



# Full wwPDB X-ray Structure Validation Report

Feb 27, 2014 – 03:47 AM GMT

PDB ID : 2C0Q  
Title : NON-AGED FORM OF MOUSE ACETYLCHOLINESTERASE INHIBITED BY TABUN  
Authors : Ekstrom, F.; Akfur, C.; Tunemalm, A.-K.; Lundberg, S.  
Deposited on : 2005-09-07  
Resolution : 2.50 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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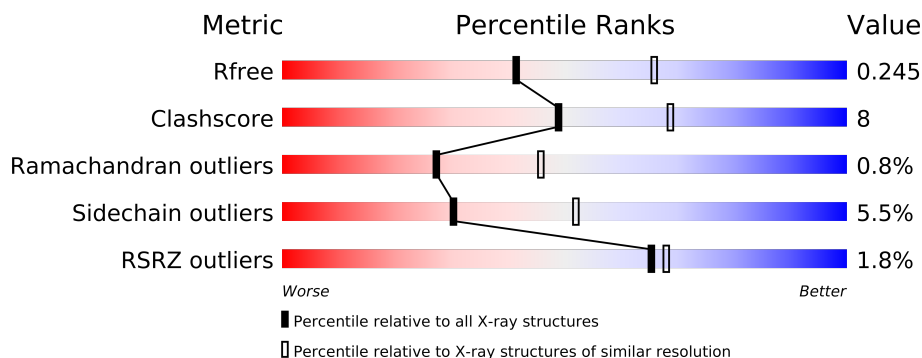
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

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))
$R_{free}$	66092	2784 (2.50-2.50)
Clashscore	79885	3562 (2.50-2.50)
Ramachandran outliers	78287	3480 (2.50-2.50)
Sidechain outliers	78261	3482 (2.50-2.50)
RSRZ outliers	66119	2785 (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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	548	
1	B	548	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	P6G	B	1545	-	X

## 2 Entry composition i

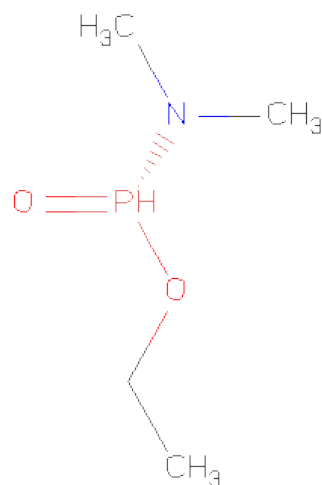
There are 4 unique types of molecules in this entry. The entry contains 8602 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

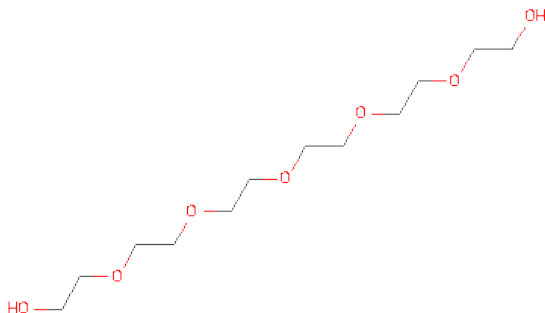
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	535	Total	C	N	O	S	0	0	0
			4177	2679	725	759	14			
1	B	534	Total	C	N	O	S	0	0	1
			4159	2670	719	756	14			

- Molecule 2 is R-ETHYL N,N-DIMETHYLPHOSPHONAMIDATE (three-letter code: NTJ) (formula: C<sub>4</sub>H<sub>12</sub>NO<sub>2</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			8	4	1	2	1		
2	B	1	Total	C	N	O	P	0	0
			8	4	1	2	1		

- Molecule 3 is HEXAETHYLENE GLYCOL (three-letter code: P6G) (formula: C<sub>12</sub>H<sub>26</sub>O<sub>7</sub>).



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

- Molecule 4 is water.

