)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.18 (at 2.54Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.189 , 0.224 0.185 , 0.211	Depositor DCC
R_{free} test set	1350 reflections (2.03%)	wwPDB-VP
Wilson B-factor (Å ²)	35.3	Xtriage
Anisotropy	0.726	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 35.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8887	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 2.74% 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: ACH, P6G, ACT

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	0.68	0/4368	0.87	3/5968 (0.1%)
1	B	0.64	0/4307	0.86	0/5886
All	All	0.66	0/8675	0.87	3/11854 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	342	GLY	CA-C-N	-6.91	117.90	122.60
1	A	342	GLY	C-N-CA	-6.91	117.90	122.60
1	A	343	VAL	N-CA-C	5.79	112.83	107.56

There are no chirality outliers.

There are no planarity outliers.

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	4220	0	4103	21	0
1	B	4179	0	4072	26	0
2	A	4	0	3	1	0
2	B	4	0	3	1	0
3	A	20	0	32	5	0
3	B	20	0	32	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	19	0	26	1	0
5	A	241	0	0	1	0
5	B	180	0	0	2	0
All	All	8887	0	8271	50	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 (50) 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:B:602:ACH:H61	3:B:603:ACH:H61	1.50	0.90
1:B:496:LYS:HG2	1:B:498:PRO:HA	1.61	0.80
1:A:4:GLU:OE1	1:A:18:ARG:HD3	1.81	0.80
1:A:197:VAL:H	1:A:223:HIS:HD2	1.43	0.67
1:A:203:ALA:HB1	2:A:544:ACT:C	2.30	0.62
1:A:197:VAL:H	1:A:223:HIS:CD2	2.18	0.60
1:A:313:GLU:HG3	5:A:2083:HOH:O	2.04	0.58
1:B:203:ALA:HB1	2:B:601:ACT:C	2.34	0.58
1:B:369[B]:GLN:HE22	1:B:405:HIS:CE1	2.22	0.56
1:B:224:ARG:HG2	1:B:325:GLN:HB2	1.88	0.56
3:B:602:ACH:C6	3:B:603:ACH:H61	2.30	0.55
1:A:337:TYR:CE2	3:A:546:ACH:H62	2.42	0.54
1:B:458:PRO:HA	1:B:465:TYR:CD2	2.44	0.52
1:A:433:ARG:CZ	1:A:437:LEU:HD23	2.40	0.51
1:A:286:TRP:CE2	3:A:545:ACH:H102	2.46	0.51
1:A:224:ARG:HG2	1:A:325:GLN:HB2	1.94	0.50
1:B:496:LYS:HA	1:B:499:GLN:HE21	1.77	0.49
1:B:211:MET:HG2	1:B:308:LEU:HD21	1.93	0.49
1:B:264:GLY:O	1:B:265:ASN:HB3	2.13	0.49
1:A:458:PRO:HA	1:A:465:TYR:CD2	2.48	0.48
1:B:495:SER:O	1:B:496:LYS:CB	2.61	0.48
1:B:316:ILE:O	1:B:421:GLN:NE2	2.47	0.48
1:A:101:VAL:HG22	1:A:147:VAL:HG22	1.96	0.47
1:A:286:TRP:CZ2	3:A:545:ACH:H102	2.48	0.47
1:B:337:TYR:CE2	3:B:603:ACH:H63	2.50	0.47
1:B:491:ASP:HB3	1:B:494:ASP:HB3	1.95	0.47
1:A:338:PHE:CE2	3:A:546:ACH:H61	2.49	0.46
1:B:134:ASP:OD1	1:B:136:ARG:HB2	2.14	0.45
1:B:200:PHE:CB	1:B:226:VAL:HB	2.46	0.45
1:A:369[B]:GLN:HE22	1:A:405:HIS:CE1	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:112:THR:HG21	1:B:143:GLY:O	2.17	0.45
1:B:525:ARG:HG2	1:B:528:THR:HB	1.98	0.45
1:B:64:THR:HG23	5:B:715:HOH:O	2.16	0.44
1:B:86:TRP:CD2	3:B:603:ACH:H22	2.52	0.44
1:A:200:PHE:CB	1:A:226:VAL:HB	2.48	0.44
1:B:329:GLY:HA3	1:B:428:TYR:CZ	2.53	0.44
1:B:337:TYR:HE2	3:B:603:ACH:H63	1.84	0.43
1:B:536:LEU:HD23	1:B:536:LEU:HA	1.80	0.43
1:B:67:ASN:ND2	5:B:766:HOH:O	2.51	0.43
1:B:300:VAL:HB	1:B:301:PRO:HD2	2.01	0.43
1:A:528:THR:O	1:A:531:PHE:HB3	2.19	0.43
1:A:367:VAL:HG12	1:A:370:ALA:HB2	2.01	0.42
1:A:452:GLU:HG2	1:A:465:TYR:OH	2.19	0.42
1:B:264:GLY:O	1:B:265:ASN:CB	2.68	0.42
1:A:381:HIS:HA	4:A:1901:P6G:H172	2.01	0.42
3:A:546:ACH:H103	3:A:546:ACH:H63	2.01	0.41
1:B:328:VAL:O	1:B:427:ALA:HA	2.21	0.41
1:A:384:ASP:OD1	1:A:384:ASP:C	2.65	0.40
1:B:329:GLY:HA3	1:B:428:TYR:CE2	2.57	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	539/543 (99%)	520 (96%)	16 (3%)	3 (1%)	21	28
1	B	532/543 (98%)	509 (96%)	20 (4%)	3 (1%)	21	28
All	All	1071/1086 (99%)	1029 (96%)	36 (3%)	6 (1%)	21	28

