



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 06:06 PM UTC

PDB ID : 2JGJ / pdb_00002jgj
Title : Crystal structure of mouse acetylcholinesterase inhibited by aged methamidophos
Authors : Hornberg, A.; Tunemalm, A.-K.; Ekstrom, F.
Deposited on : 2007-02-13
Resolution : 2.50 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

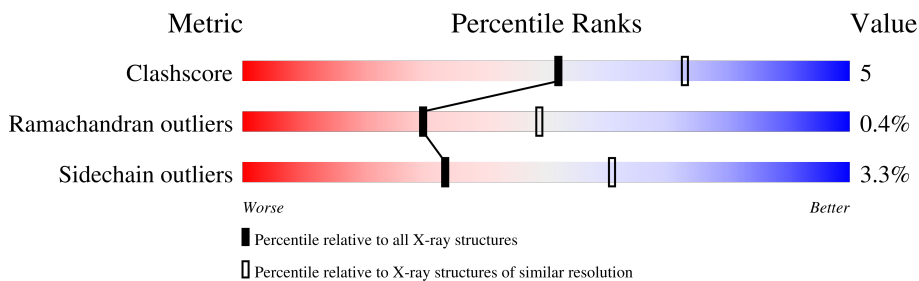
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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))
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	549	 86% 12% .
1	B	549	 82% 13% . .

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8561 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.

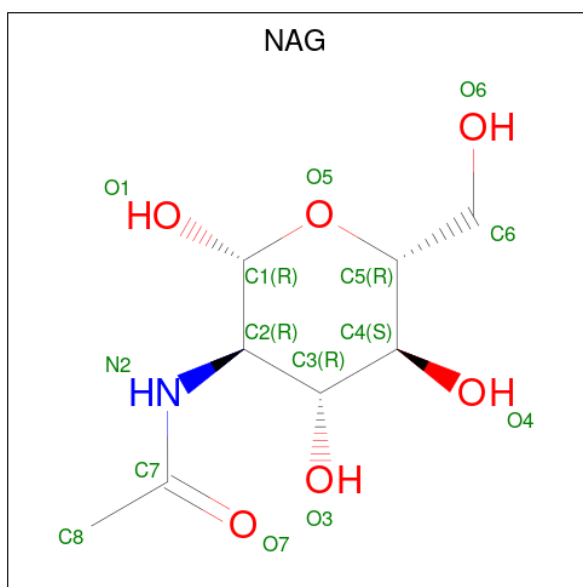
- Molecule 1 is a protein called ACETYLCHOLINESTERASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	535	Total	C	N	O	P	S	0	1	0
			4195	2685	729	765	2	14			
1	B	530	Total	C	N	O	P	S	0	1	1
			4133	2646	717	754	2	14			

There are 14 discrepancies between the modelled and reference sequences:

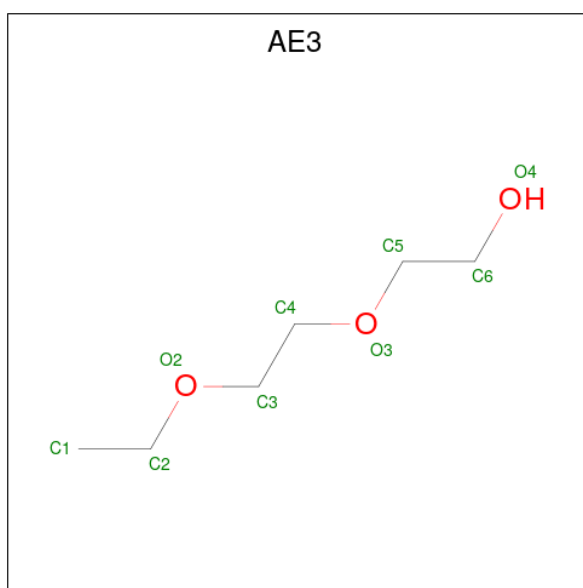
Chain	Residue	Modelled	Actual	Comment	Reference
A	203	SVV	SER	microheterogeneity	UNP P21836
A	203	SVW	SER	microheterogeneity	UNP P21836
A	544	ALA	-	expression tag	UNP P21836
A	545	THR	-	expression tag	UNP P21836
A	546	GLU	-	expression tag	UNP P21836
A	547	ALA	-	expression tag	UNP P21836
A	548	PRO	-	expression tag	UNP P21836
B	203	SVV	SER	microheterogeneity	UNP P21836
B	203	SVW	SER	microheterogeneity	UNP P21836
B	544	ALA	-	expression tag	UNP P21836
B	545	THR	-	expression tag	UNP P21836
B	546	GLU	-	expression tag	UNP P21836
B	547	ALA	-	expression tag	UNP P21836
B	548	PRO	-	expression tag	UNP P21836