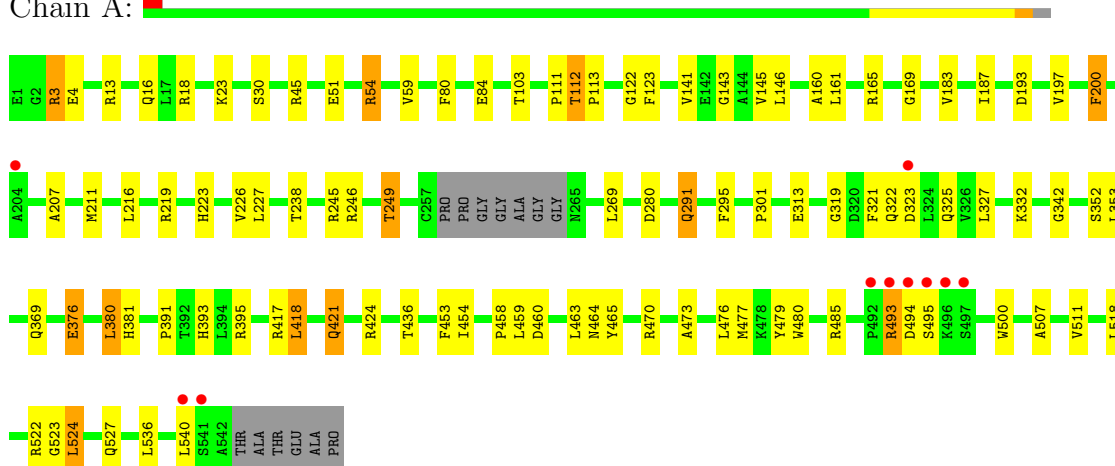
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	134	Total	O	0	0
			134	134		
4	B	97	Total	O	0	0
			97	97		

### 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.

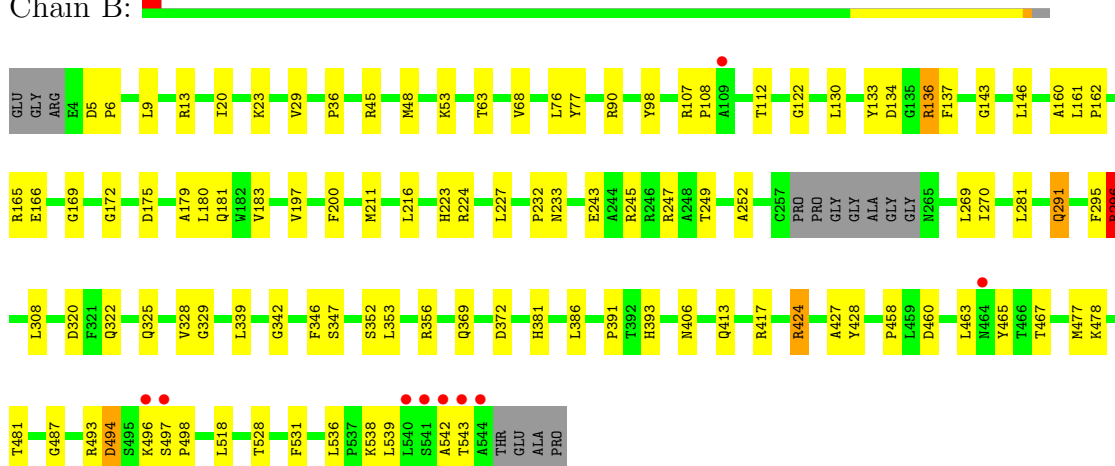
#### • Molecule 1: ACETYLCHOLINESTERASE

Chain A:



#### • Molecule 1: ACETYLCHOLINESTERASE

Chain B:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	79.62Å 112.94Å 226.16Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.17 – 2.50 29.17 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.5 (29.17-2.50) 99.5 (29.17-2.50)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.03 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.196 , 0.246 0.196 , 0.245	Depositor DCC
$R_{free}$ test set	1422 reflections (2.04%)	DCC
Wilson B-factor (Å <sup>2</sup> )	47.9	Xtriage
Anisotropy	0.123	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 24.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 70962 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	8602	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NTJ, 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	0.64	0/4300	0.73	0/5875
1	B	0.65	0/4282	0.72	1/5853 (0.0%)
All	All	0.65	0/8582	0.73	1/11728 (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	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	296	ARG	NE-CZ-NH1	5.56	123.08	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	496	LYS	Peptide
1	B	497	SER	Peptide

### 5.2 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 hydrogens

added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4177	0	4064	65	0
1	B	4159	0	4046	63	0
2	A	8	0	11	1	0
2	B	8	0	11	1	0
3	B	19	0	24	5	0
4	A	134	0	0	6	0
4	B	97	0	0	4	0
All	All	8602	0	8156	127	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 8.

