



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 07:03 PM BST

PDB ID : 5TDG
Title : Crystal structure of prefusion-stabilized bovine RSV F (DS-Cav1 variant: strain ATue51908)
Authors : Chen, L.; Zhang, B.; Kwong, P.D.
Deposited on : 2016-09-19
Resolution : 2.65 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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 : 2.13.1
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) : 2.13.1

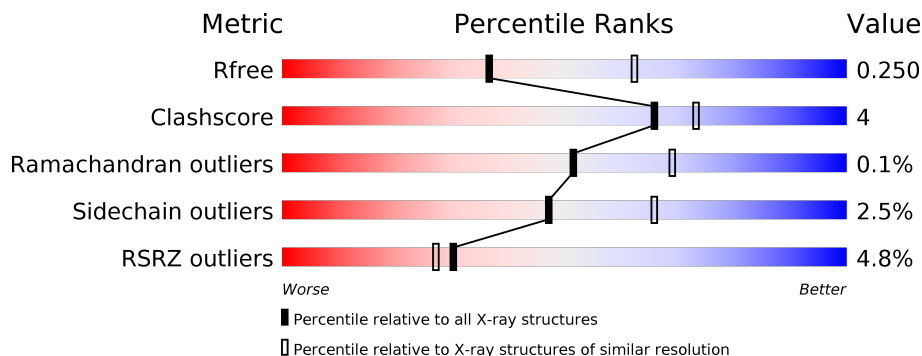
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	1332 (2.68-2.64)
Clashscore	141614	1374 (2.68-2.64)
Ramachandran outliers	138981	1349 (2.68-2.64)
Sidechain outliers	138945	1349 (2.68-2.64)
RSRZ outliers	127900	1318 (2.68-2.64)

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 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 $\leq 5\%$. 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	519	 4% 80% 12% • 8%
1	B	519	 4% 79% 12% • 8%
1	C	519	 5% 82% 10% • 8%

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 11276 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 Fusion glycoprotein F0,Fibritin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	480	3732	2355	623	731	23	0	0	0
1	B	480	3740	2360	626	731	23	0	1	0
1	C	480	3732	2355	623	731	23	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

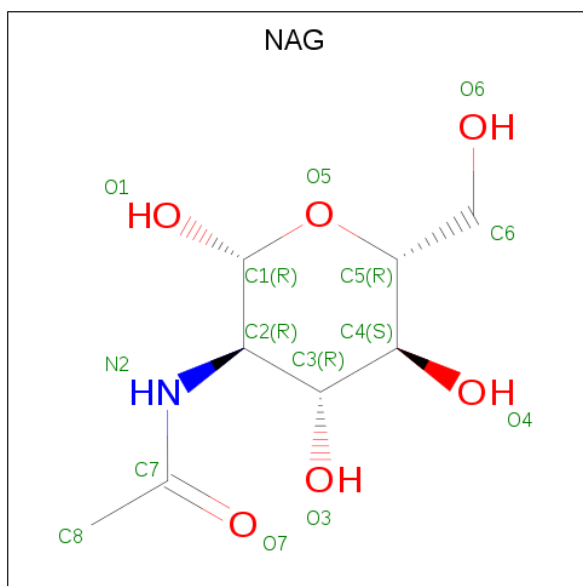
Chain	Residue	Modelled	Actual	Comment	Reference
A	155	CYS	SER	engineered mutation	UNP Q9YS24
A	190	PHE	SER	engineered mutation	UNP Q9YS24
A	207	LEU	VAL	engineered mutation	UNP Q9YS24
A	290	CYS	SER	engineered mutation	UNP Q9YS24
A	514	SER	-	linker	UNP Q9YS24
A	515	ALA	-	linker	UNP Q9YS24
A	516	ILE	-	linker	UNP Q9YS24
A	517	GLY	-	linker	UNP Q9YS24
B	155	CYS	SER	engineered mutation	UNP Q9YS24
B	190	PHE	SER	engineered mutation	UNP Q9YS24
B	207	LEU	VAL	engineered mutation	UNP Q9YS24
B	290	CYS	SER	engineered mutation	UNP Q9YS24
B	514	SER	-	linker	UNP Q9YS24
B	515	ALA	-	linker	UNP Q9YS24
B	516	ILE	-	linker	UNP Q9YS24
B	517	GLY	-	linker	UNP Q9YS24
C	155	CYS	SER	engineered mutation	UNP Q9YS24
C	190	PHE	SER	engineered mutation	UNP Q9YS24
C	207	LEU	VAL	engineered mutation	UNP Q9YS24
C	290	CYS	SER	engineered mutation	UNP Q9YS24
C	514	SER	-	linker	UNP Q9YS24
C	515	ALA	-	linker	UNP Q9YS24
C	516	ILE	-	linker	UNP Q9YS24