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



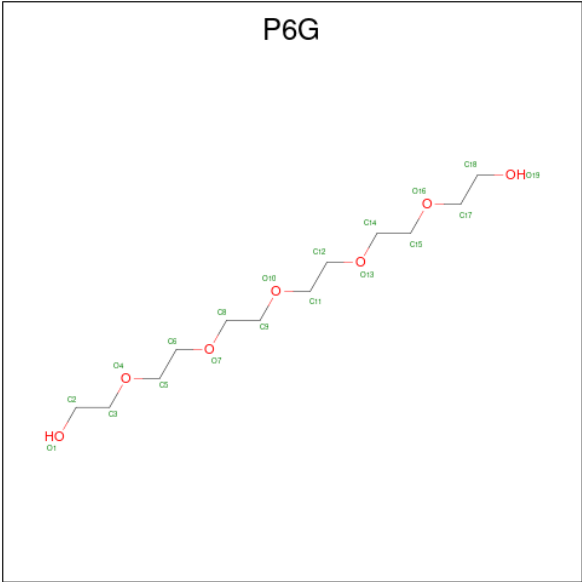
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is 2-(2-ETHOXYETHOXY)ETHANOL (CCD ID: AE3) (formula: $C_6H_{14}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			9	6	3		

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



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	101	Total	O	0	0
			101	101		
5	B	76	Total	O	0	0
			76	76		

3 Residue-property plots

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. 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. 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.

Note EDS was not executed.

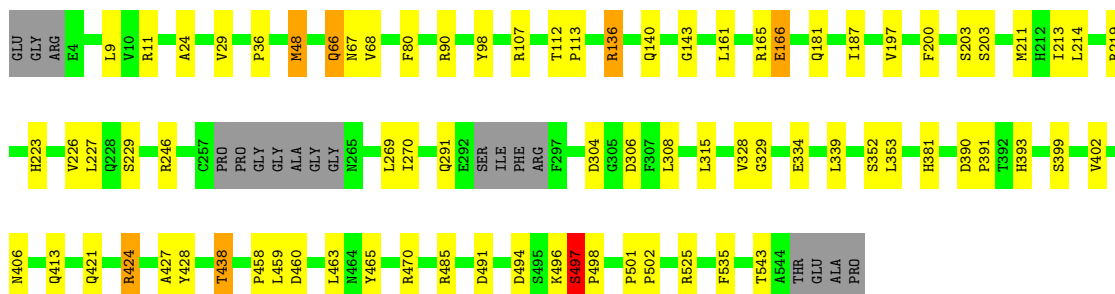
• Molecule 1: ACETYLCHOLINESTERASE

Chain A: 



• Molecule 1: ACETYLCHOLINESTERASE

Chain B: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	79.25Å 111.20Å 227.36Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.98 – 2.50	Depositor
% Data completeness (in resolution range)	99.3 (19.98-2.50)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.214 , 0.244	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8561	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SVV, NAG, SVW, P6G, AE3

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	0.66	0/4297	0.91	0/5868
1	B	0.64	1/4244 (0.0%)	0.87	0/5800
All	All	0.65	1/8541 (0.0%)	0.89	0/11668

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	543	THR	C-N	-6.59	1.24	1.33

There are no bond angle outliers.