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	265	ASN
1	B	496	LYS
1	A	496	LYS
1	A	452	GLU
1	B	497	SER
1	A	342	GLY

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	446/442 (101%)	438 (98%)	8 (2%)	51	67
1	B	440/442 (100%)	429 (98%)	11 (2%)	42	58
All	All	886/884 (100%)	867 (98%)	19 (2%)	45	63

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	ARG
1	A	326	VAL
1	A	389	GLU
1	A	413	GLN
1	A	452	GLU
1	A	524	LEU
1	A	525	ARG
1	A	543	THR
1	B	161	LEU
1	B	200	PHE
1	B	216	LEU
1	B	246	ARG
1	B	281	LEU
1	B	292	GLU
1	B	353	LEU
1	B	386	LEU
1	B	413	GLN
1	B	421	GLN

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Mol	Chain	Res	Type
1	B	493	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	100	ASN
1	A	223	HIS
1	A	287	HIS
1	A	322	GLN
1	A	499	GLN
1	B	181	GLN
1	B	405	HIS
1	B	421	GLN
1	B	474	GLN
1	B	499	GLN

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](#)

7 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
3	ACH	B	602	-	9,9,9	1.11	1 (11%)	12,12,12	0.79	0
3	ACH	A	545	-	9,9,9	1.16	1 (11%)	12,12,12	0.79	0
4	P6G	A	1901	-	18,18,18	0.53	0	17,17,17	0.30	0
2	ACT	B	601	-	3,3,3	0.71	0	3,3,3	1.22	0
3	ACH	B	603	-	9,9,9	1.17	1 (11%)	12,12,12	0.67	0
3	ACH	A	546	-	9,9,9	1.18	1 (11%)	12,12,12	0.87	0
2	ACT	A	544	-	3,3,3	0.74	0	3,3,3	1.51	1 (33%)

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
3	ACH	B	602	-	-	5/7/7/7	-
3	ACH	A	545	-	-	4/7/7/7	-
4	P6G	A	1901	-	-	6/16/16/16	-
3	ACH	B	603	-	-	2/7/7/7	-
3	ACH	A	546	-	-	3/7/7/7	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	546	ACH	O4-C5	2.89	1.47	1.33
3	B	602	ACH	O4-C5	2.59	1.45	1.33
3	B	603	ACH	O4-C5	2.53	1.45	1.33
3	A	545	ACH	O4-C5	2.52	1.45	1.33

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	544	ACT	OXT-C-CH3	2.07	123.75	115.05

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	602	ACH	C6-C5-O4-C3
3	B	602	ACH	O7-C5-O4-C3

