



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:28 AM GMT

PDB ID : 2HA0
Title : Crystal structure of mouse acetylcholinesterase complexed with 4-ketoamyltri methylammonium
Authors : Bourne, Y.; Radic, Z.; Sulzenbacher, G.; Kim, E.; Taylor, P.; Marchot, P.
Deposited on : 2006-06-12
Resolution : 2.20 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) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

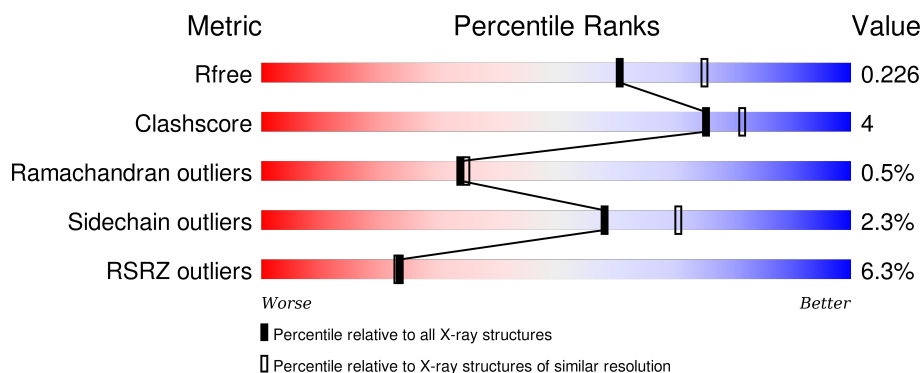
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	91344	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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.

Mol	Chain	Length	Quality of chain
1	A	543	<div> <div>5%</div> <div>90%</div> <div>7% ..</div> </div>
1	B	543	<div> <div>7%</div> <div>89%</div> <div>9% .</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	FUC	A	545	X	-	-	-
4	IOD	A	1101	-	-	X	-
4	IOD	A	1106	-	-	X	-
4	IOD	B	1114	-	-	X	-
5	NWA	A	601	-	-	-	X
6	CHH	A	1602	-	-	-	X
6	CHH	B	2602	-	-	-	X
7	P6G	A	901	-	-	-	X

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 9175 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.

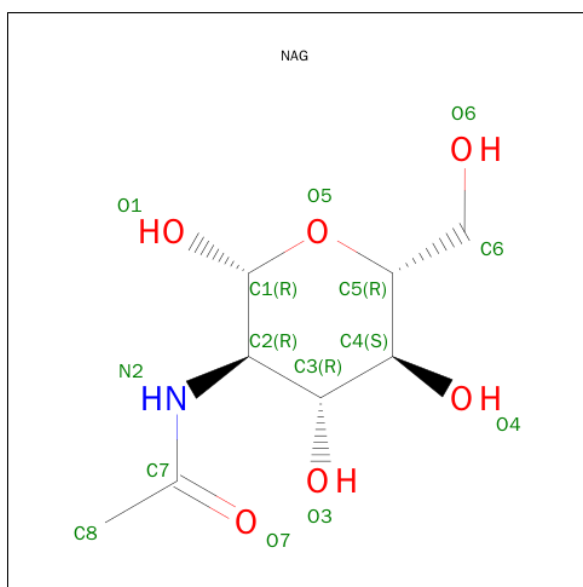
- Molecule 1 is a protein called Acetylcholinesterase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	535	Total	C	N	O	S	0	8	0
			4222	2708	739	760	15			
1	B	536	Total	C	N	O	S	0	3	0
			4196	2693	728	761	14			

- Molecule 2 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	2	Total	C	N	O	0	0
			24	14	1	9		

