Full wwPDB X-ray Structure Validation Report (i)

Aug 14, 2023 – 04:40 PM EDT

PDB ID	:	1RTK
Title	:	Crystal Structure Analysis of the Bb segment of Factor B complexed with 4-guanidinobenzoic acid
Authors	:	Ponnuraj, K.; Xu, Y.; Macon, K.; Moore, D.; Volanakis, J.E.; Narayana, S.V.
Deposited on	:	2003-12-10
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
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:

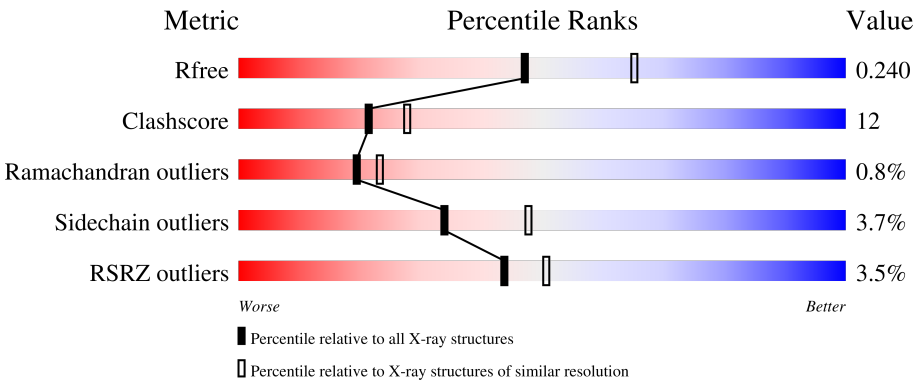
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 2.30 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}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (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 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	497	3% 75% 21% • •

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 4063 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 Complement factor B Bb fragment.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	486	3769	2391	646	711	21	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	267	VAL	CYS	engineered mutation	UNP P00751
A	428	CYS	PHE	engineered mutation	UNP P00751
A	435	CYS	ASN	engineered mutation	UNP P00751

- Molecule 2 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	I		
2	A	2	2	2	0	0

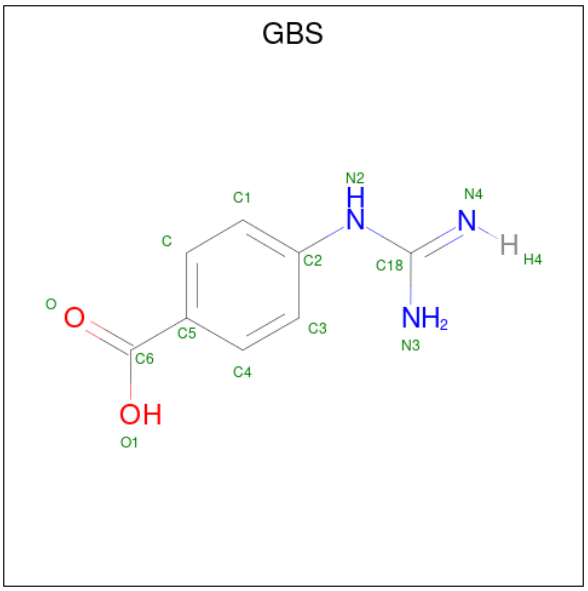
- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
3	A	7	7	7	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
4	A	1	1	1	0	0

- Molecule 5 is 4-carbamimidamidobenzoic acid (three-letter code: GBS) (formula: $C_8H_9N_3O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	A	1	12	8	3	1	0	0

- Molecule 6 is water.