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Mol	Chain	Res	Type	Atoms
3	B	603	ACH	O7-C5-O4-C3
3	B	603	ACH	C6-C5-O4-C3
3	B	602	ACH	C3-C2-N1-C9
3	A	545	ACH	C3-C2-N1-C10
3	B	602	ACH	C3-C2-N1-C8
3	B	602	ACH	C3-C2-N1-C10
3	A	546	ACH	C6-C5-O4-C3
4	A	1901	P6G	O1-C2-C3-O4
3	A	545	ACH	C3-C2-N1-C9
4	A	1901	P6G	O7-C8-C9-O10
3	A	546	ACH	O7-C5-O4-C3
3	A	545	ACH	C3-C2-N1-C8
4	A	1901	P6G	O13-C14-C15-O16
4	A	1901	P6G	C11-C12-O13-C14
4	A	1901	P6G	C2-C3-O4-C5
4	A	1901	P6G	C6-C5-O4-C3
3	A	545	ACH	C2-C3-O4-C5
3	A	546	ACH	C2-C3-O4-C5

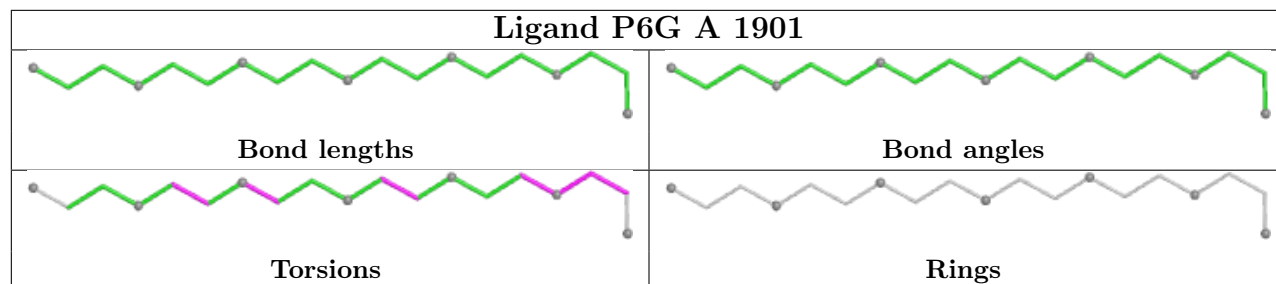
There are no ring outliers.

7 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	602	ACH	2	0
3	A	545	ACH	2	0
4	A	1901	P6G	1	0
2	B	601	ACT	1	0
3	B	603	ACH	5	0
3	A	546	ACH	3	0
2	A	544	ACT	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	537/543 (98%)	-0.22	10 (1%) 66 67	19, 34, 56, 85	6 (1%)
1	B	535/543 (98%)	-0.04	14 (2%) 57 59	25, 40, 62, 85	1 (0%)
All	All	1072/1086 (98%)	-0.13	24 (2%) 62 63	19, 37, 61, 85	7 (0%)

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	497	SER	6.4
1	B	264	GLY	5.7
1	A	543	THR	4.6
1	A	258	PRO	4.3
1	B	540	LEU	4.1
1	B	258	PRO	4.1
1	B	495	SER	4.0
1	B	496	LYS	3.8
1	A	542	ALA	3.8
1	B	493	ARG	3.8
1	A	540	LEU	3.6
1	A	541	SER	3.1
1	B	542	ALA	3.0
1	B	541	SER	2.8
1	B	323	ASP	2.6
1	A	496	LYS	2.6
1	A	492	PRO	2.3
1	B	492	PRO	2.3
1	A	2	GLY	2.2
1	A	539	LEU	2.2
1	B	257	CYS	2.2
1	A	495	SER	2.2
1	B	369[A]	GLN	2.1
1	B	256	GLY	2.1

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](#)

