



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:52 AM GMT

PDB ID : 2C0P
Title : 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 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

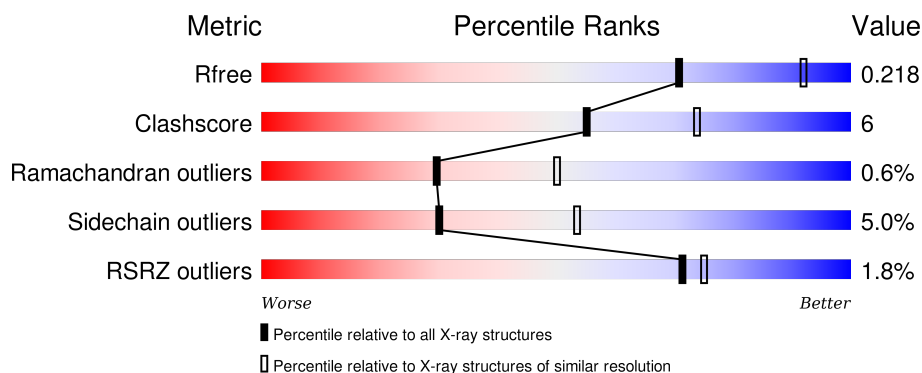
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (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.

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

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	ATJ	A	1543	-	-	-	X
2	ATJ	B	1544	-	-	-	X

2 Entry composition [i](#)

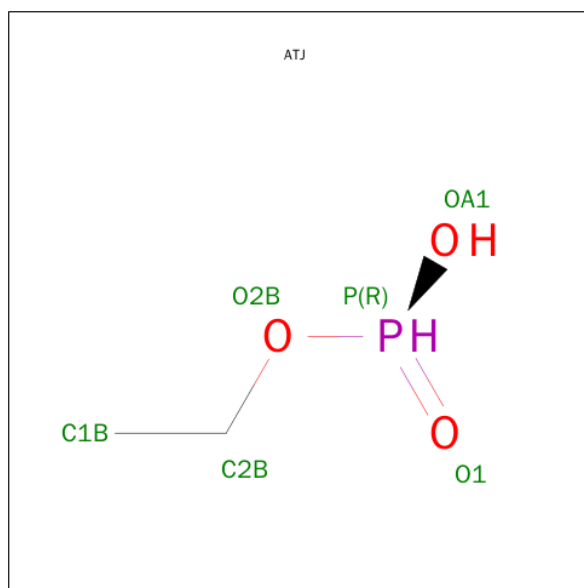
There are 3 unique types of molecules in this entry. The entry contains 8771 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	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 ETHYL HYDROGEN PHOSPHONATE (three-letter code: ATJ) (formula: $C_2H_7O_3P$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			6	2	3	1		
2	B	1	Total	C	O	P	0	0
			6	2	3	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	258	Total 258	O 258	0	0
3	B	165	Total 165	O 165	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	79.02Å 110.88Å 226.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.82 – 2.50 28.81 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.2 (28.82-2.50) 99.2 (28.81-2.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.49 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.182 , 0.220 0.181 , 0.218	Depositor DCC
R_{free} test set	1381 reflections (2.04%)	DCC
Wilson B-factor (Å ²)	49.6	Xtriage
Anisotropy	0.117	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 38.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 69037 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8771	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.73% 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: ATJ

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	0.59	0/4300	0.69	1/5875 (0.0%)
1	B	0.57	0/4282	0.67	0/5853
All	All	0.58	0/8582	0.68	1/11728 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	161	LEU	CA-CB-CG	-6.20	101.05	115.30

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	4177	0	4064	54	0
1	B	4159	0	4046	49	0
2	A	6	0	5	1	0
2	B	6	0	5	1	0
3	A	258	0	0	6	0
3	B	165	0	0	4	0
All	All	8771	0	8120	104	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 6.