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

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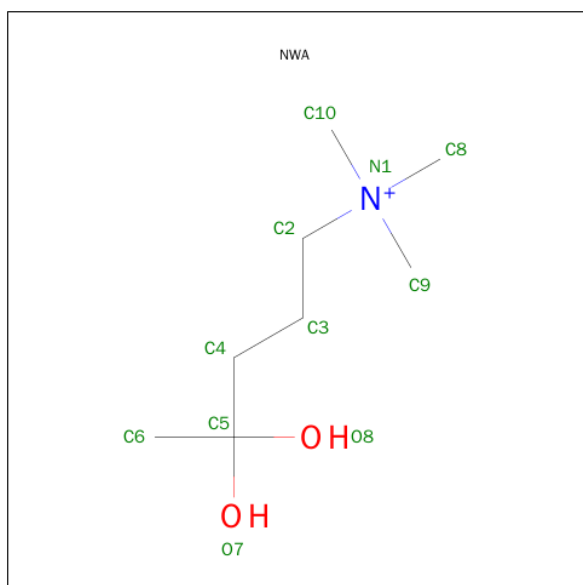
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is IODIDE ION (three-letter code: IOD) (formula: I).

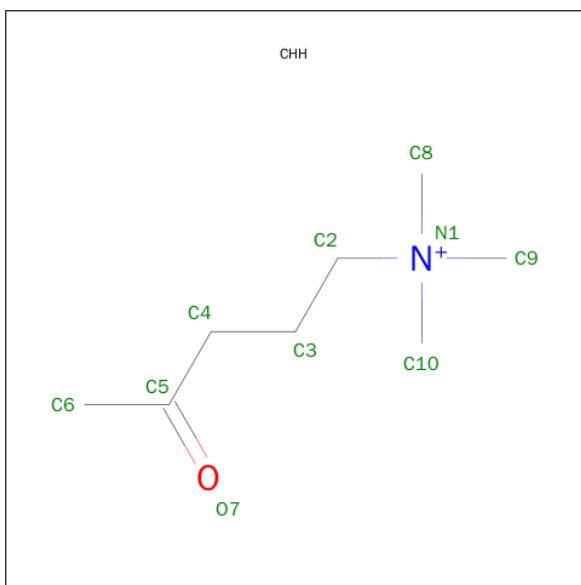
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	7	Total	I	0	0
			7	7		
4	A	7	Total	I	0	0
			7	7		

- Molecule 5 is 4,4-DIHYDROXY-N,N,N-TRIMETHYLPENTAN-1-AMINIUM (three-letter code: NWA) (formula: C₈H₂₀NO₂).



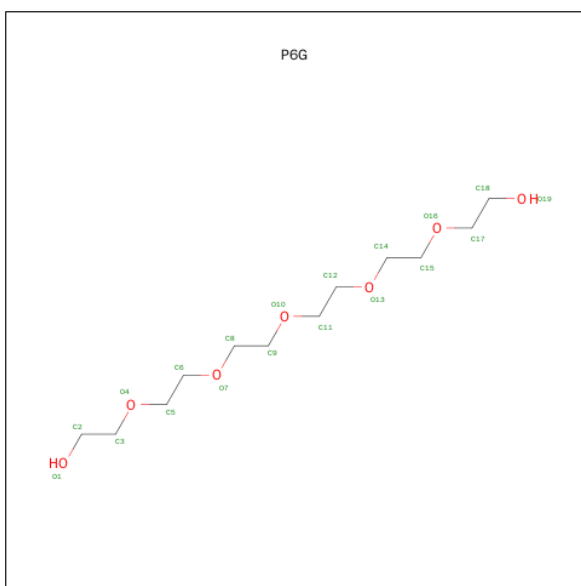
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			10	8	1	1		
5	B	1	Total	C	N	O	0	0
			10	8	1	1		

- Molecule 6 is N,N,N-TRIMETHYL-4-OXOPENTAN-1-AMINIUM (three-letter code: CHH) (formula: C₈H₁₈NO).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			10	8	1	1		
6	B	1	Total	C	N	O	0	0
			10	8	1	1		

- Molecule 7 is HEXAETHYLENE GLYCOL (three-letter code: P6G) (formula: $C_{12}H_{26}O_7$).