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	4195	0	4080	36	0
1	B	4133	0	4026	48	0
2	A	28	0	26	0	0
3	A	9	0	14	0	0
4	B	19	0	24	3	0
5	A	101	0	0	3	0
5	B	76	0	0	0	0
All	All	8561	0	8170	84	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

All (84) 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:197:VAL:H	1:B:223:HIS:HD2	1.14	0.95
1:B:424:ARG:HH11	1:B:424:ARG:HG3	1.33	0.93
1:B:497:SER:HB2	1:B:498:PRO:O	1.73	0.88
1:A:197:VAL:H	1:A:223:HIS:HD2	1.19	0.87
1:A:48:MET:HA	1:A:48:MET:HE2	1.58	0.84
1:A:48:MET:HE1	1:A:165:ARG:O	1.82	0.79
1:B:197:VAL:H	1:B:223:HIS:CD2	2.02	0.77
1:B:497:SER:HB2	1:B:498:PRO:C	2.08	0.76
1:B:48:MET:CE	1:B:166:GLU:HA	2.15	0.75
1:B:424:ARG:HG3	1:B:424:ARG:NH1	1.94	0.74
1:A:197:VAL:H	1:A:223:HIS:CD2	2.07	0.69
1:B:460:ASP:HB3	1:B:463:LEU:HD12	1.72	0.69
1:B:48:MET:HA	1:B:48:MET:HE2	1.76	0.66
1:B:48:MET:HE1	1:B:165:ARG:O	1.95	0.66
1:B:424:ARG:HH11	1:B:424:ARG:CG	2.07	0.65
1:A:369:GLN:HB3	5:A:2071:HOH:O	1.97	0.64
1:B:211:MET:HG2	1:B:308:LEU:HD21	1.80	0.64
1:B:491:ASP:HB3	1:B:494:ASP:HB3	1.80	0.63
1:B:304:ASP:OD2	1:B:306:ASP:HB3	1.99	0.62
1:A:319:GLY:O	1:A:421:GLN:NE2	2.35	0.60
1:B:112:THR:HG21	1:B:143:GLY:O	2.02	0.59
1:A:381:HIS:HA	4:B:1546:P6G:H31	1.87	0.57
1:B:381:HIS:ND1	4:B:1546:P6G:H181	2.19	0.57
1:B:227:LEU:HB2	1:B:328:VAL:HG12	1.86	0.56
1:B:48:MET:HE3	1:B:166:GLU:HA	1.87	0.56
1:A:5:ASP:HB3	1:A:8:LEU:HD12	1.89	0.55
1:B:353:LEU:HB3	1:B:391:PRO:HB2	1.90	0.54
1:A:4:GLU:OE2	1:A:18:ARG:HD3	2.07	0.54
1:B:48:MET:HE1	1:B:166:GLU:HA	1.89	0.53
1:A:373:LEU:HD23	1:A:539:LEU:HD11	1.91	0.53
1:A:224:ARG:HG2	1:A:325:GLN:HB2	1.90	0.52
1:A:376:GLU:O	1:A:380:LEU:HG	2.11	0.50
1:B:166:GLU:HG2	1:B:270:ILE:HD13	1.92	0.50
1:B:48:MET:HE3	1:B:166:GLU:C	2.36	0.50
1:A:101:VAL:HG22	1:A:147:VAL:HG22	1.94	0.49
1:A:395:ARG:HD2	1:A:396:ASP:OD1	2.12	0.49
1:A:494:ASP:OD1	1:A:497:SER:HB2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:511:VAL:HB	1:A:518:LEU:HD22	1.95	0.49
1:B:66:GLN:HE21	1:B:67:ASN:H	1.60	0.49
1:A:509:GLN:HB2	5:A:2096:HOH:O	2.11	0.48