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Chain	Residue	Modelled	Actual	Comment	Reference
C	517	GLY	-	linker	UNP Q9YS24

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		

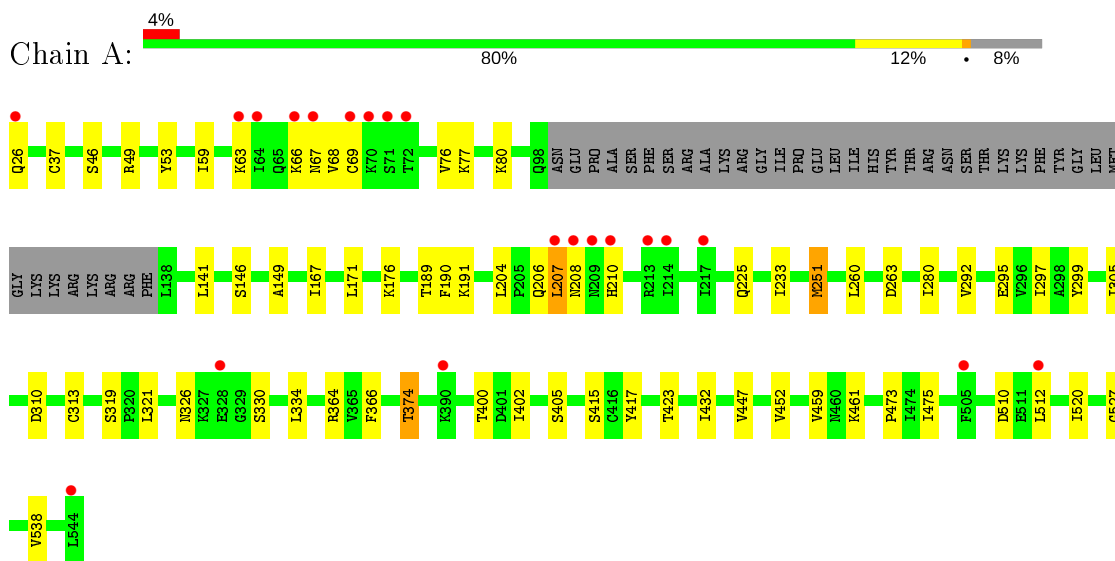
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	7	Total	O	0	0
			7	7		
3	B	15	Total	O	0	0
			15	15		
3	C	8	Total	O	0	0
			8	8		

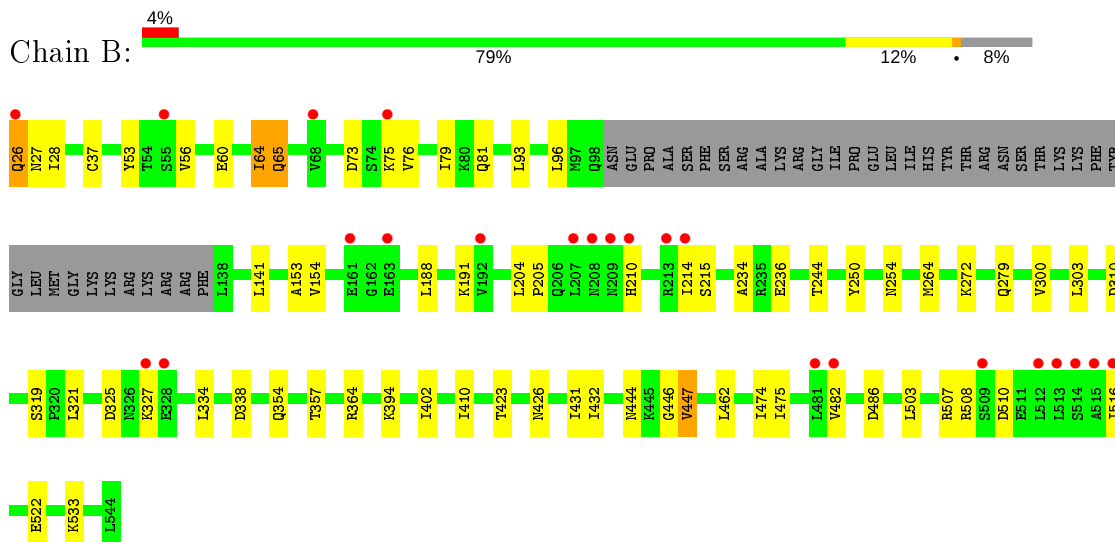
3 Residue-property plots [i](#)