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

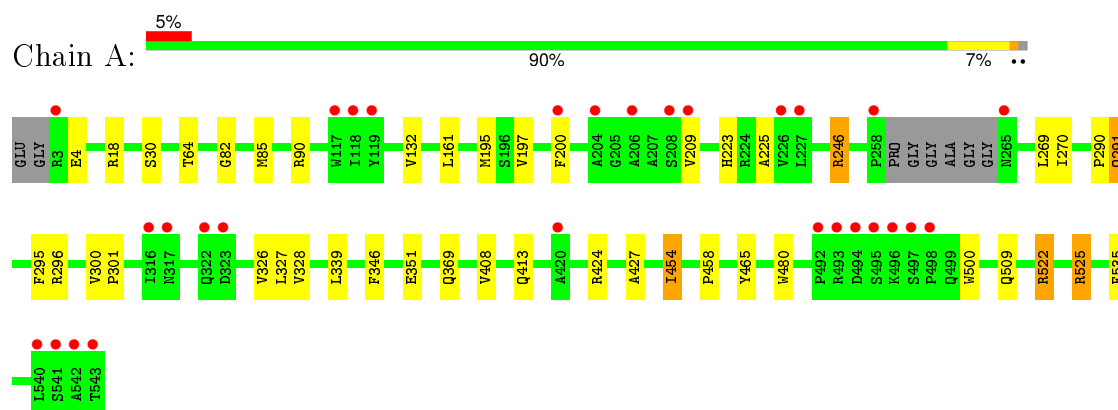
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	336	Total 336	O 336	0	0
8	B	296	Total 296	O 296	0	0

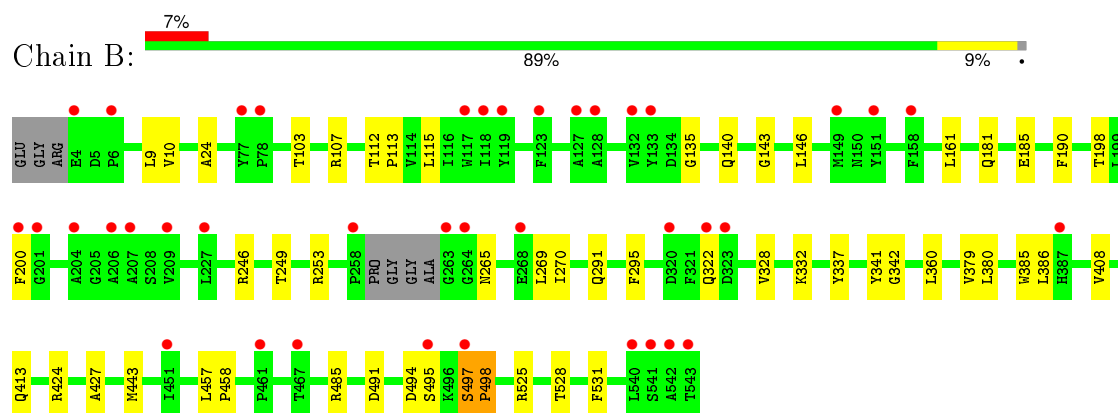
3 Residue-property plots

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.

• 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	79.23Å 111.80Å 226.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.20 37.40 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.0 (30.00-2.20) 97.5 (37.40-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.83 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.182 , 0.219 0.196 , 0.226	Depositor DCC
R_{free} test set	2015 reflections (2.04%)	DCC
Wilson B-factor (Å ²)	36.8	Xtriage
Anisotropy	0.759	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 53.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 101055 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9175	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.55% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: NAG, CHH, FUC, P6G, IOD, NWA

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	0.52	0/4381	0.66	2/5983 (0.0%)
1	B	0.48	0/4332	0.63	0/5918
All	All	0.50	0/8713	0.65	2/11901 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
2	A	1	0
All	All	1	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	246	ARG	NE-CZ-NH2	-6.52	117.04	120.30
1	A	246	ARG	NE-CZ-NH1	5.07	122.83	120.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	545	FUC	C1

