



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 05:30 AM GMT

PDB ID : 4F9L
Title : Crystal Structure of the Human BTN3A1 Ectodomain in Complex with the 20.1 Single Chain Antibody
Authors : Palakodeti, A.; Sandstrom, A.; Sundaresan, L.; Harly, C.; Nedellec, S.; Olive, D.; Scotet, E.; Bonneville, M.; Adams, E.J.
Deposited on : 2012-05-18
Resolution : 3.14 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

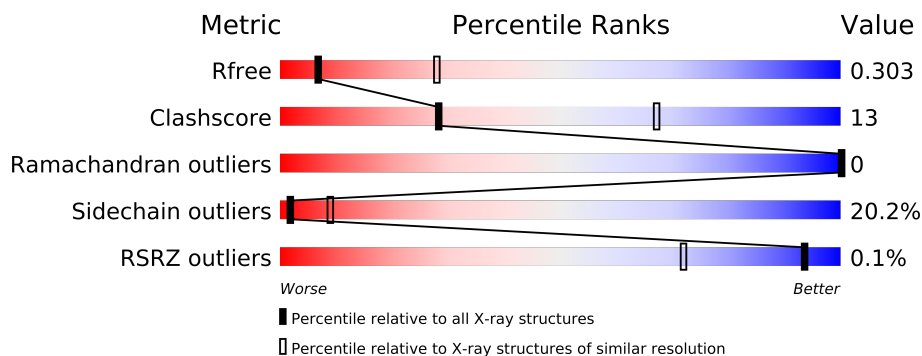
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 3.14 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}	66092	1337 (3.20-3.08)
Clashscore	79885	1656 (3.20-3.08)
Ramachandran outliers	78287	1614 (3.20-3.08)
Sidechain outliers	78261	1613 (3.20-3.08)
RSRZ outliers	66119	1338 (3.20-3.08)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	220	
1	B	220	
2	C	259	
2	D	259	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	NAG	A	301	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6598 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Butyrophilin subfamily 3 member A1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	214	Total	C	N	O	S	0	0	0
			1528	963	262	295	8			
1	B	213	Total	C	N	O	S	0	0	0
			1523	963	264	289	7			

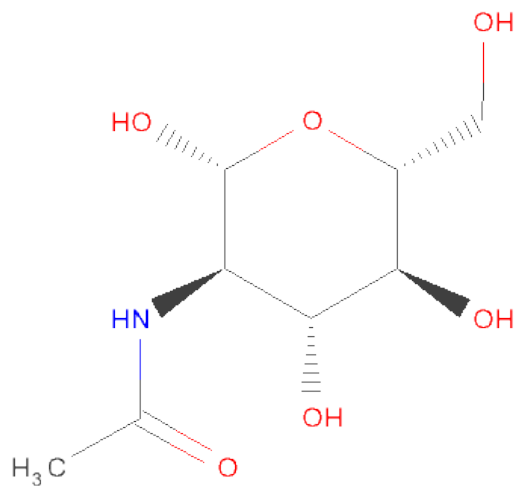
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	ALA	-	EXPRESSION TAG	UNP O00481
A	-1	ASP	-	EXPRESSION TAG	UNP O00481
A	0	LEU	-	EXPRESSION TAG	UNP O00481
B	-2	ALA	-	EXPRESSION TAG	UNP O00481
B	-1	ASP	-	EXPRESSION TAG	UNP O00481
B	0	LEU	-	EXPRESSION TAG	UNP O00481

- Molecule 2 is a protein called 20.1 anti-BTN3A1 antibody fragment.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	232	Total	C	N	O	S	0	0	0
			1763	1112	294	352	5			
2	C	232	Total	C	N	O	S	0	0	0
			1756	1106	292	353	5			

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: C₈H₁₅NO₆).



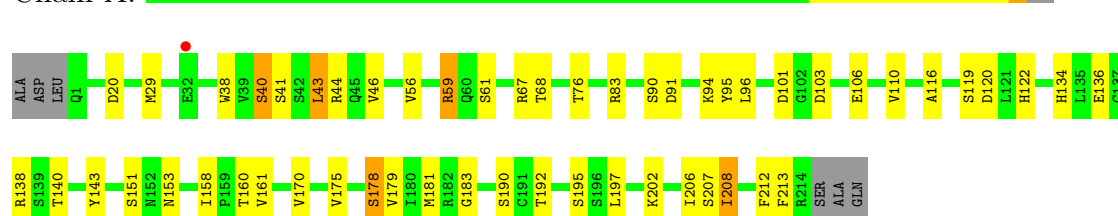
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		

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.

