



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:57 AM GMT

PDB ID : 2JGJ
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

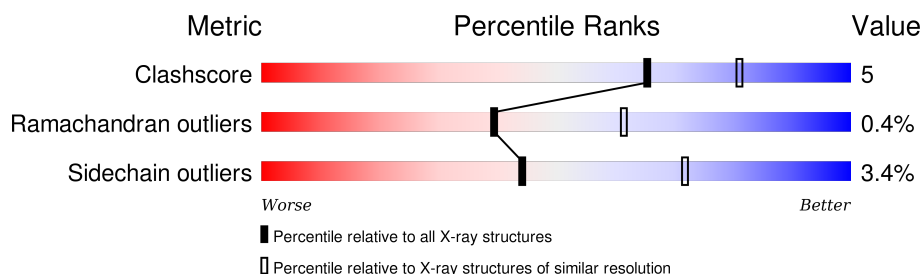
1 Overall quality at a glance

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	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	549	
1	B	549	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8607 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.

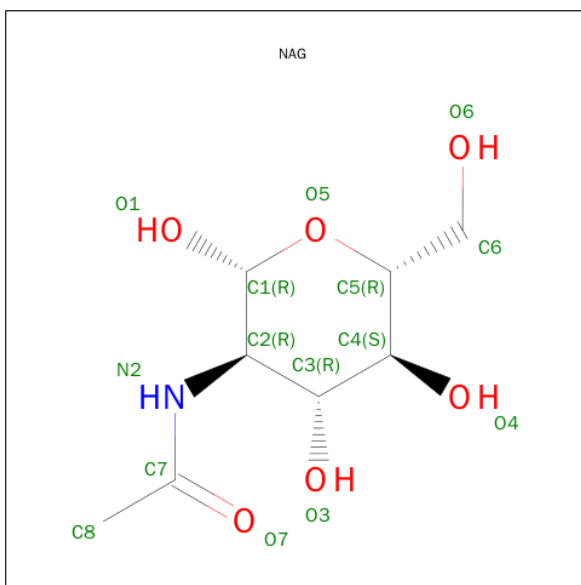
- Molecule 1 is a protein called ACETYLCHOLINESTERASE.

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	534	Total	C	N	O	P	S	0	1	1
			4179	2676	725	762	2	14			

There are 14 discrepancies between the modelled and reference sequences:

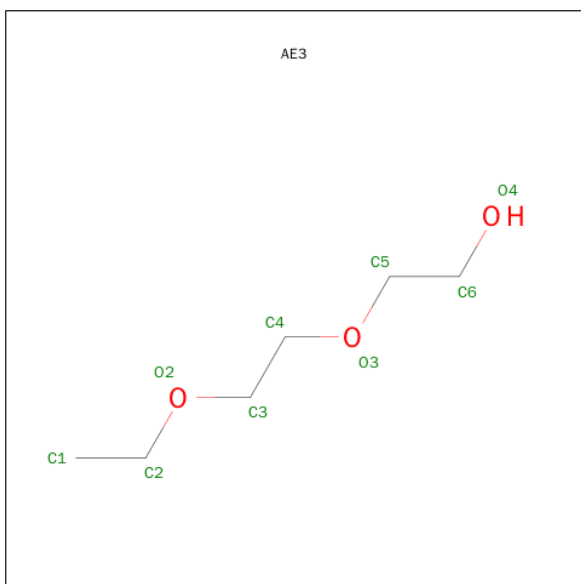
Chain	Residue	Modelled	Actual	Comment	Reference
A	203	SVV	SER	MICROHETEROGENEITY	UNP P21836
A	203	SVW	SER	MICROHETEROGENEITY	UNP P21836
A	544	ALA	-	EXPRESSION TAG	UNP P21836
A	545	THR	-	EXPRESSION TAG	UNP P21836
A	546	GLU	-	EXPRESSION TAG	UNP P21836
A	547	ALA	-	EXPRESSION TAG	UNP P21836
A	548	PRO	-	EXPRESSION 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 SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: C₈H₁₅NO₆).