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	497	SER	Peptide

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	4222	0	4111	30	0
1	B	4196	0	4089	28	0
2	A	24	0	22	0	0
3	A	14	0	13	0	0
3	B	14	0	13	0	0
4	A	7	0	0	5	0
4	B	7	0	0	6	0
5	A	10	0	18	0	0
5	B	10	0	18	0	0
6	A	10	0	18	2	0
6	B	10	0	18	5	0
7	A	19	0	26	2	0
8	A	336	0	0	6	0
8	B	296	0	0	4	0
All	All	9175	0	8346	65	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 (65) 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)
4:B:1102:IOD:I	8:B:2767:HOH:O	2.48	1.01
4:B:1114:IOD:I	6:B:2602:CHH:O7	2.51	0.97
1:B:161:LEU:HD11	1:B:269:LEU:HD22	1.48	0.95
4:A:1106:IOD:I	6:A:1602:CHH:O7	2.63	0.86
1:A:161:LEU:HD11	1:A:269:LEU:HD22	1.59	0.83
1:A:296:ARG:HE	1:A:369:GLN:HE22	1.27	0.82
1:B:112:THR:HG21	1:B:143:GLY:O	1.82	0.79
4:B:1114:IOD:I	6:B:2602:CHH:C5	3.11	0.67
4:B:1114:IOD:I	6:B:2602:CHH:H41	2.64	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:1105:IOD:I	8:B:2863:HOH:O	2.84	0.65
1:A:85[B]:MET:HE1	8:A:1697:HOH:O	2.00	0.60
1:B:181[A]:GLN:OE1	8:B:2841:HOH:O	2.17	0.59
4:A:1104:IOD:I	8:A:1839:HOH:O	2.88	0.57
4:B:1114:IOD:I	6:B:2602:CHH:C4	3.22	0.57
1:A:4:GLU:OE1	1:A:18:ARG:HD3	2.05	0.57
1:A:197:VAL:H	1:A:223:HIS:HD2	1.55	0.53
1:A:327:LEU:HD11	1:A:500:TRP:CH2	2.44	0.53
1:B:491:ASP:HB3	1:B:494:ASP:HB3	1.91	0.53
1:A:197:VAL:H	1:A:223:HIS:CD2	2.28	0.51
1:A:291:GLN:NE2	8:A:1800:HOH:O	2.43	0.51
1:A:326:VAL:HG12	1:A:328:VAL:HG13	1.94	0.50
1:A:85[B]:MET:CE	8:A:1697:HOH:O	2.59	0.49
1:B:112:THR:HG22	1:B:113:PRO:HD2	1.95	0.49
1:A:290:PRO:HD2	4:A:1101:IOD:I	2.83	0.48
1:A:458:PRO:HA	1:A:465:TYR:CD2	2.48	0.48
1:B:103:THR:HG21	1:B:190:PHE:HB3	1.94	0.48
1:B:380:LEU:HD22	1:B:385:TRP:CZ2	2.49	0.48
1:A:64:THR:HB	1:A:90[B]:ARG:NH1	2.29	0.47
1:B:24:ALA:HB3	1:B:140:GLN:HG3	1.96	0.47
