Full wwPDB X-ray Structure Validation Report (i)

Aug 26, 2023 – 11:19 PM EDT

PDB ID	:	3F96
Title	:	Crystal structure of human plasma platelet activating factor acetylhydrolase covalently inhibited by sarin
Authors	:	Samanta, U.; Bahnson, B.J.
Deposited on	:	2008-11-13
Resolution	:	2.10 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

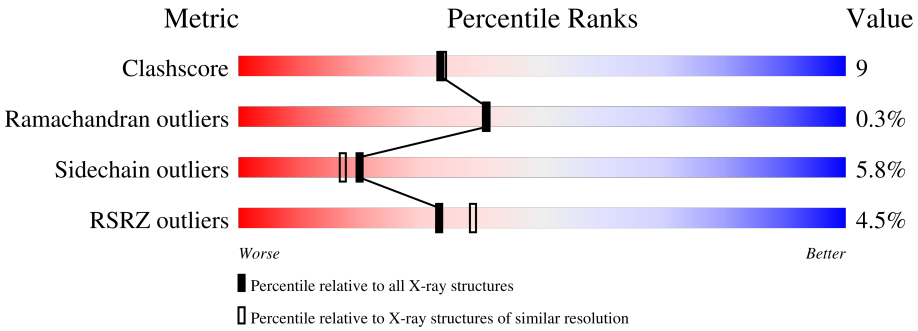
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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 <=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	383	6% 71% 24%
1	B	383	2% 77% 18%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 6196 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 Platelet-activating factor acetylhydrolase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	371	Total	C	N	O	P	S	0	3	0
			3000	1919	513	554	1	13			
1	B	371	Total	C	N	O	P	S	0	3	0
			3000	1920	513	553	1	13			

- Molecule 2 is water.

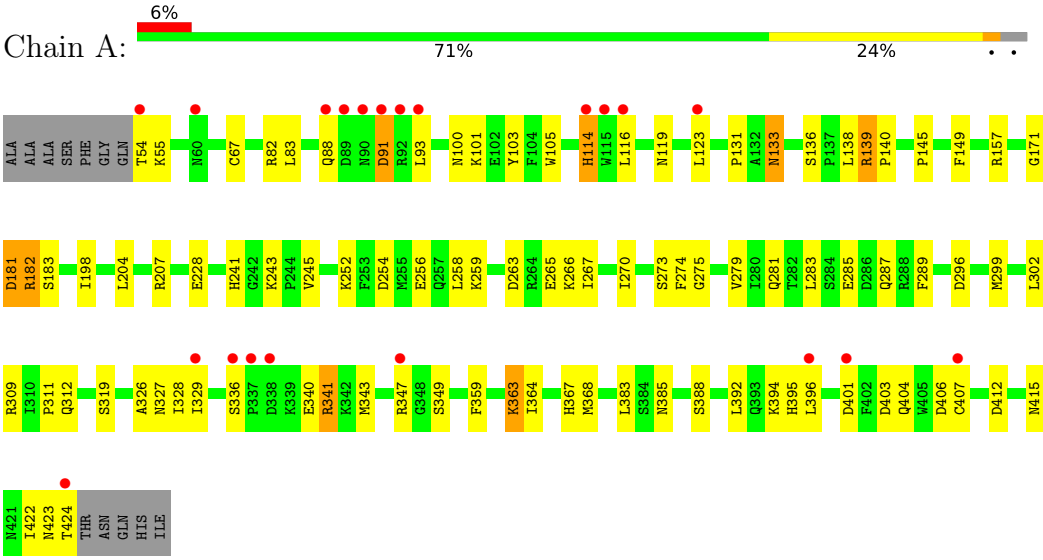
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	86	Total	O	0	0
			86	86		
2	B	110	Total	O	0	0
			110	110		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

