



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:32 AM GMT

PDB ID : 2DFP
Title : X-RAY STRUCTURE OF AGED DI-ISOPROPYL-PHOSPHORO-FLUORIDE (DFP) BOUND TO ACETYLCHOLINESTERASE
Authors : Kryger, G.; Millard, C.B.; Silman, I.; Sussman, J.L.
Deposited on : 1998-12-07
Resolution : 2.30 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

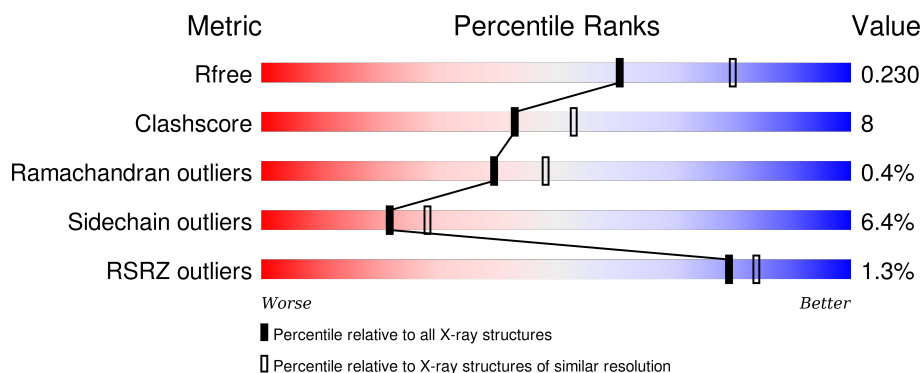
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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	534	<div> <div></div> <div>77%</div> <div>19%</div> <div>..</div> </div>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4728 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.

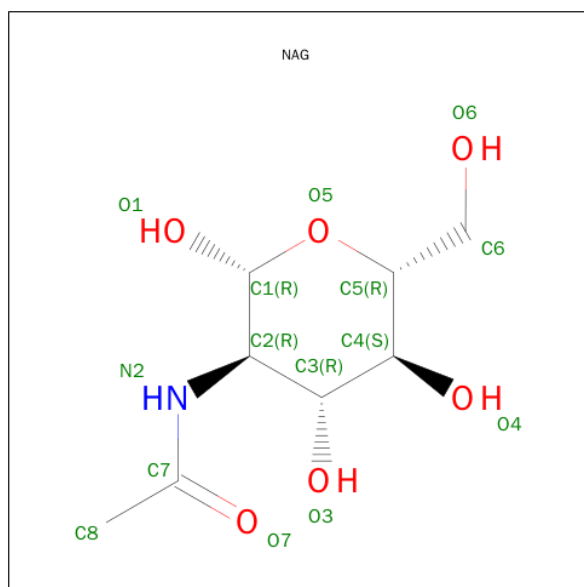
- Molecule 1 is a protein called PROTEIN (ACETYLCHOLINESTERASE).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	534	Total	C	N	O	P	S	0	0	0
			4270	2734	724	789	1	22			

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

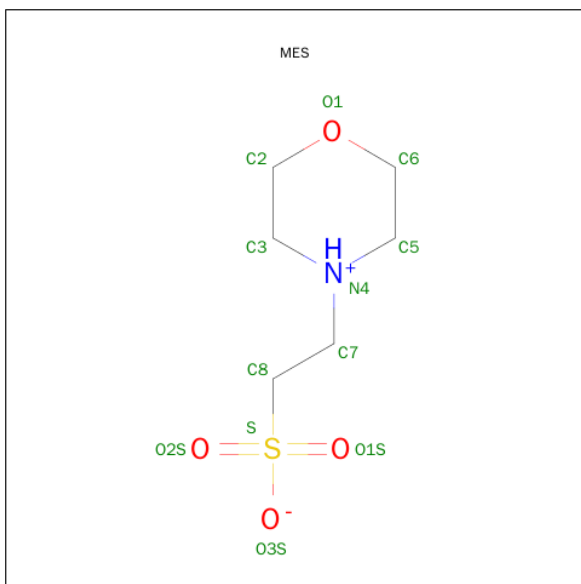
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	2	Total	C	N	O	0	0
			28	16	2	10		
2	A	2	Total	C	N	O	0	0
			28	16	2	10		