All (127) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:376:GLU:OE2	1:B:538:LYS:HE3	1.59	1.03
1:B:197:VAL:H	1:B:223:HIS:HD2	1.13	0.92
1:A:3:ARG:HH11	1:A:3:ARG:HG3	1.33	0.91
1:A:197:VAL:H	1:A:223:HIS:HD2	1.25	0.83
1:B:369:GLN:HB2	4:B:2065:HOH:O	1.80	0.80
1:A:103:THR:HG22	1:A:145:VAL:HG22	1.65	0.78
1:A:219:ARG:HA	1:A:219:ARG:HE	1.51	0.76
1:A:54:ARG:HH11	1:A:54:ARG:CG	2.03	0.72
1:B:197:VAL:H	1:B:223:HIS:CD2	2.04	0.69
1:A:3:ARG:NH1	1:A:3:ARG:HG3	2.09	0.68
1:B:458:PRO:HA	1:B:465:TYR:CD2	2.29	0.68
1:B:493:ARG:O	1:B:494:ASP:HB2	1.92	0.68
1:A:291:GLN:HE22	1:A:369:GLN:NE2	1.92	0.66
1:A:219:ARG:HA	1:A:219:ARG:NE	2.09	0.66
1:A:353:LEU:HB3	1:A:391:PRO:HB2	1.78	0.66
1:A:54:ARG:HG2	1:A:54:ARG:HH11	1.59	0.65
1:B:291:GLN:HE22	1:B:369:GLN:NE2	1.95	0.65
1:B:227:LEU:HB2	1:B:328:VAL:HG12	1.80	0.64
1:B:161:LEU:HD12	1:B:270:ILE:HD11	1.79	0.63
1:A:369:GLN:HB2	4:A:2104:HOH:O	1.99	0.62
1:A:113:PRO:HG2	1:A:485:ARG:HG2	1.82	0.62
1:B:424:ARG:HB2	1:B:424:ARG:HH11	1.64	0.62
1:B:320:ASP:OD1	1:B:322:GLN:HG2	2.00	0.61
1:A:54:ARG:CB	1:A:54:ARG:HH11	2.13	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:48:MET:HE1	1:B:166:GLU:HA	1.83	0.61
1:A:527:GLN:HE21	3:B:1545:P6G:H171	1.66	0.61
1:A:493:ARG:HB2	4:A:2122:HOH:O	2.01	0.60
1:A:381:HIS:HA	3:B:1545:P6G:H31	1.84	0.59
1:A:424:ARG:HD2	4:A:2112:HOH:O	2.03	0.59
1:A:380:LEU:HB3	3:B:1545:P6G:H51	1.84	0.58
1:A:197:VAL:H	1:A:223:HIS:CD2	2.14	0.58
1:B:460:ASP:HB3	1:B:463:LEU:HD12	1.86	0.58
1:A:380:LEU:HB3	3:B:1545:P6G:C5	2.34	0.57
1:A:122:GLY:HA2	2:A:1543:NTJ:H2C3	1.86	0.57
1:B:107:ARG:HB3	4:B:2020:HOH:O	2.04	0.56
1:A:207:ALA:O	1:A:211:MET:HG2	2.06	0.56
1:B:48:MET:HE1	1:B:165:ARG:O	2.05	0.55
1:A:319:GLY:O	1:A:421:GLN:HG2	2.07	0.55
1:B:245:ARG:O	1:B:249:THR:HG23	2.06	0.55
1:B:68:VAL:HG23	1:B:90:ARG:HB2	1.89	0.54
1:B:112:THR:HG21	1:B:143:GLY:O	2.07	0.54
1:A:219:ARG:CA	1:A:219:ARG:HE	2.20	0.53
1:A:54:ARG:HG2	1:A:54:ARG:NH1	2.25	0.52
1:A:313:GLU:HB2	4:A:2067:HOH:O	2.09	0.52
1:B:477:MET:O	1:B:481:THR:OG1	2.24	0.51
1:A:245:ARG:O	1:A:249:THR:CG2	2.59	0.51
1:A:161:LEU:HD11	1:A:269:LEU:HD22	1.93	0.50
1:A:352:SER:O	1:A:395:ARG:HG3	2.11	0.50
1:B:493:ARG:O	1:B:494:ASP:CB	2.59	0.50
1:A:112:THR:HG21	1:A:143:GLY:O	2.12	0.49
1:B:29:VAL:HG21	1:B:136:ARG:HB2	1.93	0.48
1:B:166:GLU:HG2	1:B:270:ILE:HD13	1.96	0.48
1:B:45:ARG:NH2	1:B:48:MET:SD	2.87	0.48
1:B:498:PRO:HD2	1:B:518:LEU:HB2	1.94	0.48
1:A:245:ARG:O	1:A:249:THR:HG23	2.13	0.48
1:A:80:PHE:O	1:A:84:GLU:HG2	2.14	0.48
1:B:161:LEU:HD12	1:B:270:ILE:CD1	2.44	0.47
1:A:4:GLU:OE2	1:A:18:ARG:HD3	2.14	0.47
1:B:528:THR:O	1:B:531:PHE:HB3	2.14	0.47
1:A:219:ARG:NE	1:A:219:ARG:CA	2.69	0.47
1:B:393:HIS:HB3	4:B:2069:HOH:O	2.13	0.47
1:B:381:HIS:CE1	3:B:1545:P6G:H181	2.50	0.47
1:B:20:ILE:HB	1:B:63:THR:HB	1.95	0.47
1:B:328:VAL:O	1:B:427:ALA:HA	2.15	0.47
1:B:161:LEU:HD11	1:B:269:LEU:HD22	1.96	0.47