1:B:68:VAL:HG23	1:B:90:ARG:HB2	1.95	0.48
1:A:113:PRO:HG2	1:A:485:ARG:HG2	1.96	0.48
1:A:228:GLN:NE2	1:A:480:TRP:HE1	2.13	0.47
1:B:200:PHE:HB2	1:B:226:VAL:HB	1.97	0.46
1:A:373:LEU:CD2	1:A:539:LEU:HD11	2.46	0.46
1:A:472:PHE:CZ	1:A:476:LEU:HD11	2.51	0.46
1:B:200:PHE:CB	1:B:226:VAL:HB	2.46	0.46
1:A:48:MET:HE3	1:A:166:GLU:C	2.41	0.45
1:A:118:ILE:O	1:A:205:GLY:HA3	2.16	0.45
1:A:202:GLU:HG2	1:A:228:GLN:O	2.17	0.45
1:B:197:VAL:N	1:B:223:HIS:HD2	1.97	0.45
1:A:491:ASP:HB3	1:A:494:ASP:HB3	1.99	0.45
1:A:433:ARG:HD3	5:A:2086:HOH:O	2.17	0.45
1:A:459:LEU:HD23	1:A:470:ARG:HG2	1.99	0.45
1:B:161:LEU:HD11	1:B:269:LEU:HD23	1.99	0.45
1:B:213:ILE:O	1:B:219:ARG:HD3	2.18	0.44
1:B:339:LEU:HD11	1:B:399:SER:HA	1.99	0.44
1:A:103:THR:HG21	1:A:190:PHE:HB3	1.99	0.44
1:B:24:ALA:HB3	1:B:140:GLN:HG3	2.00	0.44
1:B:80:PHE:CE1	1:B:438:THR:HB	2.54	0.43
1:B:214:LEU:HD22	1:B:315:LEU:HB3	2.01	0.43
1:B:390:ASP:OD2	1:B:393:HIS:ND1	2.46	0.43
1:B:459:LEU:HD22	1:B:470:ARG:HG2	2.00	0.43
1:B:328:VAL:O	1:B:427:ALA:HA	2.18	0.42
1:B:113:PRO:HG2	1:B:485:ARG:HG2	2.01	0.42
1:B:329:GLY:HA3	1:B:428:TYR:CZ	2.55	0.42
1:B:29:VAL:HG21	1:B:136:ARG:HB2	2.00	0.42
1:B:459:LEU:CD2	1:B:470:ARG:HG2	2.50	0.42
1:B:535:PHE:CD2	4:B:1546:P6G:H82	2.55	0.41
1:A:228:GLN:HE21	1:A:480:TRP:HE1	1.66	0.41
1:B:458:PRO:HA	1:B:465:TYR:CD2	2.55	0.41
1:A:7:GLN:O	1:A:7:GLN:HG3	2.19	0.41
1:A:219:ARG:HD2	1:A:219:ARG:HA	1.85	0.41
1:A:433:ARG:CZ	1:A:437:LEU:HD23	2.51	0.41
1:B:36:PRO:HB3	1:B:98:TYR:CE1	2.55	0.41
1:A:200:PHE:HB2	1:A:226:VAL:HB	2.03	0.41
1:B:187:ILE:HD12	1:B:187:ILE:HA	1.98	0.41
1:B:229:SER:OG	1:B:334:GLU:OE2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:ASN:O	1:A:147:VAL:HA	2.21	0.40
1:A:384:ASP:OD1	1:A:384:ASP:C	2.65	0.40
1:B:501:PRO:HA	1:B:502:PRO:HD3	2.00	0.40
1:A:176:GLN:OE1	1:A:208:SER:HB3	2.22	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	522/549 (95%)	496 (95%)	24 (5%)	2 (0%)	30	49
1	B	525/549 (96%)	505 (96%)	18 (3%)	2 (0%)	30	49
All	All	1047/1098 (95%)	1001 (96%)	42 (4%)	4 (0%)	30	49