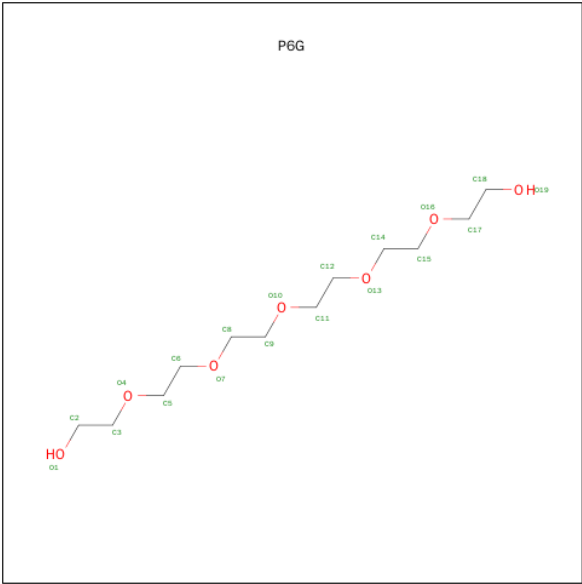
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is 2-(2-ETHOXYETHOXY)ETHANOL (three-letter code: 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 (three-letter code: P6G) (formula: C₁₂H₂₆O₇).



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

- Molecule 5 is water.

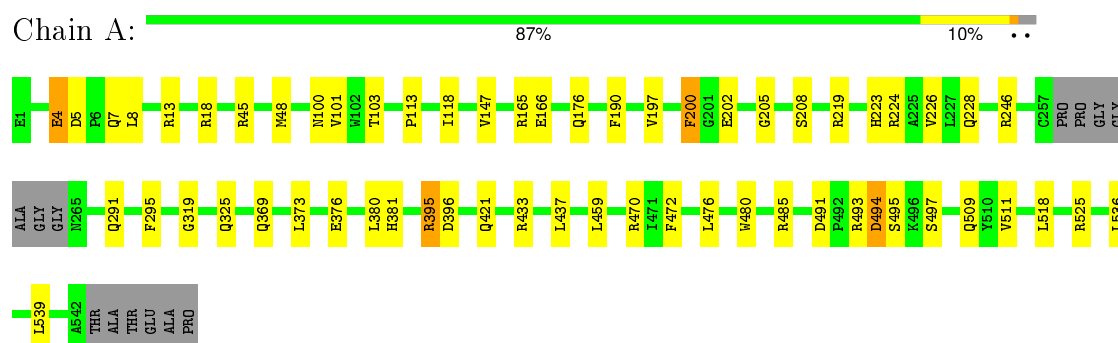
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	101	Total	O	0	0
			101	101		
5	B	76	Total	O	0	0
			76	76		

3 Residue-property plots

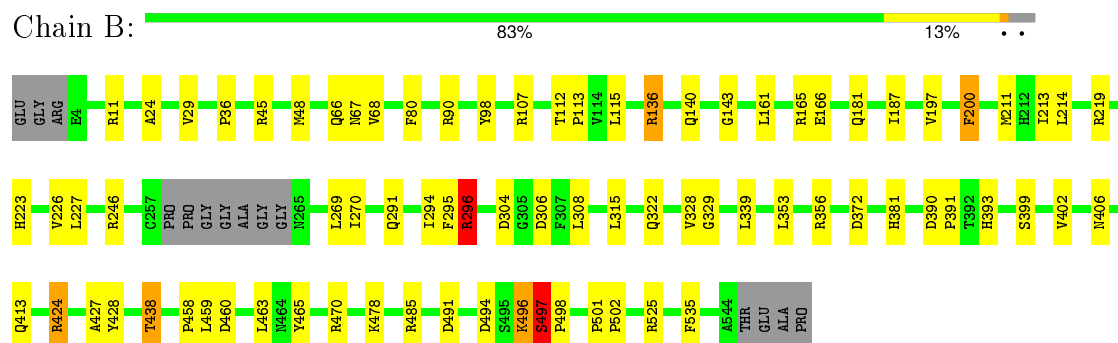
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

• Molecule 1: ACETYLCHOLINESTERASE



• Molecule 1: ACETYLCHOLINESTERASE



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	79.25 Å 111.20 Å 227.36 Å 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	8607	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

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: SVV, SVW, AE3, 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	0.56	0/4297	0.67	1/5868 (0.0%)
1	B	0.54	0/4281	0.62	2/5849 (0.0%)
All	All	0.55	0/8578	0.65	3/11717 (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	B	115	LEU	CA-CB-CG	5.22	127.30	115.30
1	A	395	ARG	NE-CZ-NH2	-5.06	117.77	120.30
1	B	296	ARG	NE-CZ-NH1	5.00	122.80	120.30