1:B:135:GLY:HA3	1:B:146:LEU:HD22	1.96	0.47
1:A:509:GLN:HE21	1:A:522[A]:ARG:NH2	2.13	0.47
1:A:454:ILE:CD1	1:A:480:TRP:CZ2	2.98	0.45
1:B:113:PRO:HG2	1:B:485:ARG:HG2	1.97	0.45
1:A:209:VAL:CG1	1:A:225:ALA:HB1	2.47	0.45
1:B:249:THR:HG22	1:B:253[A]:ARG:NH2	2.31	0.45
1:A:351:GLU:OE1	8:A:1787:HOH:O	2.21	0.45
1:B:408:VAL:HG11	1:B:525:ARG:HG3	1.99	0.45
1:A:195:MET:HE3	8:A:1836:HOH:O	2.17	0.45
4:A:1106:IOD:I	6:A:1602:CHH:C5	3.35	0.45
1:A:296:ARG:HE	1:A:369:GLN:NE2	2.05	0.44
1:A:535:PHE:CE2	7:A:901:P6G:H112	2.53	0.43
1:B:360:LEU:HD22	1:B:379:VAL:HG21	1.99	0.43
1:A:291:GLN:HB2	4:A:1101:IOD:I	2.89	0.43
1:B:337:TYR:HA	1:B:443:MET:CE	2.48	0.43
1:B:115:LEU:HD23	1:B:198:THR:HB	1.99	0.43
1:B:161:LEU:HD12	1:B:270:ILE:HD11	2.00	0.43
1:B:328:VAL:O	1:B:427:ALA:HA	2.17	0.43
1:B:181[B]:GLN:HE21	1:B:185:GLU:HG3	1.84	0.43
1:B:341:TYR:CZ	6:B:2602:CHH:H63	2.54	0.43
1:A:82:GLY:HA2	1:A:85[B]:MET:HE3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:901:P6G:H61	1:B:380:LEU:HB3	2.01	0.43
1:A:339:LEU:HD13	1:A:346:PHE:CE2	2.54	0.42
1:A:326:VAL:HG12	1:A:328:VAL:CG1	2.50	0.42
1:B:528:THR:O	1:B:531:PHE:HB3	2.20	0.42
1:B:10:VAL:HG22	1:B:107:ARG:NH1	2.35	0.42
1:B:161:LEU:HD12	1:B:270:ILE:CG1	2.50	0.42
1:B:380:LEU:HD22	1:B:385:TRP:HZ2	1.85	0.42
1:A:522[B]:ARG:CZ	1:B:386:LEU:HD22	2.50	0.41
1:A:161:LEU:HD12	1:A:270:ILE:CG1	2.50	0.41
1:A:328:VAL:O	1:A:427:ALA:HA	2.20	0.41
1:B:457:LEU:N	1:B:458:PRO:CD	2.84	0.41
1:B:332:LYS:NZ	8:B:2863:HOH:O	2.46	0.41
1:A:300:VAL:HB	1:A:301:PRO:HD2	2.03	0.41
1:A:408:VAL:HG11	1:A:525:ARG:HG3	2.03	0.41
1:A:522[B]:ARG:NH2	1:B:386:LEU:HD22	2.36	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	539/543 (99%)	523 (97%)	16 (3%)	0	100	100
1	B	535/543 (98%)	515 (96%)	15 (3%)	5 (1%)	21	19
All	All	1074/1086 (99%)	1038 (97%)	31 (3%)	5 (0%)	34	35