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.

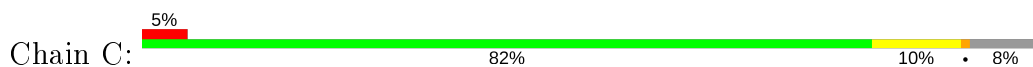
- Molecule 1: Fusion glycoprotein F0,Fibrin

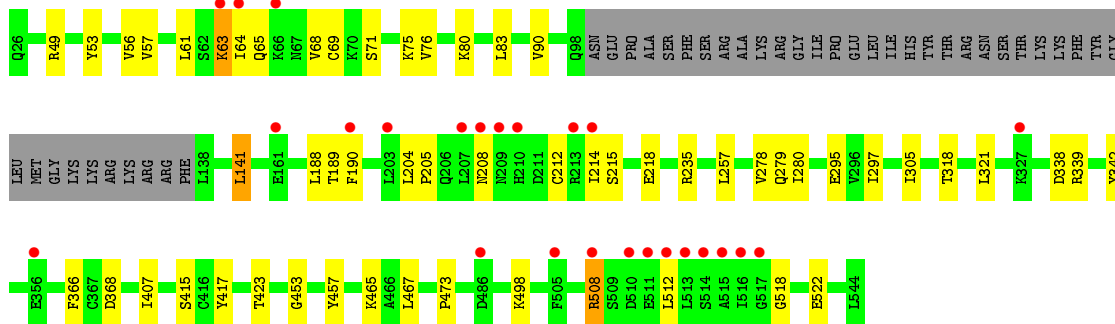


- Molecule 1: Fusion glycoprotein F0,Fibrin



- Molecule 1: Fusion glycoprotein F0,Fibrin





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.07Å 127.03Å 92.43Å 90.00° 93.91° 90.00°	Depositor
Resolution (Å)	92.21 – 2.65 43.30 – 2.65	Depositor EDS
% Data completeness (in resolution range)	96.5 (92.21-2.65) 96.5 (43.30-2.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.51 (at 2.65Å)	Xtrriage
Refinement program	REFMAC 5.8.0155	Depositor
R, R_{free}	0.205 , 0.249 0.207 , 0.250	Depositor DCC
R_{free} test set	2358 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	67.3	Xtrriage
Anisotropy	0.041	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 51.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11276	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.81% 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, 0.333 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: NAG

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	0.27	0/3788	0.47	0/5136
1	B	0.27	0/3799	0.47	0/5150
1	C	0.27	0/3788	0.47	0/5136
All	All	0.27	0/11375	0.47	0/15422

There are no bond length outliers.

There are no bond angle outliers.

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	3732	0	3757	36	0
1	B	3740	0	3770	37	0
1	C	3732	0	3757	31	0
2	A	14	0	13	0	0
2	B	14	0	13	0	0
2	C	14	0	13	0	0
3	A	7	0	0	0	0
3	B	15	0	0	2	0
3	C	8	0	0	0	0
All	All	11276	0	11323	91	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 4.