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	493	ARG
1	A	494	ASP
1	B	496	LYS
1	B	497	SER

5.3.2 Protein sidechains [i](#)

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	439/445 (99%)	427 (97%)	12 (3%)	39	67
1	B	434/445 (98%)	417 (96%)	17 (4%)	28	55
All	All	873/890 (98%)	844 (97%)	29 (3%)	33	61

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	GLU
1	A	13	ARG
1	A	45	ARG
1	A	246	ARG
1	A	291	GLN
1	A	326	VAL
1	A	441	LEU
1	A	457	LEU
1	A	475	ARG
1	A	495	SER
1	A	525	ARG
1	A	536	LEU
1	B	9	LEU
1	B	11	ARG
1	B	48	MET
1	B	66	GLN
1	B	107	ARG
1	B	136	ARG
1	B	166	GLU
1	B	181	GLN
1	B	246	ARG
1	B	291	GLN
1	B	352	SER
1	B	413	GLN
1	B	421	GLN
1	B	424	ARG
1	B	438	THR
1	B	497	SER
1	B	525	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	66	GLN

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Mol	Chain	Res	Type
1	A	223	HIS
1	A	228	GLN
1	A	265	ASN
1	A	284	HIS
1	A	287	HIS
1	A	291	GLN
1	A	317	ASN
1	A	322	GLN
1	A	405	HIS
1	A	413	GLN
1	A	421	GLN
1	A	533	ASN
1	B	66	GLN
1	B	223	HIS
1	B	291	GLN
1	B	317	ASN
1	B	322	GLN
1	B	405	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues 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$
1	SVW	A	203[B]	-	7,9,10	1.65	1 (14%)	5,12,14	5.66	4 (80%)
1	SVV	A	203[A]	1	7,9,10	1.39	2 (28%)	5,12,14	3.16	4 (80%)
1	SVV	B	203[A]	1	7,9,10	1.57	2 (28%)	5,12,14	3.23	4 (80%)
1	SVW	B	203[B]	-	7,9,10	1.69	1 (14%)	5,12,14	3.76	5 (100%)

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
1	SVW	A	203[B]	-	-	2/4/8/10	-
1	SVV	A	203[A]	1	-	2/4/8/10	-
1	SVV	B	203[A]	1	-	2/4/8/10	-
1	SVW	B	203[B]	-	-	2/4/8/10	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	203[B]	SVW	P1-O3	3.97	1.52	1.46
1	A	203[B]	SVW	P1-O3	3.70	1.51	1.46
1	B	203[A]	SVV	P1-O2	3.24	1.51	1.46
1	A	203[A]	SVV	P1-O2	2.31	1.49	1.46
1	A	203[A]	SVV	P1-O3	-2.13	1.51	1.56
1	B	203[A]	SVV	P1-O3	-2.04	1.51	1.56

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	203[B]	SVW	OG-P1-N2	9.36	132.89	107.63
1	A	203[B]	SVW	OG-P1-O3	-7.13	92.94	115.71
1	B	203[B]	SVW	OG-P1-O3	-6.47	95.04	115.71
1	A	203[A]	SVV	OG-P1-N4	-4.93	94.32	107.63
1	B	203[A]	SVV	O3-P1-O2	4.06	120.77	110.26
1	B	203[A]	SVV	OG-P1-O2	-3.72	103.83	115.71
1	B	203[A]	SVV	OG-P1-N4	-3.63	97.82	107.63
1	A	203[B]	SVW	O4-P1-O3	3.29	118.78	110.26
1	B	203[B]	SVW	O4-P1-O3	3.27	118.73	110.26
1	A	203[A]	SVV	OG-CB-CA	3.19	111.25	108.14
1	A	203[B]	SVW	OG-CB-CA	3.19	111.25	108.14
1	A	203[A]	SVV	O3-P1-O2	2.82	117.56	110.26
1	B	203[B]	SVW	OG-P1-N2	2.72	114.97	107.63
1	A	203[A]	SVV	OG-P1-O2	2.56	123.89	115.71
1	B	203[A]	SVV	OG-CB-CA	2.47	110.55	108.14
1	B	203[B]	SVW	OG-CB-CA	2.47	110.55	108.14
1	B	203[B]	SVW	P1-OG-CB	-2.12	111.33	119.24

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	203[A]	SVV	CB-OG-P1-O2
1	A	203[B]	SVW	CB-OG-P1-O3
1	B	203[A]	SVV	CB-OG-P1-O2
1	A	203[A]	SVV	N-CA-CB-OG
1	A	203[B]	SVW	N-CA-CB-OG
1	B	203[A]	SVV	N-CA-CB-OG
1	B	203[B]	SVW	N-CA-CB-OG
1	B	203[B]	SVW	CB-OG-P1-O3

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](#)