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	265	ASN
1	B	498	PRO
1	B	495	SER

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Mol	Chain	Res	Type
1	B	497	SER
1	B	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	448/443 (101%)	436 (97%)	12 (3%)	52	64
1	B	443/443 (100%)	434 (98%)	9 (2%)	63	76
All	All	891/886 (101%)	870 (98%)	21 (2%)	58	69

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	SER
1	A	132	VAL
1	A	200	PHE
1	A	246	ARG
1	A	291	GLN
1	A	295	PHE
1	A	413	GLN
1	A	424	ARG
1	A	454	ILE
1	A	522[A]	ARG
1	A	522[B]	ARG
1	A	525	ARG
1	B	9	LEU
1	B	200	PHE
1	B	246	ARG
1	B	291	GLN
1	B	295	PHE
1	B	322	GLN
1	B	413	GLN
1	B	424	ARG
1	B	498	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	100	ASN
1	A	223	HIS
1	A	291	GLN
1	A	322	GLN
1	A	369	GLN
1	A	381	HIS
1	A	509	GLN
1	B	291	GLN
1	B	381	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

2 carbohydrates 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	544	1,2	14,14,15	0.61	0	15,19,21	1.37	2 (13%)
2	FUC	A	545	2	10,10,11	0.69	0	14,14,16	2.17	3 (21%)

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	544	1,2	-	0/6/23/26	0/1/1/1
2	FUC	A	545	2	1/1/4/5	0/0/17/20	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	A	545	FUC	C1-C2-C3	-6.24	102.16	109.54
2	A	545	FUC	C2-C3-C4	-2.12	107.43	111.04
2	A	544	NAG	O3-C3-C2	2.07	113.22	109.11
2	A	545	FUC	O5-C5-C4	2.63	114.08	109.53
2	A	544	NAG	C1-O5-C5	3.31	116.45	112.25

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	545	FUC	C1

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.6 Ligand geometry [i](#)

Of 21 ligands modelled in this entry, 14 are monoatomic - leaving 7 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	$\# Z > 2$
6	CHH	A	1602	-	9,9,9	0.88	0	11,12,12	0.67	0
5	NWA	A	601	1	9,9,10	0.71	0	11,12,15	0.53	0
3	NAG	A	701	1	14,14,15	0.50	0	15,19,21	1.11	1 (6%)
7	P6G	A	901	-	18,18,18	2.22	6 (33%)	17,17,17	1.35	2 (11%)
3	NAG	B	1601	1	14,14,15	0.49	0	15,19,21	1.91	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	CHH	B	2602	-	9,9,9	0.85	0	11,12,12	0.69	0
5	NWA	B	601	1	9,9,10	0.71	0	11,12,15	0.33	0

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
6	CHH	A	1602	-	-	0/7/7/7	0/0/0/0
5	NWA	A	601	1	-	0/7/7/8	0/0/0/0
3	NAG	A	701	1	-	0/6/23/26	0/1/1/1
7	P6G	A	901	-	-	0/16/16/16	0/0/0/0
3	NAG	B	1601	1	-	0/6/23/26	0/1/1/1
6	CHH	B	2602	-	-	0/7/7/7	0/0/0/0
5	NWA	B	601	1	-	0/7/7/8	0/0/0/0

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	901	P6G	O7-C6	2.48	1.52	1.42
7	A	901	P6G	O16-C15	3.42	1.56	1.42
7	A	901	P6G	O19-C18	3.46	1.60	1.42
7	A	901	P6G	O4-C3	3.49	1.56	1.42
7	A	901	P6G	O13-C12	4.12	1.59	1.42
7	A	901	P6G	O10-C9	4.48	1.61	1.42

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	901	P6G	O10-C11-C12	-2.02	101.38	110.36
3	A	701	NAG	O5-C5-C6	2.14	111.97	107.35
7	A	901	P6G	O1-C2-C3	2.98	130.41	112.03
3	B	1601	NAG	C1-O5-C5	6.71	120.76	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1602	CHH	2	0
7	A	901	P6G	2	0
6	B	2602	CHH	5	0

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	535/543 (98%)	0.11	29 (5%)	29	37, 53, 74, 105	0
1	B	536/543 (98%)	0.28	39 (7%)	18	41, 58, 79, 107	0
All	All	1071/1086 (98%)	0.20	68 (6%)	23	37, 55, 78, 107	0