1:B:130:LEU:HD12	1:B:133:TYR:CE2	2.50	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:233:ASN:HD22	1:B:413:GLN:HE21	1.61	0.47
1:B:224:ARG:HG2	1:B:325:GLN:HB2	1.97	0.47
1:A:493:ARG:O	1:A:495:SER:N	2.48	0.46
1:A:23:LYS:HG2	4:A:2002:HOH:O	2.14	0.46
1:A:511:VAL:HG11	1:A:518:LEU:HD13	1.96	0.46
1:B:122:GLY:HA2	2:B:1544:NTJ:H2C3	1.97	0.46
1:A:470:ARG:HG2	1:A:470:ARG:HH11	1.81	0.46
1:A:226:VAL:HG22	1:A:327:LEU:HB3	1.97	0.46
1:A:327:LEU:HD11	1:A:500:TRP:CH2	2.51	0.46
1:A:238:THR:HA	1:A:301:PRO:O	2.16	0.46
1:A:393:HIS:HD2	4:A:2107:HOH:O	2.00	0.45
1:B:36:PRO:HB3	1:B:98:TYR:CE1	2.51	0.45
1:B:233:ASN:ND2	1:B:413:GLN:HE21	2.15	0.45
1:B:224:ARG:HD3	1:B:487:GLY:HA2	1.97	0.45
1:A:507:ALA:O	1:A:522:ARG:NH1	2.49	0.45
1:A:463:LEU:O	1:A:464:ASN:HB2	2.17	0.45
1:B:134:ASP:OD2	1:B:136:ARG:HD2	2.17	0.44
1:B:162:PRO:O	1:B:245:ARG:NH1	2.46	0.44
1:B:13:ARG:HD2	4:B:2037:HOH:O	2.17	0.44
1:A:458:PRO:HA	1:A:465:TYR:CD2	2.52	0.44
1:A:111:PRO:HB2	1:A:193:ASP:HB2	2.00	0.44
1:A:200:PHE:CB	1:A:226:VAL:HB	2.47	0.44
1:B:291:GLN:HE22	1:B:369:GLN:HE21	1.66	0.44
1:B:424:ARG:CB	1:B:424:ARG:HH11	2.29	0.44
1:B:339:LEU:HD13	1:B:346:PHE:CE2	2.53	0.44
1:B:243:GLU:O	1:B:247:ARG:HG3	2.18	0.44
1:B:160:ALA:HB2	1:B:169:GLY:CA	2.48	0.44
1:B:136:ARG:HG2	1:B:137:PHE:N	2.33	0.43
1:A:227:LEU:N	1:A:227:LEU:HD12	2.32	0.43
1:A:291:GLN:HE22	1:A:369:GLN:HE22	1.67	0.43
1:A:141:VAL:HG21	1:A:459:LEU:HD23	2.01	0.43
1:B:179:ALA:O	1:B:183:VAL:HG23	2.18	0.43
1:B:48:MET:CE	1:B:166:GLU:HA	2.48	0.43
1:B:296:ARG:NH2	1:B:406:ASN:OD1	2.51	0.42
1:A:473:ALA:O	1:A:477:MET:HG3	2.19	0.42
1:B:424:ARG:CG	1:B:424:ARG:HH11	2.32	0.42
1:A:321:PHE:CD2	1:A:418:LEU:HD12	2.54	0.42
1:B:353:LEU:HB3	1:B:391:PRO:HB2	2.01	0.42
1:A:479:TYR:OH	1:A:518:LEU:HG	2.18	0.42
1:B:211:MET:HG3	1:B:232:PRO:HB3	2.01	0.42
1:B:417:ARG:HE	1:B:417:ARG:HA	1.85	0.42
1:B:76:LEU:HD23	1:B:77:TYR:CE2	2.55	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:160:ALA:HB2	1:A:169:GLY:HA3	2.01	0.41
1:A:183:VAL:HG13	1:A:187:ILE:HB	2.02	0.41
1:B:539:LEU:HA	1:B:539:LEU:HD12	1.80	0.41
1:B:329:GLY:HA3	1:B:428:TYR:CE1	2.56	0.41
1:A:417:ARG:HA	1:A:417:ARG:HD2	1.82	0.41
1:B:252:ALA:HB2	1:B:269:LEU:HD21	2.02	0.41
1:A:454:ILE:HD12	1:A:480:TRP:CE2	2.55	0.41
1:B:36:PRO:HB2	1:B:53:LYS:HD3	2.01	0.41
1:B:5:ASP:HA	1:B:6:PRO:HD3	1.96	0.41
1:B:172:GLY:O	1:B:175:ASP:HB2	2.20	0.41
1:A:45:ARG:HH12	1:A:51:GLU:CD	2.21	0.41
1:A:122:GLY:O	1:A:123:PHE:HB2	2.20	0.41
1:A:16:GLN:HB2	1:A:59:VAL:HA	2.03	0.41
1:B:211:MET:HG2	1:B:308:LEU:HD21	2.03	0.41
1:A:524:LEU:HD13	1:A:524:LEU:HA	1.97	0.40
1:A:319:GLY:O	1:A:421:GLN:CG	2.69	0.40
1:A:453:PHE:HB3	1:A:476:LEU:HD12	2.03	0.40
1:B:329:GLY:HA3	1:B:428:TYR:CZ	2.55	0.40
1:A:460:ASP:HB3	1:A:463:LEU:HD12	2.04	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	531/548 (97%)	508 (96%)	20 (4%)	3 (1%)	33	55
1	B	530/548 (97%)	503 (95%)	22 (4%)	5 (1%)	25	42
All	All	1061/1096 (97%)	1011 (95%)	42 (4%)	8 (1%)	27	46