- 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		

- Molecule 4 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

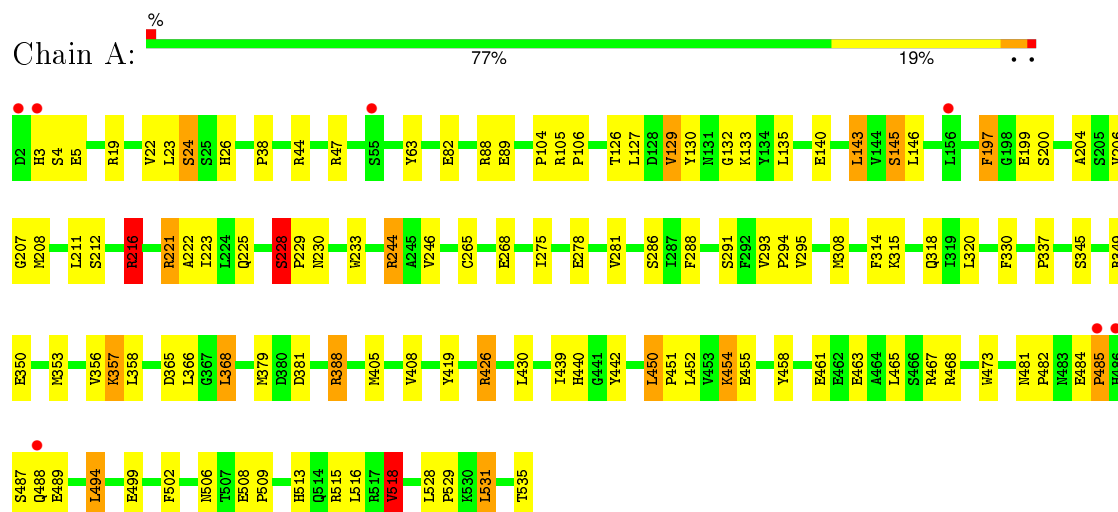
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	376	Total	O	0	0
			376	376		

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: PROTEIN (ACETYLCHOLINESTERASE)



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	112.64Å 112.64Å 136.88Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.30 19.63 – 2.20	Depositor EDS
% Data completeness (in resolution range)	93.7 (20.00-2.30) 87.5 (19.63-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.60 (at 2.21Å)	Xtriage
Refinement program	CNS 0.4	Depositor
R, R_{free}	0.186 , 0.228 0.190 , 0.230	Depositor DCC
R_{free} test set	1874 reflections (4.44%)	DCC
Wilson B-factor (Å ²)	38.0	Xtriage
Anisotropy	0.563	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 46.2	EDS
Estimated twinning fraction	0.027 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 44916 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4728	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.24% 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: MIS, NAG, MES

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	0.92	2/4380 (0.0%)	0.96	16/5944 (0.3%)

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	A	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	228	SER	CB-OG	-6.02	1.34	1.42
1	A	145	SER	CB-OG	-5.32	1.35	1.42

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	426	ARG	NE-CZ-NH2	-9.54	115.53	120.30
1	A	221	ARG	NE-CZ-NH2	-8.42	116.09	120.30
1	A	531	LEU	CA-CB-CG	7.96	133.62	115.30
1	A	426	ARG	NE-CZ-NH1	7.72	124.16	120.30
1	A	216	ARG	NE-CZ-NH1	6.48	123.54	120.30
1	A	216	ARG	NE-CZ-NH2	-6.35	117.12	120.30
1	A	129	VAL	CB-CA-C	-6.21	99.60	111.40
1	A	494	LEU	CA-CB-CG	6.06	129.24	115.30
1	A	221	ARG	NE-CZ-NH1	6.04	123.32	120.30
1	A	518	VAL	CB-CA-C	-5.89	100.20	111.40
1	A	244	ARG	NE-CZ-NH2	-5.76	117.42	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	379	MET	CG-SD-CE	5.74	109.39	100.20
1	A	308	MET	CG-SD-CE	5.48	108.96	100.20
1	A	228	SER	CB-CA-C	-5.29	100.06	110.10
1	A	388	ARG	NE-CZ-NH1	5.15	122.88	120.30
1	A	47	ARG	NE-CZ-NH1	5.05	122.82	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	442	TYR	Sidechain