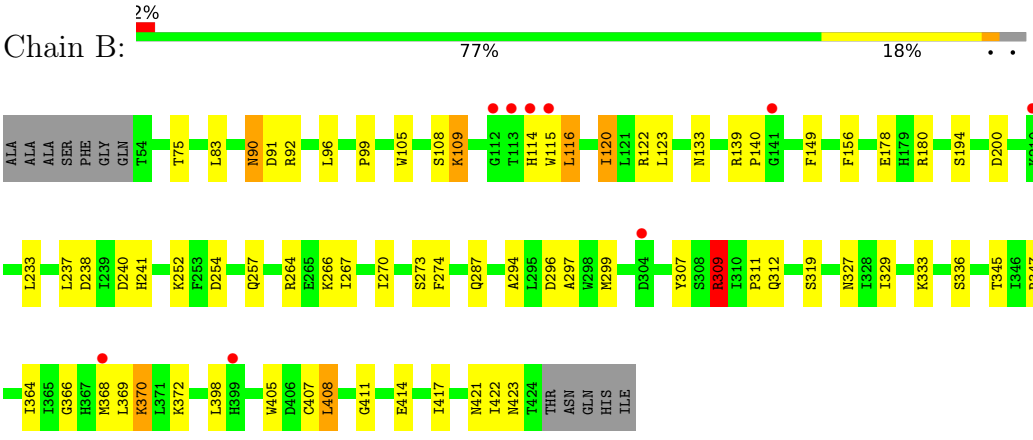
• Molecule 1: Platelet-activating factor acetylhydrolase

Chain A:



• Molecule 1: Platelet-activating factor acetylhydrolase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	116.08Å 82.45Å 96.59Å 90.00° 115.11° 90.00°	Depositor
Resolution (Å)	50.00 – 2.10 35.02 – 2.10	Depositor EDS
% Data completeness (in resolution range)	95.7 (50.00-2.10) 95.6 (35.02-2.10)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.07 (at 2.10Å)	Xtriage
Refinement program	REFMAC OF CCP4I FOR FINAL REFINEMENT	Depositor
R, R_{free}	0.206 , 0.278 0.210 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	32.5	Xtriage
Anisotropy	0.321	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 47.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6196	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.43% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 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: SGB

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	1.00	1/3063 (0.0%)	0.89	5/4140 (0.1%)
1	B	1.00	0/3063	0.94	4/4138 (0.1%)
All	All	1.00	1/6126 (0.0%)	0.91	9/8278 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	228	GLU	CB-CG	5.13	1.61	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	200	ASP	CB-CG-OD1	6.11	123.80	118.30
1	A	416	LEU	CA-CB-CG	5.93	128.94	115.30
1	A	181	ASP	CB-CG-OD1	5.91	123.62	118.30
1	B	83	LEU	CA-CB-CG	5.84	128.73	115.30
1	A	423	ASN	N-CA-C	5.70	126.39	111.00
1	A	341	ARG	NE-CZ-NH2	-5.44	117.58	120.30
1	B	309	ARG	NE-CZ-NH2	-5.37	117.62	120.30
1	B	238	ASP	CB-CG-OD1	5.25	123.02	118.30
1	A	343	MET	CG-SD-CE	5.02	108.22	100.20

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	3000	0	2952	63	0
1	B	3000	0	2957	44	0
2	A	86	0	0	1	0
2	B	110	0	0	1	0
All	All	6196	0	5909	103	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 9.