All (104) 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:424:ARG:HH11	1:B:424:ARG:HG3	1.14	1.10
1:B:197:VAL:H	1:B:223:HIS:HD2	1.10	0.96
1:A:54:ARG:HG2	1:A:54:ARG:HH11	1.28	0.94
1:B:424:ARG:HG3	1:B:424:ARG:NH1	1.81	0.85
1:B:197:VAL:H	1:B:223:HIS:CD2	1.97	0.83
1:A:433:ARG:HD3	3:A:2225:HOH:O	1.78	0.81
1:A:4:GLU:OE2	1:A:18:ARG:HD3	1.80	0.80
1:A:369:GLN:HB2	3:A:2179:HOH:O	1.81	0.80
1:A:197:VAL:H	1:A:223:HIS:HD2	1.32	0.77
1:B:424:ARG:CG	1:B:424:ARG:HH11	1.97	0.75
1:B:496:LYS:H	1:B:496:LYS:HD3	1.52	0.72
1:B:112:THR:HG21	1:B:143:GLY:O	1.89	0.71
1:B:460:ASP:HB3	1:B:463:LEU:HD12	1.74	0.70
1:A:54:ARG:HH11	1:A:54:ARG:CG	2.03	0.69
1:B:458:PRO:HA	1:B:465:TYR:CD2	2.28	0.68
1:B:211:MET:HG2	1:B:308:LEU:HD21	1.77	0.66
1:A:245:ARG:O	1:A:249:THR:HG22	1.96	0.65
1:B:296:ARG:HG2	3:B:2094:HOH:O	1.96	0.64
1:A:54:ARG:HG2	1:A:54:ARG:NH1	2.07	0.63
1:B:496:LYS:HD3	1:B:496:LYS:N	2.10	0.63
1:A:337:TYR:HA	1:A:443:MET:HE1	1.82	0.62
1:A:113:PRO:HG2	1:A:485:ARG:HG2	1.83	0.61
1:A:245:ARG:O	1:A:249:THR:CG2	2.49	0.60
1:A:76:LEU:HD23	1:A:77:TYR:CE2	2.37	0.60
1:B:316:ILE:O	1:B:421:GLN:NE2	2.33	0.60
1:A:337:TYR:HA	1:A:443:MET:CE	2.32	0.59
1:B:447:HIS:HE1	2:B:1544:ATJ:P	2.26	0.58
1:A:224:ARG:HG2	1:A:325:GLN:HB2	1.86	0.58
1:A:112:THR:HG21	1:A:143:GLY:O	2.03	0.57
1:B:296:ARG:NH2	1:B:406:ASN:OD1	2.37	0.57
1:A:227:LEU:HB2	1:A:328:VAL:HG12	1.87	0.57
1:A:291:GLN:HE22	1:A:369:GLN:NE2	2.03	0.57
1:B:80:PHE:O	1:B:84:GLU:HG2	2.05	0.56
1:B:166:GLU:HG2	1:B:270:ILE:HD13	1.88	0.55
1:A:104:PRO:HG3	1:A:143:GLY:HA2	1.90	0.53
2:A:1543:ATJ:H2B2	3:A:2258:HOH:O	2.07	0.53
1:B:224:ARG:HD3	1:B:487:GLY:HA2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:85:MET:CE	1:B:132:VAL:HG11	2.39	0.53
1:A:207:ALA:O	1:A:211:MET:HG2	2.09	0.52
1:B:328:VAL:O	1:B:427:ALA:HA	2.10	0.52
1:B:224:ARG:HD3	1:B:487:GLY:CA	2.40	0.52
1:B:160:ALA:HB2	1:B:169:GLY:HA3	1.91	0.51
1:B:29:VAL:HG21	1:B:136:ARG:HB2	1.93	0.51
1:A:24:ALA:HB3	1:A:140:GLN:HG3	1.92	0.50
1:B:224:ARG:HG3	1:B:224:ARG:HH11	1.75	0.50
1:B:293:SER:HB3	1:B:368:PRO:HB3	1.94	0.49
1:B:165:ARG:HH11	1:B:165:ARG:HB3	1.77	0.49
1:B:437:LEU:HD11	1:B:449:TYR:CD2	2.47	0.49
1:B:200:PHE:CB	1:B:226:VAL:HB	2.42	0.49
1:A:103:THR:HG21	1:A:190:PHE:HB3	1.95	0.49
1:A:507:ALA:O	1:A:522:ARG:NH1	2.46	0.49
1:A:5:ASP:HB3	1:A:8:LEU:HD12	1.96	0.48
1:B:224:ARG:HG3	1:B:224:ARG:NH1	2.28	0.48
1:B:390:ASP:OD2	1:B:393:HIS:ND1	2.47	0.48