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	4270	0	4111	69	0
2	A	56	0	50	0	0
3	A	14	0	13	1	0
4	A	12	0	13	0	0
5	A	376	0	0	9	0
All	All	4728	0	4187	70	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 8.

All (70) 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:A:22:VAL:HG13	1:A:133:LYS:HG3	1.63	0.79
1:A:468:ARG:HD3	5:A:2327:HOH:O	1.84	0.78
1:A:487:SER:OG	1:A:489:GLU:HG2	1.90	0.71
1:A:485:PRO:HA	5:A:2363:HOH:O	1.92	0.70
1:A:366:LEU:HD23	1:A:535:THR:HG21	1.77	0.65
1:A:223:ILE:HA	1:A:320:LEU:O	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:275:ILE:HA	1:A:278:GLU:OE1	1.99	0.63
1:A:345:SER:O	1:A:388:ARG:HG3	2.01	0.60
1:A:426:ARG:HD3	5:A:2085:HOH:O	2.02	0.60
1:A:5:GLU:OE2	1:A:104:PRO:HA	2.02	0.59
1:A:419:TYR:CZ	1:A:494:LEU:HD13	2.37	0.59
1:A:452:LEU:HD13	1:A:467:ARG:NH2	2.18	0.58
1:A:515:ARG:O	1:A:518:VAL:HG22	2.05	0.57
1:A:197:PHE:CB	1:A:223:ILE:HB	2.34	0.57
1:A:451:PRO:HA	1:A:458:TYR:CD2	2.41	0.55
1:A:63:TYR:CD1	1:A:126:THR:HG22	2.43	0.54
1:A:461:GLU:CD	1:A:461:GLU:H	2.10	0.54
1:A:366:LEU:CD2	1:A:535:THR:HG21	2.38	0.54
1:A:127:LEU:HD12	1:A:130:TYR:CE2	2.44	0.53
1:A:349:ARG:HD3	1:A:381:ASP:O	2.09	0.52
1:A:452:LEU:HD22	1:A:463:GLU:HG3	1.91	0.52
1:A:200:MIS:H33	1:A:233:TRP:CE2	2.45	0.52
1:A:23:LEU:HD11	1:A:452:LEU:HD12	1.93	0.50
1:A:204:ALA:O	1:A:208:MET:HG3	2.11	0.50
1:A:216:ARG:HB3	1:A:315:LYS:HB2	1.93	0.49
1:A:212:SER:O	1:A:216:ARG:HG2	2.13	0.49
1:A:405:MET:HA	1:A:408:VAL:HG12	1.94	0.48
1:A:132:GLY:HA3	1:A:143:LEU:HD22	1.94	0.48
1:A:244:ARG:HD3	1:A:291:SER:HB3	1.95	0.48
1:A:197:PHE:HB3	1:A:223:ILE:HB	1.95	0.48
1:A:197:PHE:HB2	1:A:223:ILE:HB	1.96	0.47
1:A:88:ARG:CD	5:A:2264:HOH:O	2.62	0.47
1:A:528:LEU:HB3	1:A:529:PRO:HD3	1.95	0.47