All (91) 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:250:TYR:OH	1:C:235:ARG:NH1	2.23	0.71
1:A:374:THR:HG21	1:C:453:GLY:HA3	1.73	0.69
1:B:334:LEU:HD23	1:B:475:ILE:HD13	1.76	0.66
1:C:321:LEU:HD11	1:C:473:PRO:HB3	1.76	0.65
1:A:400:THR:HG21	1:B:141:LEU:HD21	1.79	0.64
1:A:512:LEU:HD11	1:C:512:LEU:HD13	1.80	0.64
1:C:71:SER:OG	1:C:212:CYS:SG	2.57	0.62
1:B:426:ASN:ND2	1:B:446:GLY:O	2.33	0.60
1:B:432:ILE:HD11	1:B:447:VAL:HG12	1.83	0.60
1:C:257:LEU:HD23	1:C:278:VAL:HG13	1.83	0.60
1:B:486:ASP:OD2	1:C:498:LYS:NZ	2.35	0.59
1:A:167:ILE:HG23	1:A:189:THR:HG21	1.83	0.59
1:A:405:SER:HB2	1:A:452:VAL:HG21	1.84	0.59
1:C:56:VAL:HB	1:C:189:THR:HG22	1.86	0.58
1:C:63:LYS:HD2	1:C:295:GLU:HG3	1.85	0.57
1:B:154:VAL:HG23	1:B:300:VAL:HG21	1.86	0.57
1:C:64:ILE:HD11	1:C:90:VAL:HG21	1.87	0.57
1:C:338:ASP:OD1	1:C:338:ASP:N	2.38	0.57
1:B:334:LEU:HD21	1:B:474:ILE:HG13	1.88	0.56
1:A:176:LYS:NZ	1:A:263:ASP:OD2	2.36	0.55
1:B:394:LYS:NZ	3:B:5101:HOH:O	2.39	0.55
1:A:204:LEU:HG	1:A:208:ASN:HB2	1.88	0.54
1:A:206:GLN:HA	1:A:210:HIS:HB2	1.90	0.54
1:B:75:LYS:NZ	1:B:215:SER:O	2.40	0.54
1:A:171:LEU:HD13	1:A:191:LYS:HB2	1.90	0.54
1:B:510:ASP:OD1	1:C:508:ARG:NH1	2.41	0.52
1:A:334:LEU:HB2	1:A:475:ILE:HD13	1.90	0.52
1:A:59:ILE:HB	1:A:297:ILE:HB	1.92	0.51
1:A:77:LYS:HD3	1:A:80:LYS:HD2	1.91	0.51
1:B:60:GLU:HG3	1:B:191:LYS:HD3	1.92	0.51
1:A:146:SER:HB3	1:A:149:ALA:HB2	1.92	0.51
1:A:432:ILE:HD11	1:A:447:VAL:HG22	1.93	0.51
1:C:68:VAL:HG22	1:C:69:CYS:H	1.77	0.50
1:C:415:SER:HB3	1:C:417:TYR:CE2	2.48	0.49
1:A:326:ASN:HB3	1:A:330:SER:HB2	1.95	0.48
1:A:292:VAL:HG22	1:A:297:ILE:HG12	1.96	0.48
1:C:61:LEU:HD11	1:C:297:ILE:HG13	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:218:GLU:N	1:C:218:GLU:OE2	2.45	0.48
1:C:338:ASP:HB2	1:C:342:TYR:OH	2.15	0.47
1:C:76:VAL:HG22	1:C:214:ILE:HG12	1.96	0.47
1:A:63:LYS:HB2	1:A:295:GLU:HG3	1.96	0.47
1:A:461:LYS:HD2	1:B:153:ALA:HB1	1.97	0.47
1:A:321:LEU:HD11	1:A:473:PRO:HB3	1.97	0.47
1:B:272:LYS:HB2	1:B:272:LYS:HE3	1.83	0.46
1:A:520:ILE:HD11	1:C:522:GLU:HA	1.97	0.46
1:B:482:VAL:HG11	1:B:503:LEU:HD21	1.98	0.46
1:B:28:ILE:HG22	1:B:410:ILE:HD13	1.98	0.46