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	494	ASP

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Mol	Chain	Res	Type
1	B	494	ASP
1	B	542	ALA
1	B	543	THR
1	A	342	GLY
1	A	523	GLY
1	B	108	PRO
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	439/446 (98%)	412 (94%)	27 (6%)	26	45
1	B	438/446 (98%)	417 (95%)	21 (5%)	35	60
All	All	877/892 (98%)	829 (94%)	48 (6%)	30	52

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ARG
1	A	13	ARG
1	A	30	SER
1	A	54	ARG
1	A	112	THR
1	A	146	LEU
1	A	165	ARG
1	A	200	PHE
1	A	216	LEU
1	A	246	ARG
1	A	249	THR
1	A	280	ASP
1	A	291	GLN
1	A	295	PHE
1	A	322	GLN
1	A	323	ASP
1	A	325	GLN
1	A	332	LYS

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Mol	Chain	Res	Type
1	A	376	GLU
1	A	380	LEU
1	A	418	LEU
1	A	421	GLN
1	A	436	THR
1	A	493	ARG
1	A	524	LEU
1	A	536	LEU
1	A	540	LEU
1	B	9	LEU
1	B	23	LYS
1	B	136	ARG
1	B	146	LEU
1	B	180	LEU
1	B	181	GLN
1	B	200	PHE
1	B	216	LEU
1	B	281	LEU
1	B	291	GLN
1	B	295	PHE
1	B	296	ARG
1	B	347	SER
1	B	352	SER
1	B	356	ARG
1	B	372	ASP
1	B	386	LEU
1	B	424	ARG
1	B	467	THR
1	B	478	LYS
1	B	536	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	223	HIS
1	A	287	HIS
1	A	291	GLN
1	A	509	GLN
1	B	223	HIS
1	B	291	GLN
1	B	413	GLN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