1:A:19:ARG:NH2	1:A:26:HIS:HB2	2.30	0.47
1:A:454:LYS:HG3	1:A:455:GLU:N	2.30	0.47
1:A:293:VAL:HB	1:A:294:PRO:HD2	1.96	0.47
1:A:484:GLU:HB2	1:A:487:SER:HB3	1.97	0.46
1:A:24:SER:HA	5:A:2179:HOH:O	2.16	0.46
1:A:199:GLU:HA	1:A:225:GLN:O	2.16	0.45
1:A:211:LEU:HD23	1:A:314:PHE:HB3	1.99	0.45
1:A:452:LEU:HD13	1:A:467:ARG:CZ	2.45	0.45
1:A:465:LEU:HD13	1:A:506:ASN:O	2.17	0.45
1:A:88:ARG:HD2	5:A:2264:HOH:O	2.16	0.45
1:A:481:ASN:OD1	1:A:482:PRO:HD2	2.17	0.45
1:A:22:VAL:O	1:A:23:LEU:C	2.56	0.44
1:A:487:SER:OG	1:A:488:GLN:N	2.51	0.44
1:A:508:GLU:HB3	1:A:509:PRO:HD2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:450:LEU:HD23	1:A:450:LEU:N	2.33	0.43
1:A:265:CYS:O	1:A:268:GLU:HB2	2.18	0.43
1:A:82:GLU:HG2	5:A:2204:HOH:O	2.18	0.43
1:A:135:LEU:HD23	1:A:143:LEU:CD1	2.49	0.43
1:A:357:LYS:HG2	1:A:368:LEU:HD21	2.01	0.43
1:A:228:SER:HB3	1:A:230:ASN:OD1	2.19	0.43
1:A:439:ILE:HG22	1:A:440:HIS:O	2.19	0.43
1:A:206:VAL:CG1	1:A:222:ALA:HB1	2.49	0.42
1:A:353:MET:HG3	5:A:2106:HOH:O	2.18	0.42
1:A:216:ARG:HG2	1:A:216:ARG:H	1.49	0.42
1:A:349:ARG:HA	1:A:349:ARG:HD2	1.89	0.41
1:A:508:GLU:HB3	1:A:509:PRO:CD	2.51	0.41
1:A:286:SER:OG	1:A:288:PHE:O	2.38	0.41
1:A:350:GLU:HA	1:A:350:GLU:OE1	2.20	0.41
1:A:19:ARG:CZ	1:A:26:HIS:HB2	2.50	0.41
1:A:146:LEU:C	1:A:146:LEU:HD12	2.40	0.41
3:A:3001:NAG:O6	5:A:2368:HOH:O	2.22	0.41
1:A:502:PHE:CZ	1:A:513:HIS:HB2	2.55	0.41
1:A:105:ARG:HA	1:A:106:PRO:HD3	1.92	0.41
1:A:221:ARG:HD3	1:A:318:GLN:OE1	2.21	0.41
1:A:484:GLU:HB2	1:A:487:SER:CB	2.51	0.41
1:A:135:LEU:HD23	1:A:143:LEU:HD11	2.03	0.40
1:A:207:GLY:HA3	1:A:229:PRO:HD3	2.03	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	531/534 (99%)	508 (96%)	21 (4%)	2 (0%)	39 48