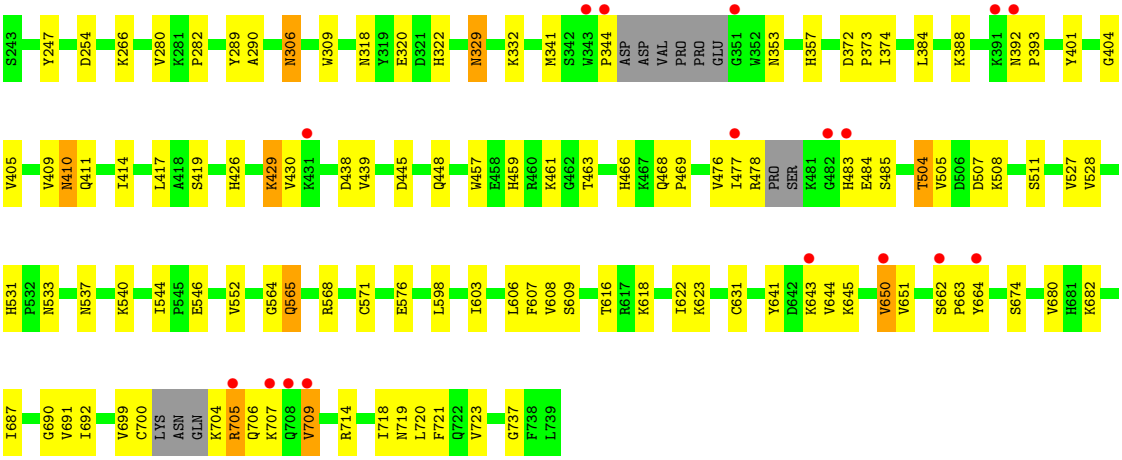
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	272	272	272	0	0

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: Complement factor B Bb fragment

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α, β, γ	98.36Å 98.36Å 125.66Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.81 – 2.30 49.18 – 2.30	Depositor EDS
% Data completeness (in resolution range)	95.8 (19.81-2.30) 95.8 (49.18-2.30)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.72 (at 2.29Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.208 , 0.245 0.201 , 0.240	Depositor DCC
R_{free} test set	861 reflections (2.83%)	wwPDB-VP
Wilson B-factor (Å^2)	27.3	Xtriage
Anisotropy	0.110	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 57.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.049 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	4063	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.91% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, NA, IOD, GBS

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	0.35	0/3843	0.61	1/5204 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	344	PRO	N-CA-CB	5.76	110.21	103.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	3769	0	3690	90	0
2	A	2	0	0	2	0
3	A	7	0	0	0	0
4	A	1	0	0	0	0
5	A	12	0	0	0	0
6	A	272	0	0	3	0
All	All	4063	0	3690	90	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 12.