All (103) 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:256:GLU:HB2	1:A:259:LYS:HE2	1.49	0.93
1:B:299:MET:H	1:B:327:ASN:HD21	1.27	0.81
1:A:299:MET:H	1:A:327:ASN:HD21	1.35	0.74
1:B:422:ILE:HG22	1:B:422:ILE:O	1.87	0.74
1:A:401:ASP:O	1:A:404:GLN:HG2	1.87	0.73
1:A:182:ARG:HH11	1:A:207:ARG:CG	2.02	0.73
1:A:383:LEU:HD22	1:A:416:LEU:HD21	1.71	0.73
1:A:311:PRO:HB2	1:A:312[B]:GLN:NE2	2.05	0.71
1:A:311:PRO:HB2	1:A:312[B]:GLN:HE22	1.56	0.70
1:A:182:ARG:HH11	1:A:207:ARG:HG3	1.63	0.63
1:A:319:SER:HA	1:A:349:SER:OG	1.99	0.62
1:B:105:TRP:O	1:B:109:LYS:HG3	2.00	0.61
1:B:307:TYR:CD1	1:B:333:LYS:O	2.55	0.60
1:B:347:ARG:NH1	1:B:414:GLU:O	2.34	0.60
1:B:309:ARG:HH11	1:B:309:ARG:CG	2.14	0.60
1:B:307:TYR:HD1	1:B:333:LYS:O	1.86	0.59
1:A:394:LYS:HB3	1:A:395:HIS:CD2	2.39	0.58
1:A:347:ARG:HD2	1:A:417:ILE:HG12	1.86	0.58
1:A:93:LEU:HB3	1:A:131:PRO:HA	1.85	0.57
1:A:182:ARG:HH11	1:A:207:ARG:HG2	1.68	0.57
1:B:114:HIS:CD2	1:B:115:TRP:H	2.23	0.57
1:A:392:LEU:O	1:A:396:LEU:HB2	2.04	0.56
1:B:216:HIS:NE2	1:B:220:GLU:OE2	2.38	0.56
1:A:101:LYS:HD2	1:A:105:TRP:CZ2	2.40	0.56
1:A:88:GLN:HA	1:A:139:ARG:HD2	1.87	0.56
1:B:311:PRO:HD2	1:B:312:GLN:OE1	2.06	0.55
1:A:265[B]:GLU:OE2	1:B:287:GLN:HG3	2.07	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:ARG:HG2	1:A:139:ARG:HH11	1.72	0.55
1:A:364:ILE:O	1:A:368:MET:HG2	2.07	0.55
1:B:90:ASN:HD22	1:B:133:ASN:HD21	1.55	0.55
1:A:309:ARG:HD3	1:B:241:HIS:CD2	2.43	0.54
1:A:182:ARG:HD3	1:A:207:ARG:HG3	1.89	0.54
1:A:326:ALA:O	1:A:329:ILE:HG22	2.08	0.54
1:B:364:ILE:O	1:B:368:MET:HG3	2.09	0.53
1:B:407:CYS:O	1:B:411:GLY:O	2.27	0.53
1:B:414:GLU:CD	1:B:414:GLU:H	2.12	0.53
1:A:182:ARG:NH1	1:A:207:ARG:HG2	2.25	0.51
1:B:216:HIS:CE1	1:B:220:GLU:OE2	2.63	0.51
1:A:299:MET:H	1:A:327:ASN:ND2	2.06	0.51
1:A:139:ARG:HG2	1:A:139:ARG:NH1	2.25	0.51
1:A:114:HIS:HD2	1:A:116:LEU:H	1.58	0.50
1:A:182:ARG:HB3	1:A:207:ARG:HG3	1.94	0.50
1:A:114:HIS:CD2	1:A:116:LEU:H	2.31	0.49
1:B:91:ASP:O	1:B:92:ARG:HG3	2.12	0.49
1:A:283:LEU:HD22	1:A:312[B]:GLN:HG2	1.95	0.48
1:A:55:LYS:HB3	1:A:359:PHE:O	2.14	0.47
1:A:157:ARG:HB3	1:A:178:GLU:HB2	1.96	0.47
1:A:133:ASN:ND2	2:A:493:HOH:O	2.47	0.47
1:B:405:TRP:HB3	1:B:408:LEU:HD22	1.97	0.47
1:A:299:MET:HE3	1:A:302:LEU:HD12	1.95	0.47
1:B:99:PRO:HB3	2:B:470:HOH:O	2.15	0.46
1:B:114:HIS:CG	1:B:115:TRP:H	2.33	0.46
1:B:254:ASP:O	1:B:257:GLN:HG3	2.15	0.46
1:A:340:GLU:C	1:A:341:ARG:HD2	2.36	0.46
1:A:133:ASN:HB3	1:A:136:SER:HB3	1.98	0.46
1:B:266:LYS:HD3	1:B:398:LEU:HD23	1.98	0.45
1:A:385:ASN:O	1:A:388:SER:HB2	2.15	0.45
1:A:287:GLN:NE2	1:B:264:ARG:HE	2.14	0.45
1:A:100:ASN:HD22	1:A:103:TYR:HE2	1.65	0.45
1:A:299:MET:N	1:A:327:ASN:HD21	2.11	0.44
1:A:275:GLY:O	1:A:279:VAL:HG23	2.18	0.43
1:A:407:CYS:HB2	1:A:412:ASP:HB3	1.99	0.43
1:B:345:THR:HB	1:B:417:ILE:HB	2.00	0.43
1:B:405:TRP:O	1:B:408:LEU:HB2	2.19	0.43
1:B:90:ASN:ND2	1:B:133:ASN:HD21	2.16	0.43
1:B:139:ARG:HA	1:B:140:PRO:HD3	1.76	0.43
1:B:421:ASN:O	1:B:423:ASN:N	2.52	0.43
1:A:254:ASP:OD2	1:A:256:GLU:HG2	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:369:LEU:O	1:B:370:LYS:HB2	2.18	0.43
1:B:366:GLY:HA3	1:B:372:LYS:HD2	1.99	0.42
1:A:267:ILE:HG22	1:A:289:PHE:CD1	2.55	0.42
1:B:149:PHE:HA	1:B:270:ILE:O	2.20	0.42
1:A:139:ARG:HA	1:A:140:PRO:HD3	1.85	0.42
1:A:133:ASN:CG	1:A:136:SER:HB2	2.40	0.42
1:A:181:ASP:OD1	1:A:183:SER:OG	2.30	0.42
1:A:420:THR:HG23	1:A:422:ILE:O	2.20	0.42
1:B:116:LEU:O	1:B:120:ILE:HG23	2.20	0.42
1:B:319:SER:HA	1:B:349:SER:OG	2.20	0.41
1:A:138:LEU:HD22	1:A:258:LEU:HD23	2.01	0.41
1:A:241:HIS:CE1	1:B:309:ARG:HD3	2.55	0.41
1:A:363:LYS:O	1:A:367:HIS:HB2	2.19	0.41
1:B:347:ARG:HG2	1:B:417:ILE:HG13	2.01	0.41
1:A:364:ILE:O	1:A:368:MET:CG	2.68	0.41
1:B:96:LEU:HD23	1:B:99:PRO:HA	2.02	0.41
1:B:114:HIS:HD2	1:B:116:LEU:H	1.68	0.41
1:B:294:ALA:HB1	1:B:297:ALA:HB2	2.03	0.41
1:A:243:LYS:HD3	1:A:245:VAL:HG23	2.03	0.41
1:A:263:ASP:OD2	1:A:266:LYS:HD2	2.21	0.41
1:A:383:LEU:HD22	1:A:416:LEU:CD2	2.45	0.41
1:B:114:HIS:CD2	1:B:115:TRP:N	2.88	0.41
1:A:149:PHE:HA	1:A:270:ILE:O	2.19	0.41
1:B:237:LEU:O	1:B:240:ASP:HB3	2.21	0.41
1:A:67:CYS:SG	1:A:82:ARG:HD3	2.61	0.41
1:A:281:GLN:NE2	1:A:285:GLU:OE2	2.49	0.41
1:A:328:ILE:HG21	1:A:420:THR:HG21	2.02	0.41
1:A:403:ASP:HA	1:A:406:ASP:OD1	2.20	0.41
1:A:415:ASN:C	1:A:416:LEU:HD23	2.41	0.41
1:B:156:PHE:HB2	1:B:178:GLU:OE2	2.22	0.40
1:B:233:LEU:HD11	1:B:267:ILE:HD13	2.02	0.40
1:A:145:PRO:HD2	1:A:171:GLY:O	2.21	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	370/383 (97%)	354 (96%)	14 (4%)	2 (0%)	29 26
1	B	370/383 (97%)	354 (96%)	16 (4%)	0	100 100
All	All	740/766 (97%)	708 (96%)	30 (4%)	2 (0%)	41 41