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	4195	0	4080	36	0
1	B	4179	0	4064	46	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	76	0	0	0	0
All	All	8607	0	8208	82	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 (82) 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:48:MET:HE1	1:B:166:GLU:HA	1.42	1.01
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:B:197:VAL:H	1:B:223:HIS:CD2	2.02	0.77
1:B:424:ARG:NH1	1:B:424:ARG:HG3	1.94	0.74
1:B:48:MET:CE	1:B:166:GLU:HA	2.15	0.74
1:B:497:SER:HB2	1:B:498:PRO:C	2.08	0.72
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:A:48:MET:HE1	1:A:165:ARG:O	1.94	0.67
1:B:424:ARG:CG	1:B:424:ARG:HH11	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:48:MET:HE1	1:A:166:GLU:HA	1.84	0.59
1:B:48:MET:HE1	1:B:165:ARG:O	2.03	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: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: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:A:48:MET:CE	1:A:48:MET:HA	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:A:511:VAL:HB	1:A:518:LEU:HD22	1.95	0.49
1:B:296:ARG:NH2	1:B:406:ASN:OD1	2.46	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:48:MET:HE1	1:B:166:GLU:CA	2.29	0.46
1:B:200:PHE:CB	1:B:226:VAL:HB	2.46	0.46
1:A:118:ILE:O	1:A:205:GLY:HA3	2.16	0.45
1:B:197:VAL:N	1:B:223:HIS:HD2	1.97	0.45
1:A:202:GLU:HG2	1:A:228:GLN:O	2.17	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:B:161:LEU:HD11	1:B:269:LEU:HD23	1.99	0.45
1:A:459:LEU:HD23	1:A:470:ARG:HG2	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:A:48:MET:HE1	1:A:166:GLU:CA	2.48	0.43
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:294:ILE:HD11	1:B:402:VAL:HG21	2.01	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:459:LEU:CD2	1:B:470:ARG:HG2	2.50	0.42
1:B:29:VAL:HG21	1:B:136:ARG:HB2	2.00	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:HG3	1:A:7:GLN:O	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:219:ARG:HA	1:A:219:ARG:HD2	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:HA	1:B:187:ILE:HD12	1.98	0.41
1:B:48:MET:HA	1:B:48:MET:CE	2.52	0.40
1:A:100:ASN:O	1:A:147:VAL:HA	2.21	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	530/549 (96%)	504 (95%)	24 (4%)	2 (0%)	39	61
1	B	529/549 (96%)	509 (96%)	18 (3%)	2 (0%)	39	61
All	All	1059/1098 (96%)	1013 (96%)	42 (4%)	4 (0%)	39	61

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 ⓘ

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%)	429 (98%)	10 (2%)	58	83
1	B	438/445 (98%)	418 (95%)	20 (5%)	33	57
All	All	877/890 (98%)	847 (97%)	30 (3%)	44	72

All (30) 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	200	PHE
1	A	246	ARG
1	A	291	GLN
1	A	295	PHE
1	A	495	SER
1	A	525	ARG
1	A	536	LEU
1	B	11	ARG
1	B	45	ARG
1	B	107	ARG
1	B	136	ARG
1	B	181	GLN
1	B	200	PHE
1	B	246	ARG
1	B	291	GLN
1	B	295	PHE
1	B	296	ARG
1	B	322	GLN
1	B	356	ARG
1	B	372	ASP
1	B	413	GLN
1	B	424	ARG
1	B	438	THR
1	B	478	LYS

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Mol	Chain	Res	Type
1	B	496	LYS
1	B	497	SER
1	B	525	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	66	GLN
1	A	223	HIS
1	A	228	GLN
1	A	287	HIS
1	A	291	GLN
1	A	317	ASN
1	A	405	HIS
1	A	533	ASN
1	B	66	GLN
1	B	223	HIS
1	B	291	GLN
1	B	317	ASN

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	SVV	A	203[A]	1	7,9,10	1.58	1 (14%)	7,12,14	3.37	4 (57%)
1	SVW	A	203[B]	-	7,9,10	2.03	1 (14%)	7,12,14	7.99	5 (71%)
1	SVV	B	203[A]	1	7,9,10	1.89	1 (14%)	7,12,14	4.66	4 (57%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	SVW	B	203[B]	-	7,9,10	2.14	1 (14%)	7,12,14	7.28	4 (57%)