3 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	NTJ	A	1543	1	7,7,7	24.98	3 (42%)	7,8,8	1.72	1 (14%)
2	NTJ	B	1544	1	7,7,7	23.17	3 (42%)	7,8,8	5.17	2 (28%)
3	P6G	B	1545	-	18,18,18	1.70	5 (27%)	17,17,17	2.28	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	NTJ	A	1543	1	-	1/2/7/7	0/0/0/0
2	NTJ	B	1544	1	-	0/2/7/7	0/0/0/0
3	P6G	B	1545	-	-	0/16/16/16	0/0/0/0

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1543	NTJ	P1-N1	-65.53	1.47	1.61
2	B	1544	NTJ	P1-N1	-60.66	1.48	1.61
2	B	1544	NTJ	P1-O2	-8.07	1.44	1.58
2	A	1543	NTJ	P1-O2	-8.04	1.44	1.58
2	B	1544	NTJ	P1-O1	-3.51	1.43	1.48
2	A	1543	NTJ	P1-O1	-3.03	1.44	1.48
3	B	1545	P6G	C17-C18	-2.78	1.34	1.49
3	B	1545	P6G	C9-C8	-2.76	1.34	1.48
3	B	1545	P6G	C3-C2	-2.74	1.34	1.49
3	B	1545	P6G	C15-C14	-2.70	1.34	1.48
3	B	1545	P6G	C6-C5	-2.48	1.35	1.48

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1544	NTJ	O1-P1-N1	-13.30	111.98	115.60
3	B	1545	P6G	O7-C8-C9	3.60	126.81	110.47
3	B	1545	P6G	O7-C6-C5	3.55	126.56	110.47
2	A	1543	NTJ	O1-P1-N1	-3.53	114.64	115.60
3	B	1545	P6G	O4-C5-C6	3.00	124.08	110.47
3	B	1545	P6G	O10-C9-C8	2.93	123.79	110.47
3	B	1545	P6G	O16-C15-C14	2.88	123.54	110.47
3	B	1545	P6G	O13-C14-C15	2.76	122.98	110.47
3	B	1545	P6G	O4-C3-C2	2.51	122.68	110.61
2	B	1544	NTJ	P1-O2-C3	-2.43	114.36	120.78
3	B	1545	P6G	C5-O4-C3	2.28	123.42	113.38

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1543	NTJ	P1-O2-C3-C4

There are no ring outliers.

## 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 ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	535/548 (97%)	-0.22	10 (1%) 64 66	29, 43, 62, 86	0
1	B	534/548 (97%)	-0.12	9 (1%) 67 69	31, 48, 68, 88	0
All	All	1069/1096 (97%)	-0.17	19 (1%) 65 68	29, 45, 67, 88	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	544	ALA	9.3
1	B	543	THR	4.9
1	A	495	SER	4.3
1	A	493	ARG	4.1
1	A	541	SER	3.6
1	A	492	PRO	3.5
1	B	497	SER	3.4
1	A	496	LYS	3.1
1	B	109	ALA	2.8
1	B	541	SER	2.8
1	B	496	LYS	2.7
1	A	497	SER	2.6
1	B	542	ALA	2.6
1	A	540	LEU	2.5
1	B	540	LEU	2.4
1	A	204	ALA	2.2
1	A	323	ASP	2.1
1	B	464	ASN	2.1
1	A	494	ASP	2.0

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

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

### 6.3 Carbohydrates

There are no carbohydrates in this entry.

### 6.4 Ligands

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, 95<sup>th</sup> 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	P6G	B	1545	19/19	0.19	3.87	64,70,75,75	0
2	NTJ	A	1543	8/8	0.16	-0.13	39,43,46,47	0
2	NTJ	B	1544	8/8	0.12	-0.50	45,49,54,57	0

### 6.5 Other polymers

There are no such residues in this entry.