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	114	HIS
1	A	91	ASP

5.3.2 Protein sidechains (i)

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	322/328 (98%)	303 (94%)	19 (6%)	19 17
1	B	322/328 (98%)	304 (94%)	18 (6%)	21 18
All	All	644/656 (98%)	607 (94%)	37 (6%)	20 18

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	54	THR
1	A	83	LEU
1	A	91	ASP
1	A	119	ASN
1	A	123	LEU
1	A	133	ASN
1	A	139	ARG
1	A	180	ARG
1	A	182	ARG
1	A	198	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	204	LEU
1	A	252	LYS
1	A	274	PHE
1	A	296	ASP
1	A	304	ASP
1	A	336	SER
1	A	363	LYS
1	A	416	LEU
1	A	424	THR
1	B	75	THR
1	B	90	ASN
1	B	108	SER
1	B	109	LYS
1	B	116	LEU
1	B	120	ILE
1	B	122	ARG
1	B	123	LEU
1	B	180	ARG
1	B	194	SER
1	B	252	LYS
1	B	274	PHE
1	B	296	ASP
1	B	309	ARG
1	B	329	ILE
1	B	336	SER
1	B	370	LYS
1	B	408	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	ASN
1	A	100	ASN
1	A	114	HIS
1	A	119	ASN
1	A	133	ASN
1	A	135	ASN
1	A	327	ASN
1	A	415	ASN
1	B	90	ASN
1	B	100	ASN
1	B	114	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	135	ASN
1	B	287	GLN
1	B	327	ASN
1	B	423	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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	SGB	A	273[B]	-	10,12,13	4.13	3 (30%)	9,16,18	1.78	3 (33%)
1	SGB	B	273[A]	-	10,12,13	3.88	3 (30%)	9,16,18	2.68	3 (33%)
1	SGB	B	273[B]	-	10,12,13	3.84	3 (30%)	9,16,18	2.42	2 (22%)
1	SGB	A	273[A]	-	10,12,13	4.15	3 (30%)	9,16,18	1.62	2 (22%)