1:A:76:VAL:HG12	1:A:80:LYS:HE3	1.97	0.45
1:A:37:CYS:SG	1:A:319:SER:HB3	2.57	0.45
1:B:37:CYS:SG	1:B:319:SER:HB3	2.56	0.45
1:C:53:TYR:HB2	1:C:305:ILE:HD11	1.98	0.45
1:B:402:ILE:HG21	1:C:141:LEU:HD12	1.99	0.45
1:B:279:GLN:NE2	3:B:5104:HOH:O	2.49	0.45
1:B:354:GLN:O	1:B:357:THR:HG22	2.17	0.45
1:C:75:LYS:NZ	1:C:215:SER:O	2.46	0.44
1:B:522:GLU:N	1:C:518:GLY:O	2.50	0.44
1:B:37:CYS:HB2	1:B:321:LEU:HD13	1.99	0.44
1:A:310:ASP:OD1	1:A:364:ARG:NH2	2.40	0.44
1:C:57:VAL:HG22	1:C:190:PHE:CZ	2.53	0.43
1:B:236:GLU:HG2	1:B:244:THR:HG21	1.99	0.43
1:A:66:LYS:O	1:A:68:VAL:N	2.52	0.43
1:B:73:ASP:HB3	1:B:76:VAL:HG23	2.01	0.43
1:C:280:ILE:HG21	1:C:366:PHE:CG	2.52	0.43
1:C:49:ARG:HE	1:C:368:ASP:CG	2.22	0.43
1:A:53:TYR:HB2	1:A:305:ILE:HD11	2.01	0.43
1:B:310:ASP:OD1	1:B:364:ARG:NH2	2.36	0.43
1:B:444:ASN:ND2	1:B:462:LEU:O	2.48	0.43
1:A:510:ASP:OD1	1:B:508:ARG:NH1	2.51	0.43
1:B:53:TYR:CE2	1:B:264:MET:HG2	2.54	0.43
1:C:204:LEU:N	1:C:205:PRO:HD2	2.34	0.42
1:B:338:ASP:N	1:B:338:ASP:OD1	2.47	0.42
1:C:407:ILE:HD11	1:C:457:TYR:HB3	2.02	0.42
1:A:46:SER:HB3	1:A:313:CYS:SG	2.59	0.42
1:B:64:ILE:O	1:B:65:GLN:HG2	2.20	0.42
1:C:465:LYS:HE2	1:C:467:LEU:HD11	2.02	0.42
1:A:402:ILE:HA	1:A:402:ILE:HD12	1.87	0.42
1:A:280:ILE:HG21	1:A:366:PHE:CG	2.55	0.42
1:B:79:ILE:HG13	1:B:214:ILE:HG12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:423:THR:HG21	1:B:431:ILE:HD13	2.02	0.41
1:C:65:GLN:NE2	1:C:208:ASN:OD1	2.53	0.41
1:A:251:MET:HE2	1:A:299:TYR:CE2	2.56	0.41
1:A:225:GLN:OE1	1:B:81:GLN:NE2	2.53	0.41
1:A:233:ILE:HG23	1:A:251:MET:HE1	2.02	0.41
1:A:527:GLY:O	1:B:533:LYS:HE2	2.20	0.41
1:A:76:VAL:O	1:A:80:LYS:HG3	2.20	0.41
1:A:69:CYS:SG	1:A:207:LEU:HD23	2.61	0.41
1:B:205:PRO:O	1:B:210:HIS:ND1	2.54	0.41
1:B:26:GLN:HB3	1:B:26:GLN:HE21	1.63	0.41
1:A:415:SER:HB3	1:A:417:TYR:CE2	2.56	0.41
1:C:318:THR:HG23	1:C:339:ARG:HG2	2.02	0.41
1:B:93:LEU:HD21	1:B:234:ALA:HA	2.02	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	476/519 (92%)	449 (94%)	26 (6%)	1 (0%)	47	64
1	B	477/519 (92%)	453 (95%)	23 (5%)	1 (0%)	47	64
1	C	476/519 (92%)	447 (94%)	29 (6%)	0	100	100
All	All	1429/1557 (92%)	1349 (94%)	78 (6%)	2 (0%)	51	69