All (90) 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:508:LYS:HA	1:A:508:LYS:HE2	1.40	1.00
1:A:374:ILE:HD13	1:A:417:LEU:HD23	1.58	0.86
1:A:459:HIS:HD2	1:A:461:LYS:H	1.30	0.80
1:A:392:ASN:N	1:A:393:PRO:HD3	1.97	0.79
1:A:643:LYS:HG2	6:A:833:HOH:O	1.86	0.74
1:A:531:HIS:HD2	1:A:533:ASN:H	1.35	0.72
1:A:623:LYS:HE3	1:A:662:SER:O	1.91	0.71
1:A:463:THR:H	1:A:466:HIS:HD2	1.39	0.69
1:A:306:ASN:C	1:A:306:ASN:HD22	1.97	0.68
1:A:576:GLU:HG3	1:A:737:GLY:O	1.94	0.68
1:A:410:ASN:C	1:A:410:ASN:HD22	1.97	0.67
1:A:476:VAL:HB	1:A:484:GLU:HB3	1.79	0.65
1:A:417:LEU:HD12	6:A:918:HOH:O	1.98	0.64
1:A:463:THR:H	1:A:466:HIS:CD2	2.15	0.64
1:A:341:MET:HE2	1:A:384:LEU:HD11	1.79	0.63
1:A:429:LYS:HE3	1:A:429:LYS:HA	1.81	0.62
1:A:373:PRO:HB2	1:A:417:LEU:HD21	1.82	0.61
1:A:247:TYR:OH	1:A:357:HIS:HD2	1.83	0.61
1:A:644:VAL:HG11	1:A:650:VAL:CG1	2.32	0.60
1:A:409:VAL:CG1	1:A:414:ILE:HD12	2.32	0.60
1:A:374:ILE:HD13	1:A:417:LEU:CD2	2.32	0.59
1:A:459:HIS:CD2	1:A:461:LYS:H	2.16	0.59
1:A:329:ASN:ND2	1:A:332:LYS:H	2.01	0.58
1:A:544:ILE:CD1	1:A:650:VAL:HG12	2.36	0.56
1:A:603:ILE:HB	1:A:622:ILE:HB	1.89	0.55
1:A:392:ASN:N	1:A:393:PRO:CD	2.69	0.54
1:A:409:VAL:HG13	1:A:414:ILE:HD12	1.90	0.53
1:A:609:SER:OG	1:A:705:ARG:NH1	2.37	0.53
1:A:663:PRO:HG2	1:A:664:TYR:HD1	1.74	0.53
1:A:508:LYS:HA	1:A:508:LYS:CE	2.25	0.52
1:A:477:ILE:HG23	1:A:511:SER:HB2	1.91	0.52
1:A:616:THR:HG23	1:A:618:LYS:HE3	1.92	0.52
1:A:404:GLY:O	1:A:430:VAL:HG23	2.10	0.52
1:A:306:ASN:ND2	1:A:309:TRP:H	2.08	0.51
1:A:341:MET:CE	1:A:384:LEU:HD11	2.40	0.51
1:A:405:VAL:HG22	1:A:430:VAL:HG21	1.92	0.50
1:A:445:ASP:OD2	1:A:448:GLN:HG2	2.11	0.50
1:A:700:CYS:HA	1:A:704:LYS:O	2.12	0.50
1:A:318:ASN:ND2	1:A:320:GLU:H	2.09	0.49
1:A:438:ASP:OD2	1:A:459:HIS:HE1	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:289:TYR:HA	1:A:322:HIS:CE1	2.46	0.49
1:A:531:HIS:CD2	1:A:533:ASN:H	2.24	0.49
1:A:691:VAL:HG23	1:A:720:LEU:HD21	1.94	0.49
1:A:699:VAL:O	1:A:706:GLN:HB2	2.12	0.49
1:A:484:GLU:HG3	1:A:485:SER:N	2.26	0.49
1:A:527:VAL:HG22	1:A:528:VAL:N	2.27	0.49
1:A:571:CYS:HB2	1:A:687:ILE:HD13	1.94	0.49
1:A:598:LEU:HA	1:A:603:ILE:HD13	1.94	0.49
1:A:564:GLY:O	1:A:568:ARG:HG2	2.13	0.48
1:A:466:HIS:O	1:A:469:PRO:HG3	2.13	0.48
1:A:478:ARG:H	1:A:483:HIS:CD2	2.31	0.48
1:A:537:ASN:OD1	1:A:540:LYS:HE3	2.13	0.48
1:A:372:ASP:OD2	1:A:374:ILE:HG12	2.14	0.47
1:A:318:ASN:HD22	1:A:320:GLU:H	1.62	0.47
1:A:401:TYR:CE1	1:A:439:VAL:HG13	2.49	0.47
1:A:329:ASN:C	1:A:329:ASN:HD22	2.17	0.47
1:A:699:VAL:HG11	1:A:709:VAL:HB	1.97	0.47
1:A:477:ILE:HG13	1:A:483:HIS:NE2	2.30	0.47
1:A:280:VAL:HG12	1:A:282:PRO:HD3	1.97	0.46
1:A:468:GLN:HG2	1:A:608:VAL:HG21	1.97	0.46
1:A:616:THR:CG2	1:A:618:LYS:HE3	2.45	0.46
1:A:606:LEU:C	1:A:606:LEU:HD12	2.36	0.46
1:A:680:VAL:HG12	1:A:682:LYS:HG3	1.97	0.46
1:A:466:HIS:HE1	2:A:741:IOD:I	2.68	0.46
1:A:618:LYS:NZ	1:A:705:ARG:CZ	2.79	0.46
1:A:392:ASN:H	1:A:393:PRO:HD3	1.77	0.45
1:A:457:TRP:CH2	1:A:459:HIS:HB3	2.51	0.45
1:A:419:SER:HB2	1:A:426:HIS:CD2	2.51	0.45
1:A:650:VAL:HG22	1:A:651:VAL:HG23	1.99	0.45
1:A:457:TRP:CZ3	1:A:459:HIS:HB3	2.52	0.44
1:A:411:GLN:OE1	1:A:429:LYS:NZ	2.48	0.44
1:A:631:CYS:SG	1:A:714:ARG:HD2	2.58	0.44
1:A:565:GLN:NE2	1:A:565:GLN:H	2.16	0.44
1:A:663:PRO:HG2	1:A:664:TYR:CD1	2.53	0.44
1:A:531:HIS:HE1	2:A:740:IOD:I	2.71	0.43
1:A:719:ASN:OD1	1:A:721:PHE:HB2	2.18	0.43
1:A:504:THR:HG22	1:A:507:ASP:OD2	2.18	0.43
1:A:618:LYS:HZ3	1:A:705:ARG:NE	2.16	0.43
1:A:650:VAL:CG2	1:A:651:VAL:N	2.82	0.43
1:A:607:PHE:HB2	1:A:692:ILE:HD11	2.01	0.43
1:A:531:HIS:HB2	1:A:552:VAL:HG23	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:720:LEU:HA	1:A:723:VAL:HG22	2.00	0.42
1:A:429:LYS:HA	1:A:429:LYS:CE	2.48	0.42
1:A:544:ILE:HD11	1:A:650:VAL:HG12	2.01	0.42
1:A:641:TYR:CE2	1:A:650:VAL:HG21	2.54	0.42
1:A:318:ASN:HD22	1:A:320:GLU:N	2.18	0.41
1:A:682:LYS:HE3	6:A:912:HOH:O	2.21	0.41
1:A:306:ASN:C	1:A:306:ASN:ND2	2.69	0.41
1:A:690:GLY:HA2	1:A:718:ILE:O	2.21	0.41
1:A:247:TYR:OH	1:A:357:HIS:CD2	2.70	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	478/497 (96%)	458 (96%)	16 (3%)	4 (1%)	19 23