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	HIS
1	A	485	PRO

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	466/466 (100%)	436 (94%)	30 (6%)	22	28

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	SER
1	A	24	SER
1	A	38	PRO
1	A	44	ARG
1	A	89	GLU
1	A	129	VAL
1	A	140	GLU
1	A	143	LEU
1	A	145	SER
1	A	197	PHE
1	A	216	ARG
1	A	228	SER
1	A	246	VAL
1	A	281	VAL
1	A	295	VAL
1	A	330	PHE
1	A	337	PRO
1	A	356	VAL
1	A	357	LYS
1	A	358	LEU
1	A	365	ASP
1	A	368	LEU
1	A	430	LEU
1	A	450	LEU
1	A	454	LYS

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Mol	Chain	Res	Type
1	A	473	TRP
1	A	499	GLU
1	A	516	LEU
1	A	518	VAL
1	A	531	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	68	GLN
1	A	526	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	MIS	A	200	1	11,12,13	1.72	2 (18%)	11,16,18	1.49	2 (18%)

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	MIS	A	200	1	-	0/11/13/15	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	200	MIS	P-O3P	-4.80	1.47	1.60
1	A	200	MIS	P-OG	-2.32	1.48	1.59

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	200	MIS	O-C-CA	-3.04	117.57	125.49
1	A	200	MIS	P-O3P-C1	2.94	130.16	119.41

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	200	MIS	1	0

5.5 Carbohydrates [i](#)

4 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	3002	1,2	14,14,15	0.72	0	15,19,21	0.92	0
2	NAG	A	3003	2	14,14,15	1.38	1 (7%)	15,19,21	1.33	1 (6%)
2	NAG	A	3004	1,2	14,14,15	1.42	3 (21%)	15,19,21	1.03	1 (6%)
2	NAG	A	3005	2	14,14,15	1.15	2 (14%)	15,19,21	0.96	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	NAG	A	3002	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	3003	2	-	0/6/23/26	0/1/1/1
2	NAG	A	3004	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	3005	2	-	0/6/23/26	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	3005	NAG	C8-C7	2.00	1.54	1.50
2	A	3004	NAG	O5-C5	2.06	1.48	1.43
2	A	3005	NAG	C1-C2	2.08	1.55	1.52
2	A	3004	NAG	O5-C1	2.13	1.47	1.43
2	A	3004	NAG	C1-C2	2.97	1.56	1.52
2	A	3003	NAG	C4-C5	3.08	1.59	1.53

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	3003	NAG	C2-N2-C7	-4.77	116.91	123.04
2	A	3004	NAG	C2-N2-C7	-2.68	119.59	123.04

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.6 Ligand geometry [i](#)

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	$\# Z > 2$
3	NAG	A	3001	1	14,14,15	1.10	0	15,19,21	0.92	1 (6%)
4	MES	A	4001	-	11,12,12	6.09	6 (54%)	14,16,16	2.69	6 (42%)

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
3	NAG	A	3001	1	-	0/6/23/26	0/1/1/1
4	MES	A	4001	-	-	0/6/14/14	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	4001	MES	C7-C8	-3.25	1.41	1.52
4	A	4001	MES	C7-N4	-2.76	1.40	1.47
4	A	4001	MES	C3-C2	-2.33	1.40	1.50
4	A	4001	MES	O2S-S	9.90	1.76	1.45
4	A	4001	MES	O1S-S	10.85	1.79	1.45
4	A	4001	MES	O3S-S	12.47	1.78	1.46

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	4001	MES	O3S-S-O2S	-3.28	103.99	111.61
3	A	3001	NAG	C2-N2-C7	-2.70	119.56	123.04
4	A	4001	MES	O3S-S-O1S	-2.61	105.55	111.61
4	A	4001	MES	O1-C2-C3	-2.36	106.43	111.84
4	A	4001	MES	C7-C8-S	3.56	123.54	112.51
4	A	4001	MES	O2S-S-C8	3.62	110.00	106.91
4	A	4001	MES	O1S-S-C8	6.78	112.69	106.91

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	3001	NAG	1	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

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	533/534 (99%)	-0.43	7 (1%) 79 84	25, 39, 60, 91	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	ASP	7.1
1	A	3	HIS	6.7
1	A	486	HIS	4.6
1	A	488	GLN	4.1
1	A	485	PRO	3.6
1	A	55	SER	3.0
1	A	156	LEU	2.2

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

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
1	MIS	A	200	13/14	0.99	0.07	-	26,28,33,34	0

6.3 Carbohydrates

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	NAG	A	3005	14/15	0.78	0.48	-	67,73,75,76	0
2	NAG	A	3002	14/15	0.92	0.24	-	45,51,58,63	0
2	NAG	A	3004	14/15	0.91	0.36	-	70,72,73,73	0
2	NAG	A	3003	14/15	0.85	0.44	-	61,69,73,75	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(\AA^2)	Q<0.9
4	MES	A	4001	12/12	0.95	0.16	1.22	64,66,67,67	0
3	NAG	A	3001	14/15	0.87	0.27	-	67,69,72,74	0

6.5 Other polymers [i](#)

There are no such residues in this entry.