1:B:68:VAL:HG11	1:B:88:PRO:HB3	1.96	0.48
1:A:458:PRO:HA	1:A:465:TYR:CD2	2.49	0.47
1:B:160:ALA:HB2	1:B:169:GLY:CA	2.44	0.47
1:A:433:ARG:CZ	1:A:437:LEU:HD23	2.45	0.47
1:A:203:SER:HB2	1:A:447:HIS:NE2	2.28	0.47
1:A:219:ARG:HA	1:A:219:ARG:HD2	1.65	0.47
1:A:29:VAL:HG21	1:A:136:ARG:HB2	1.97	0.47
1:A:80:PHE:O	1:A:84:GLU:HG2	2.14	0.47
1:B:165:ARG:NH1	1:B:165:ARG:HB3	2.30	0.46
1:B:113:PRO:HG2	1:B:485:ARG:HG2	1.98	0.46
1:B:393:HIS:HB3	3:B:2116:HOH:O	2.17	0.45
1:B:353:LEU:HB3	1:B:391:PRO:HB2	1.98	0.45
1:A:291:GLN:HE22	1:A:369:GLN:HE22	1.63	0.45
1:A:200:PHE:CB	1:A:226:VAL:HB	2.46	0.45
1:A:68:VAL:HG23	1:A:90:ARG:HB2	1.99	0.45
1:A:291:GLN:NE2	1:A:369:GLN:NE2	2.64	0.45
1:A:39:GLU:OE2	1:A:54:ARG:HB2	2.17	0.45
1:B:136:ARG:HG2	1:B:137:PHE:N	2.32	0.45
1:B:176:GLN:OE1	1:B:208:SER:HB3	2.18	0.44
1:B:369:GLN:HE22	1:B:405:HIS:CE1	2.36	0.44
1:A:141:VAL:HG21	1:A:459:LEU:HD23	2.00	0.43
1:A:397:ALA:O	1:A:401:VAL:HG23	2.17	0.43
1:A:453:PHE:HB3	1:A:476:LEU:HD12	2.00	0.43
1:B:453:PHE:HB3	1:B:476:LEU:HD12	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:459:LEU:HD11	1:A:474:GLN:HG3	2.00	0.43
1:A:355:SER:OG	1:A:358:GLN:HG3	2.18	0.43
1:A:393:HIS:HB2	3:A:2209:HOH:O	2.17	0.43
1:B:48:MET:SD	3:B:2066:HOH:O	2.61	0.43
1:A:46:ARG:HD3	1:A:47:PHE:CZ	2.54	0.43
1:A:21:ARG:HG3	1:A:105:TYR:CE1	2.54	0.43
1:A:527:GLN:HG3	3:A:2252:HOH:O	2.19	0.42
1:B:528:THR:O	1:B:531:PHE:HB3	2.20	0.42
1:A:472:PHE:CZ	1:A:476:LEU:HD11	2.54	0.42
1:B:45:ARG:HD2	1:B:51:GLU:OE1	2.20	0.42
1:A:122:GLY:O	1:A:123:PHE:HB2	2.20	0.42
1:A:243:GLU:OE1	1:A:246:ARG:NH1	2.53	0.42
1:A:541:SER:O	1:A:542:ALA:HB2	2.20	0.42
1:B:10:VAL:HG23	1:B:32:PHE:CE2	2.55	0.42
1:A:85:MET:CE	1:A:132:VAL:HG11	2.49	0.42
1:B:302:VAL:HG13	1:B:304:ASP:HB3	2.02	0.41
1:B:408:VAL:HG11	1:B:525:ARG:HG3	2.01	0.41
1:A:118:ILE:O	1:A:205:GLY:HA3	2.20	0.41
1:A:88:PRO:HD3	3:A:2060:HOH:O	2.20	0.41
1:B:130:LEU:HD12	1:B:133:TYR:CE2	2.56	0.41
1:A:408:VAL:HG11	1:A:525:ARG:HG3	2.03	0.41
1:B:497:SER:H	1:B:498:PRO:HA	1.84	0.41
1:A:463:LEU:O	1:A:464:ASN:HB2	2.21	0.40
1:A:353:LEU:HB3	1:A:391:PRO:HB2	2.03	0.40
1:A:54:ARG:NH1	1:A:54:ARG:CG	2.72	0.40
1:B:119:TYR:HB2	3:B:2057:HOH:O	2.20	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%)	506 (95%)	24 (4%)	1 (0%)	52	75
1	B	530/548 (97%)	500 (94%)	25 (5%)	5 (1%)	21	37
All	All	1061/1096 (97%)	1006 (95%)	49 (5%)	6 (1%)	30	50