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	67	ASN
1	B	64	ILE

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	433/467 (93%)	422 (98%)	11 (2%)	47	66
1	B	434/467 (93%)	420 (97%)	14 (3%)	39	56
1	C	433/467 (93%)	425 (98%)	8 (2%)	59	75
All	All	1300/1401 (93%)	1267 (98%)	33 (2%)	47	66

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	GLN
1	A	49	ARG
1	A	141	LEU
1	A	190	PHE
1	A	207	LEU
1	A	251	MET
1	A	260	LEU
1	A	374	THR
1	A	423	THR
1	A	459	VAL
1	A	538	VAL
1	B	26	GLN
1	B	27	ASN
1	B	56	VAL
1	B	65	GLN
1	B	96	LEU
1	B	188	LEU
1	B	204	LEU
1	B	254	ASN
1	B	303	LEU
1	B	325	ASP
1	B	327	LYS
1	B	447	VAL
1	B	507	ARG
1	B	516	ILE
1	C	63	LYS

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Mol	Chain	Res	Type
1	C	80	LYS
1	C	83	LEU
1	C	141	LEU
1	C	188	LEU
1	C	279	GLN
1	C	423	THR
1	C	508	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	26	GLN

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](#)

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	NAG	C	5001	1	14,14,15	0.42	0	17,19,21	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	A	5001	1	14,14,15	0.29	0	17,19,21	0.50	0
2	NAG	B	5001	1	14,14,15	0.28	0	17,19,21	0.42	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	C	5001	1	-	2/6/23/26	0/1/1/1
2	NAG	A	5001	1	-	2/6/23/26	0/1/1/1
2	NAG	B	5001	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	5001	NAG	O5-C5-C6-O6
2	C	5001	NAG	C4-C5-C6-O6
2	A	5001	NAG	O5-C5-C6-O6
2	A	5001	NAG	C4-C5-C6-O6

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

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	480/519 (92%)	0.21	21 (4%) 34 31	46, 73, 125, 191	0
1	B	480/519 (92%)	0.19	23 (4%) 30 27	48, 73, 127, 197	0
1	C	480/519 (92%)	0.17	25 (5%) 27 24	48, 77, 133, 172	0
All	All	1440/1557 (92%)	0.19	69 (4%) 30 27	46, 74, 129, 197	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	209	ASN	7.4
1	B	209	ASN	6.9
1	A	210	HIS	6.7
1	B	208	ASN	6.7
1	B	328	GLU	6.6
1	B	513	LEU	6.0
1	A	72	THR	5.7
1	B	516	ILE	5.3
1	A	208	ASN	5.2
1	A	26	GLN	5.1
1	C	517	GLY	5.1
1	B	161	GLU	5.0
1	C	512	LEU	4.9
1	C	511	GLU	4.4
1	C	64	ILE	4.4
1	C	514	SER	4.0
1	B	214	ILE	3.9
1	C	209	ASN	3.8
1	B	210	HIS	3.8
1	B	512	LEU	3.7
1	C	208	ASN	3.6
1	C	516	ILE	3.6
1	C	63	LYS	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	481	LEU	3.6
1	C	510	ASP	3.4
1	A	66	LYS	3.3
1	A	69	CYS	3.2
1	A	64	ILE	3.1
1	A	328	GLU	3.1
1	B	515	ALA	3.1
1	A	544	LEU	3.0
1	C	513	LEU	3.0
1	A	207	LEU	2.9
1	C	515	ALA	2.9
1	C	161	GLU	2.9
1	A	70	LYS	2.9
1	B	213	ARG	2.8
1	A	505	PHE	2.7
1	A	217	ILE	2.6
1	A	390	LYS	2.6
1	B	55	SER	2.6
1	C	356	GLU	2.5
1	A	213	ARG	2.5
1	C	327	LYS	2.5
1	B	68	VAL	2.5
1	B	327	LYS	2.4
1	A	214	ILE	2.4
1	A	71	SER	2.4
1	B	514	SER	2.4
1	A	67	ASN	2.4
1	C	213	ARG	2.3
1	B	26	GLN	2.3
1	C	486	ASP	2.3
1	C	207	LEU	2.3
1	A	512	LEU	2.2
1	C	505	PHE	2.2
1	C	203	LEU	2.2
1	B	192	VAL	2.1
1	C	214	ILE	2.1
1	B	207	LEU	2.1
1	B	509	SER	2.1
1	B	75	LYS	2.1
1	B	482	VAL	2.1
1	C	210	HIS	2.1
1	C	190	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	63	LYS	2.0
1	C	66	LYS	2.0
1	B	163	GLU	2.0
1	C	508	ARG	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(\AA^2)	Q<0.9
2	NAG	B	5001	14/15	0.71	0.26	135,136,143,143	0
2	NAG	C	5001	14/15	0.79	0.29	105,116,124,125	0
2	NAG	A	5001	14/15	0.80	0.23	131,145,150,150	0

6.5 Other polymers [i](#)

There are no such residues in this entry.