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	707	LYS
1	A	645	LYS
1	A	290	ALA
1	A	353	ASN

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	407/439 (93%)	392 (96%)	15 (4%)	34 48

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	254	ASP
1	A	266	LYS
1	A	306	ASN
1	A	329	ASN
1	A	388	LYS
1	A	410	ASN
1	A	429	LYS
1	A	504	THR
1	A	505	VAL
1	A	546	GLU
1	A	565	GLN
1	A	650	VAL
1	A	674	SER
1	A	705	ARG
1	A	709	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	260	ASN
1	A	270	ASN
1	A	306	ASN
1	A	315	ASN
1	A	318	ASN
1	A	329	ASN
1	A	357	HIS
1	A	410	ASN
1	A	413	ASN
1	A	415	ASN
1	A	423	ASN
1	A	459	HIS
1	A	466	HIS
1	A	483	HIS
1	A	531	HIS
1	A	565	GLN

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Mol	Chain	Res	Type
1	A	591	GLN
1	A	681	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 11 ligands modelled in this entry, 10 are monoatomic - leaving 1 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	$\#\|Z\| > 2$
5	GBS	A	750	1	12,12,13	1.98	5 (41%)	15,15,17	0.96	1 (6%)

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
5	GBS	A	750	1	-	0/6/6/8	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	750	GBS	C18-N2	-3.01	1.34	1.37
5	A	750	GBS	O-C6	2.98	1.31	1.21
5	A	750	GBS	C3-C2	2.79	1.43	1.39
5	A	750	GBS	C-C1	2.58	1.43	1.38
5	A	750	GBS	C-C5	2.14	1.43	1.39

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	750	GBS	O-C6-C5	-2.08	117.86	124.59

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	486/497 (97%)	-0.20	17 (3%) 44 51	15, 30, 46, 63	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	709	VAL	4.6
1	A	707	LYS	4.3
1	A	391	LYS	4.2
1	A	392	ASN	4.0
1	A	343	TRP	4.0
1	A	344	PRO	3.1
1	A	482	GLY	3.0
1	A	431	LYS	2.9
1	A	708	GLN	2.9
1	A	477	ILE	2.8
1	A	664	TYR	2.7
1	A	662	SER	2.4
1	A	705	ARG	2.2
1	A	483	HIS	2.1
1	A	643	LYS	2.1
1	A	650	VAL	2.0
1	A	351	GLY	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 monosaccharides 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. 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	B-factors(Å^2)	Q<0.9
5	GBS	A	750	12/13	0.94	0.12	24,26,30,30	0
3	NA	A	748	1/1	0.95	0.23	32,32,32,32	0
3	NA	A	744	1/1	0.95	0.37	14,14,14,14	0
4	MG	A	749	1/1	0.96	0.11	32,32,32,32	0
3	NA	A	747	1/1	0.96	0.27	38,38,38,38	0
3	NA	A	743	1/1	0.97	0.30	4,4,4,4	0
3	NA	A	745	1/1	0.97	0.35	7,7,7,7	0
3	NA	A	746	1/1	0.98	0.24	16,16,16,16	0
3	NA	A	742	1/1	0.99	0.27	4,4,4,4	0
2	IOD	A	740	1/1	0.99	0.09	31,31,31,31	0
2	IOD	A	741	1/1	0.99	0.08	29,29,29,29	0

6.5 Other polymers (i)

There are no such residues in this entry.