4 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	NAG	A	1546	1	14,14,15	0.56	0	17,19,21	1.41	1 (5%)
3	AE3	A	1547	-	8,8,8	1.03	0	7,7,7	0.55	0
2	NAG	A	1545	1	14,14,15	0.89	1 (7%)	17,19,21	1.70	2 (11%)
4	P6G	B	1546	-	18,18,18	1.79	5 (27%)	17,17,17	2.01	9 (52%)

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	NAG	A	1546	1	-	2/6/23/26	0/1/1/1
3	AE3	A	1547	-	-	3/6/6/6	-
2	NAG	A	1545	1	-	2/6/23/26	0/1/1/1
4	P6G	B	1546	-	-	6/16/16/16	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1546	P6G	C9-C8	-3.10	1.33	1.49
4	B	1546	P6G	C17-C18	-3.04	1.33	1.49
4	B	1546	P6G	C3-C2	-2.97	1.33	1.49
4	B	1546	P6G	C15-C14	-2.93	1.34	1.49
4	B	1546	P6G	C6-C5	-2.90	1.34	1.49
2	A	1545	NAG	C1-C2	2.67	1.56	1.52

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1545	NAG	C1-O5-C5	5.53	119.60	112.19
2	A	1546	NAG	C1-O5-C5	4.36	118.03	112.19
4	B	1546	P6G	O7-C8-C9	3.03	124.18	110.35
4	B	1546	P6G	O7-C6-C5	2.97	123.90	110.35
4	B	1546	P6G	O16-C15-C14	2.65	122.42	110.35
4	B	1546	P6G	O13-C14-C15	2.62	122.31	110.35
4	B	1546	P6G	O4-C5-C6	2.61	122.25	110.35
4	B	1546	P6G	O16-C17-C18	2.40	120.71	110.11
4	B	1546	P6G	O10-C9-C8	2.33	120.97	110.35
4	B	1546	P6G	C5-O4-C3	2.23	123.01	113.26
2	A	1545	NAG	O3-C3-C2	2.12	113.81	109.40
4	B	1546	P6G	O4-C3-C2	2.04	119.12	110.11

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1545	NAG	C8-C7-N2-C2
2	A	1545	NAG	O7-C7-N2-C2
2	A	1546	NAG	C8-C7-N2-C2
2	A	1546	NAG	O7-C7-N2-C2
3	A	1547	AE3	O2-C3-C4-O3
4	B	1546	P6G	O4-C5-C6-O7

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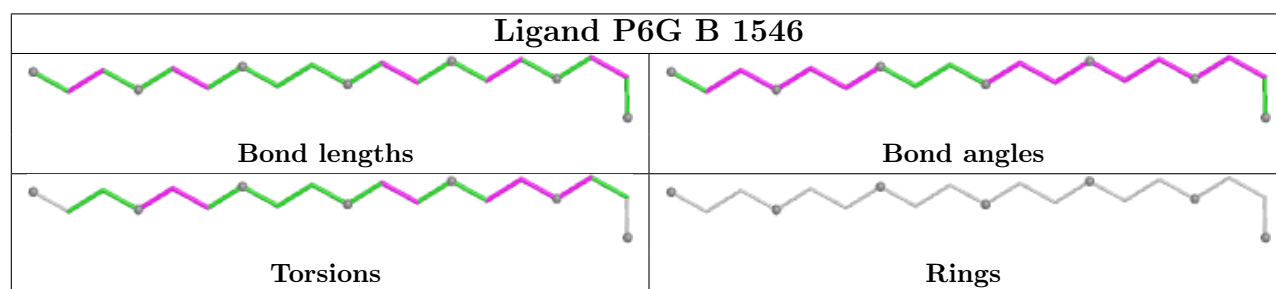
Mol	Chain	Res	Type	Atoms
4	B	1546	P6G	O13-C14-C15-O16
4	B	1546	P6G	O7-C8-C9-O10
4	B	1546	P6G	C6-C5-O4-C3
4	B	1546	P6G	C14-C15-O16-C17
3	A	1547	AE3	C3-C4-O3-C5
4	B	1546	P6G	C2-C3-O4-C5
3	A	1547	AE3	C4-C3-O2-C2

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1546	P6G	3	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.