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	494	ASP
1	B	337	TYR
1	B	543	THR
1	B	496	LYS
1	B	497	SER
1	B	541	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	439/446 (98%)	418 (95%)	21 (5%)	31	55
1	B	438/446 (98%)	415 (95%)	23 (5%)	28	50
All	All	877/892 (98%)	833 (95%)	44 (5%)	30	53

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ARG
1	A	13	ARG
1	A	21	ARG
1	A	23	LYS
1	A	54	ARG
1	A	70	TYR
1	A	200	PHE
1	A	211	MET
1	A	216	LEU
1	A	249	THR

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Mol	Chain	Res	Type
1	A	291	GLN
1	A	295	PHE
1	A	322	GLN
1	A	356	ARG
1	A	380	LEU
1	A	418	LEU
1	A	478	LYS
1	A	493	ARG
1	A	524	LEU
1	A	525	ARG
1	A	536	LEU
1	B	9	LEU
1	B	23	LYS
1	B	136	ARG
1	B	161	LEU
1	B	165	ARG
1	B	180	LEU
1	B	181	GLN
1	B	200	PHE
1	B	246	ARG
1	B	281	LEU
1	B	291	GLN
1	B	295	PHE
1	B	296	ARG
1	B	348	LYS
1	B	352	SER
1	B	356	ARG
1	B	386	LEU
1	B	424	ARG
1	B	441	LEU
1	B	467	THR
1	B	496	LYS
1	B	497	SER
1	B	536	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

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

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Mol	Chain	Res	Type
1	B	291	GLN
1	B	447	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

2 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	ATJ	A	1543	1	1,5,5	0.80	0	1,5,5	0.28	0
2	ATJ	B	1544	1	1,5,5	1.00	0	1,5,5	0.62	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
2	ATJ	A	1543	1	-	0/1/3/3	0/0/0/0
2	ATJ	B	1544	1	-	0/1/3/3	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1543	ATJ	1	0
2	B	1544	ATJ	1	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 [i](#)

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

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	535/548 (97%)	-0.30	10 (1%) 70 73	29, 45, 70, 114	0
1	B	534/548 (97%)	-0.22	9 (1%) 73 76	31, 51, 77, 117	0
All	All	1069/1096 (97%)	-0.26	19 (1%) 71 75	29, 47, 75, 117	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	543	THR	5.5
1	A	540	LEU	4.1
1	B	541	SER	3.7
1	B	542	ALA	3.5
1	A	497	SER	3.5
1	A	495	SER	3.4
1	A	496	LYS	3.3
1	B	544	ALA	3.3
1	A	493	ARG	2.9
1	A	76	LEU	2.7
1	A	541	SER	2.5
1	B	492	PRO	2.4
1	B	110	SER	2.2
1	A	226	VAL	2.1
1	A	165	ARG	2.1
1	B	42	VAL	2.1
1	B	165	ARG	2.1
1	B	497	SER	2.1
1	A	204	ALA	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](#)

There are no carbohydrates 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. 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(\AA^2)	Q<0.9
2	ATJ	B	1544	6/6	0.95	0.25	4.14	42,45,61,63	0
2	ATJ	A	1543	6/6	0.98	0.28	2.54	38,40,56,59	0

6.5 Other polymers [i](#)

There are no such residues in this entry.