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	SVV	A	203[A]	1	-	0/4/8/10	0/0/0/0
1	SVW	A	203[B]	-	-	1/4/8/10	0/0/0/0
1	SVV	B	203[A]	1	-	0/4/8/10	0/0/0/0
1	SVW	B	203[B]	-	-	1/4/8/10	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	203[A]	SVV	P1-O2	3.14	1.49	1.46
1	B	203[A]	SVV	P1-O2	4.35	1.51	1.46
1	A	203[B]	SVW	P1-O3	4.95	1.51	1.46
1	B	203[B]	SVW	P1-O3	5.30	1.52	1.46

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	203[B]	SVW	OG-P1-O3	-20.16	92.94	115.97
1	B	203[B]	SVW	OG-P1-O3	-18.32	95.04	115.97
1	B	203[A]	SVV	OG-P1-O2	-10.62	103.83	115.97
1	B	203[B]	SVW	P1-OG-CB	-3.14	111.33	120.45
1	A	203[A]	SVV	O-C-CA	-2.53	118.91	125.49
1	A	203[B]	SVW	O-C-CA	-2.53	118.91	125.49
1	B	203[A]	SVV	P1-OG-CB	-2.46	113.30	120.45
1	B	203[B]	SVW	OG-CB-CA	2.66	110.55	108.27
1	B	203[A]	SVV	OG-CB-CA	2.66	110.55	108.27
1	A	203[A]	SVV	O3-P1-O2	2.95	117.56	110.07
1	A	203[B]	SVW	OG-P1-N2	3.01	132.89	107.98
1	B	203[B]	SVW	O4-P1-O3	3.41	118.73	110.07
1	A	203[B]	SVW	O4-P1-O3	3.43	118.78	110.07
1	A	203[A]	SVV	OG-CB-CA	3.49	111.25	108.27
1	A	203[B]	SVW	OG-CB-CA	3.49	111.25	108.27
1	B	203[A]	SVV	O3-P1-O2	4.22	120.77	110.07
1	A	203[A]	SVV	OG-P1-O2	6.94	123.89	115.97

There are no chirality outliers.

All (2) torsion outliers are listed below:

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

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates 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	1545	1	14,14,15	0.84	1 (7%)	15,19,21	1.87	2 (13%)
2	NAG	A	1546	1	14,14,15	0.54	0	15,19,21	1.49	1 (6%)
3	AE3	A	1547	-	8,8,8	1.02	0	7,7,7	0.56	0
4	P6G	B	1546	-	18,18,18	1.73	5 (27%)	17,17,17	2.02	8 (47%)

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	1545	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1546	1	-	0/6/23/26	0/1/1/1
3	AE3	A	1547	-	-	0/6/6/6	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	P6G	B	1546	-	-	0/16/16/16	0/0/0/0

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1546	P6G	C9-C8	-2.99	1.33	1.48
4	B	1546	P6G	C17-C18	-2.91	1.33	1.49
4	B	1546	P6G	C3-C2	-2.85	1.33	1.49
4	B	1546	P6G	C15-C14	-2.83	1.34	1.48
4	B	1546	P6G	C6-C5	-2.80	1.34	1.48
2	A	1545	NAG	C1-C2	2.54	1.56	1.52

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1546	P6G	O16-C17-C18	2.23	120.71	110.43
4	B	1546	P6G	C5-O4-C3	2.26	123.01	113.31
2	A	1545	NAG	O3-C3-C2	2.37	113.81	109.11
4	B	1546	P6G	O10-C9-C8	2.38	120.97	110.36
4	B	1546	P6G	O4-C5-C6	2.67	122.25	110.36
4	B	1546	P6G	O13-C14-C15	2.69	122.31	110.36
4	B	1546	P6G	O16-C15-C14	2.71	122.42	110.36
4	B	1546	P6G	O7-C6-C5	3.04	123.90	110.36
4	B	1546	P6G	O7-C8-C9	3.11	124.18	110.36
2	A	1546	NAG	C1-O5-C5	4.56	118.03	112.25
2	A	1545	NAG	C1-O5-C5	5.80	119.60	112.25

There are no chirality outliers.

There are no torsion outliers.

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

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.