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	495	SER	8.0
1	B	543	THR	6.8
1	B	542	ALA	6.7
1	B	497	SER	6.3
1	A	541	SER	6.2
1	A	542	ALA	5.6
1	A	497	SER	5.5
1	A	496	LYS	5.3
1	A	493	ARG	5.2
1	B	118	ILE	4.4
1	B	541	SER	4.4
1	B	264	GLY	4.1
1	A	494	ASP	3.9
1	B	540	LEU	3.8
1	B	263	GLY	3.7
1	B	117	TRP	3.6
1	A	323	ASP	3.6
1	A	317	ASN	3.6
1	B	467	THR	3.4
1	A	498	PRO	3.4
1	B	323	ASP	3.2
1	A	118	ILE	3.1
1	B	119	TYR	3.1
1	A	540	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	495	SER	3.0
1	A	492	PRO	3.0
1	A	543	THR	3.0
1	A	227	LEU	2.9
1	B	258	PRO	2.9
1	A	204	ALA	2.9
1	B	320	ASP	2.9
1	A	265	ASN	2.8
1	B	128	ALA	2.8
1	B	151	TYR	2.7
1	B	4	GLU	2.7
1	B	461	PRO	2.6
1	A	117	TRP	2.6
1	B	149	MET	2.6
1	B	201	GLY	2.6
1	B	204	ALA	2.6
1	B	451	ILE	2.5
1	B	158	PHE	2.5
1	A	316	ILE	2.5
1	B	207	ALA	2.4
1	B	77	TYR	2.4
1	B	322	GLN	2.4
1	A	206	ALA	2.3
1	B	200	PHE	2.3
1	A	3	ARG	2.3
1	B	268	GLU	2.3
1	A	119	TYR	2.2
1	A	322	GLN	2.2
1	A	420	ALA	2.2
1	B	133	TYR	2.2
1	B	227	LEU	2.2
1	B	127	ALA	2.2
1	A	226	VAL	2.2
1	A	208	SER	2.2
1	A	200	PHE	2.1
1	A	258	PRO	2.1
1	B	209	VAL	2.1
1	B	123	PHE	2.1
1	B	78	PRO	2.1
1	A	209	VAL	2.1
1	B	206	ALA	2.1
1	B	387	HIS	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	132	VAL	2.0
1	B	6	PRO	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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	NAG	A	544	14/15	0.87	0.39	-	79,84,87,90	0
2	FUC	A	545	10/11	0.90	0.52	-	92,94,94,95	0

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
6	CHH	B	2602	10/10	0.79	0.41	10.28	76,76,77,77	10
6	CHH	A	1602	10/10	0.86	0.33	6.66	71,73,74,75	10
7	P6G	A	901	19/19	0.90	0.19	2.64	47,64,73,74	0
5	NWA	A	601	10/11	0.97	0.27	2.01	42,46,47,48	0
5	NWA	B	601	10/11	0.97	0.26	1.49	45,52,54,54	0
4	IOD	A	1106	1/1	0.99	0.13	-0.05	55,55,55,55	1
4	IOD	B	1114	1/1	0.89	0.10	-1.91	72,72,72,72	1
4	IOD	A	1101	1/1	0.99	0.04	-2.45	49,49,49,49	1
4	IOD	B	1102	1/1	0.99	0.04	-2.63	54,54,54,54	1
4	IOD	B	1109	1/1	0.99	0.10	-	47,47,47,47	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	IOD	B	1112	1/1	0.97	0.05	-	71,71,71,71	1
4	IOD	B	1113	1/1	0.94	0.06	-	79,79,79,79	1
4	IOD	B	1107	1/1	0.95	0.04	-	88,88,88,88	1
4	IOD	A	1110	1/1	0.97	0.03	-	64,64,64,64	1
4	IOD	B	1105	1/1	0.99	0.06	-	57,57,57,57	1
3	NAG	A	701	14/15	0.72	0.43	-	82,87,88,89	0
4	IOD	A	1108	1/1	0.97	0.05	-	70,70,70,70	1
4	IOD	A	1103	1/1	0.96	0.05	-	55,55,55,55	1
3	NAG	B	1601	14/15	0.59	0.37	-	86,90,94,94	0
4	IOD	A	1111	1/1	0.99	0.06	-	53,53,53,53	1
4	IOD	A	1104	1/1	0.99	0.09	-	52,52,52,52	1

6.5 Other polymers [i](#)

There are no such residues in this entry.