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	SGB	A	273[B]	-	-	4/10/13/15	-
1	SGB	B	273[A]	-	-	1/10/13/15	-
1	SGB	B	273[B]	-	-	3/10/13/15	-
1	SGB	A	273[A]	-	-	1/10/13/15	-

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	273[A]	SGB	P1-O1	9.39	1.61	1.47
1	B	273[B]	SGB	P1-O1	9.39	1.61	1.47
1	A	273[A]	SGB	P1-O1	8.90	1.61	1.47
1	A	273[B]	SGB	P1-O1	8.90	1.61	1.47
1	A	273[A]	SGB	P1-OG	7.92	1.68	1.58
1	A	273[B]	SGB	P1-OG	7.92	1.68	1.58
1	B	273[A]	SGB	P1-OG	5.70	1.65	1.58
1	B	273[B]	SGB	P1-OG	5.70	1.65	1.58
1	B	273[A]	SGB	O-C	4.85	1.39	1.19
1	B	273[B]	SGB	O-C	4.85	1.39	1.19
1	A	273[A]	SGB	O-C	4.70	1.38	1.19
1	A	273[B]	SGB	O-C	4.70	1.38	1.19

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	273[A]	SGB	OG-CB-CA	5.91	113.90	108.14
1	B	273[B]	SGB	OG-CB-CA	5.91	113.90	108.14
1	B	273[A]	SGB	O1-P1-C1	-3.30	102.63	114.83
1	B	273[B]	SGB	O1-P1-C1	-3.08	103.44	114.83
1	A	273[B]	SGB	O1-P1-C1	-2.96	103.90	114.83
1	B	273[A]	SGB	P1-O2-C2	2.58	130.42	123.40
1	A	273[A]	SGB	OG-P1-C1	2.53	112.40	105.41
1	A	273[A]	SGB	O1-P1-C1	-2.43	105.85	114.83
1	A	273[B]	SGB	P1-O2-C2	2.25	129.51	123.40
1	A	273[B]	SGB	OG-P1-O2	2.13	113.32	104.17

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	273[B]	SGB	C2-O2-P1-O1
1	A	273[B]	SGB	C2-O2-P1-O1
1	B	273[B]	SGB	CB-OG-P1-O2
1	A	273[B]	SGB	C4-C2-O2-P1
1	A	273[A]	SGB	N-CA-CB-OG
1	A	273[B]	SGB	N-CA-CB-OG
1	B	273[A]	SGB	N-CA-CB-OG
1	B	273[B]	SGB	N-CA-CB-OG
1	A	273[B]	SGB	C3-C2-O2-P1

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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, 95^{th} 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	370/383 (96%)	0.42	24 (6%) 18 23	18, 38, 58, 84	0
1	B	370/383 (96%)	0.04	9 (2%) 59 64	17, 31, 52, 74	0
All	All	740/766 (96%)	0.23	33 (4%) 33 38	17, 34, 56, 84	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	89	ASP	9.3
1	A	92	ARG	9.1
1	A	54	THR	7.7
1	A	115	TRP	5.7
1	B	115	TRP	5.6
1	A	90	ASN	5.5
1	A	91	ASP	5.2
1	A	114	HIS	5.2
1	A	338	ASP	4.5
1	A	93	LEU	4.3
1	A	407	CYS	4.0
1	A	329	ILE	4.0
1	B	114	HIS	4.0
1	A	417	ILE	3.3
1	A	116	LEU	3.1
1	A	88	GLN	2.9
1	A	396	LEU	2.9
1	A	336	SER	2.7
1	B	141	GLY	2.5
1	A	60	ASN	2.5
1	A	347	ARG	2.5
1	A	308	SER	2.4
1	B	210	LYS	2.4
1	A	304	ASP	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	424	THR	2.4
1	B	112	GLY	2.4
1	A	337	PRO	2.3
1	B	113	THR	2.2
1	B	399	HIS	2.1
1	A	401	ASP	2.1
1	A	123	LEU	2.1
1	B	304	ASP	2.0
1	B	368	MET	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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. The B-factors column lists the minimum, median, 95^{th} 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	B-factors(Å^2)	Q<0.9
1	SGB	A	273[A]	13/14	0.67	0.36	26,38,52,56	5
1	SGB	A	273[B]	13/14	0.67	0.36	26,38,53,56	5
1	SGB	B	273[A]	13/14	0.67	0.37	21,37,50,54	5
1	SGB	B	273[B]	13/14	0.67	0.37	21,37,52,54	5

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.