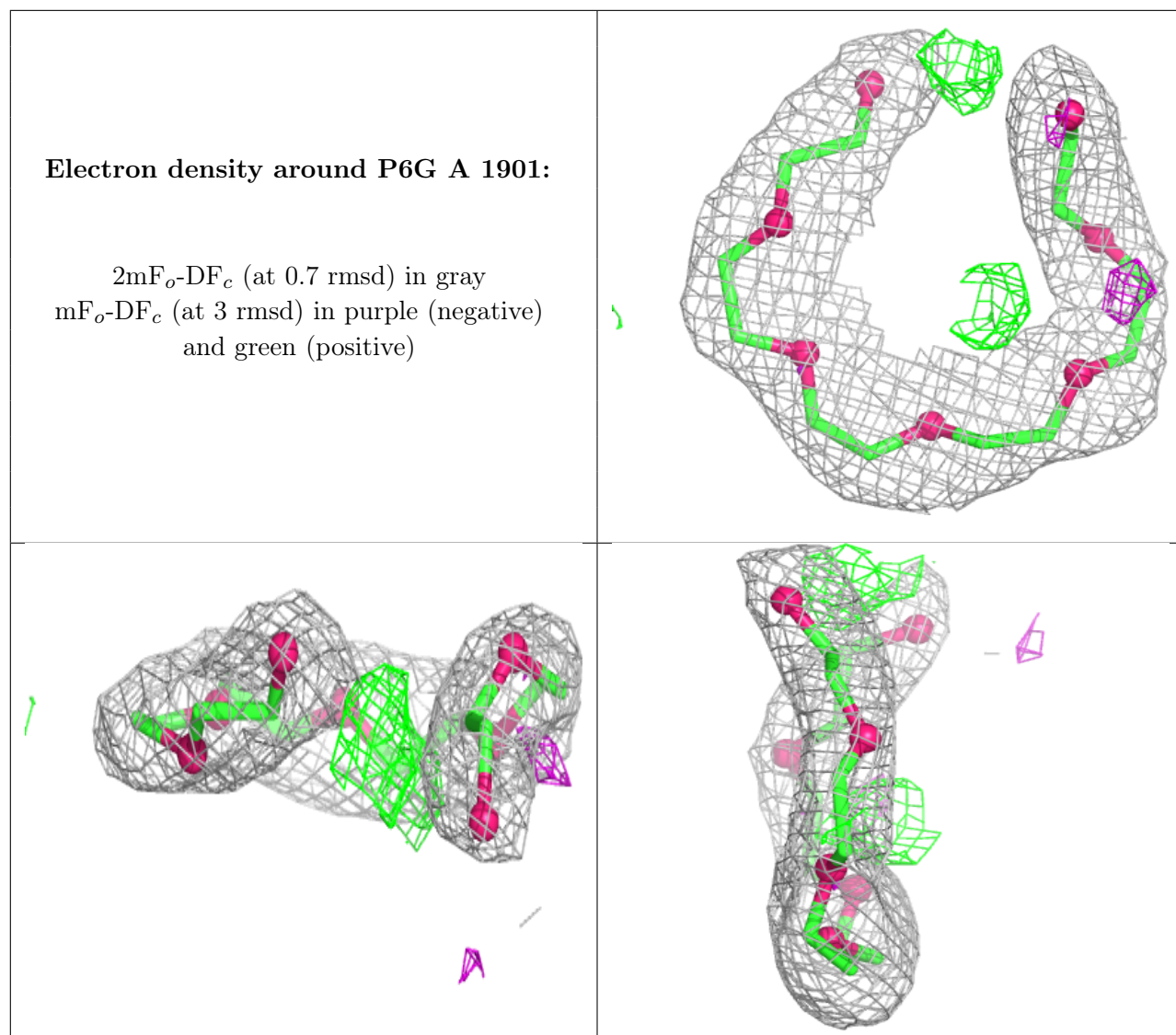
There are no oligosaccharides in this entry.

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
3	ACH	B	602	10/10	0.90	0.19	60,63,65,66	0
3	ACH	A	546	10/10	0.91	0.16	42,48,59,60	0
4	P6G	A	1901	19/19	0.91	0.14	52,57,60,60	0
3	ACH	B	603	10/10	0.92	0.14	51,52,56,56	0
2	ACT	B	601	4/4	0.93	0.14	39,40,40,40	0
3	ACH	A	545	10/10	0.94	0.12	44,47,47,48	0
2	ACT	A	544	4/4	0.96	0.08	34,35,35,35	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.