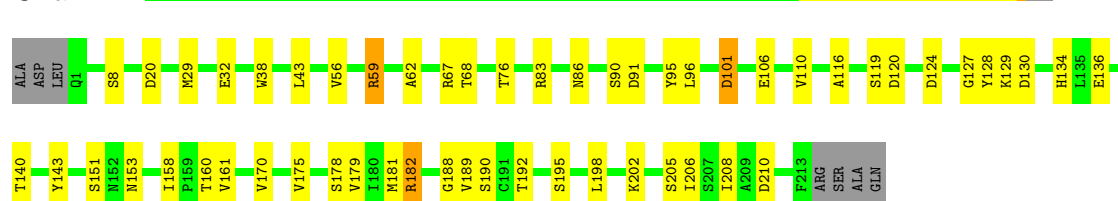
- Molecule 1: Butyrophilin subfamily 3 member A1

Chain A:



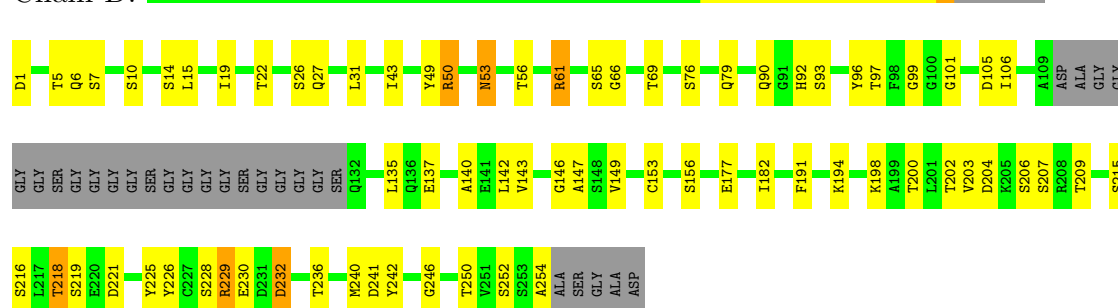
- Molecule 1: Butyrophilin subfamily 3 member A1

Chain B:



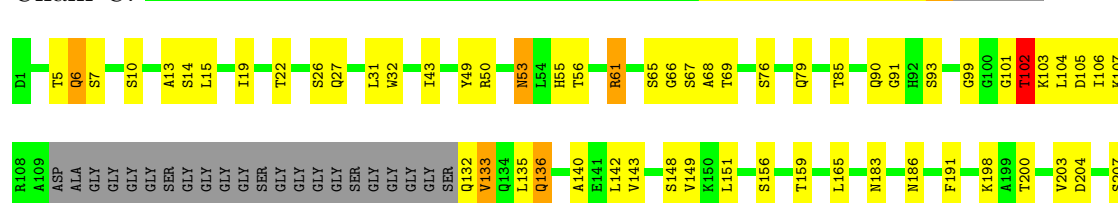
- Molecule 2: 20.1 anti-BTN3A1 antibody fragment

Chain D:



- Molecule 2: 20.1 anti-BTN3A1 antibody fragment

Chain C:



S215	S216	L217	T218	S219	F220	D221	S228	R229	D232	D238	D241	Y242	Q245	S253	A254	ALA	SER	GLY	ALA	ASP
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4 Data and refinement statistics

Property	Value	Source
Space group	P 4	Depositor
Cell constants a, b, c, α , β , γ	165.14Å 165.14Å 53.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.80 – 3.14 45.80 – 3.14	Depositor EDS
% Data completeness (in resolution range)	99.7 (45.80-3.14) 99.8 (45.80-3.14)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.75 (at 3.12Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.2_869)	Depositor
R, R_{free}	0.254 , 0.303 0.256 , 0.303	Depositor DCC
R_{free} test set	1325 reflections (5.13%)	DCC
Wilson B-factor (Å ²)	75.2	Xtriage
Anisotropy	0.269	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 43.3	EDS
Estimated twinning fraction	0.021 for h,-k,-l	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 25839 reflections	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	6598	wwPDB-VP
Average B, all atoms (Å ²)	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.98% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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	0.38	0/1560	0.60	0/2131
1	B	0.41	0/1555	0.64	1/2124 (0.0%)
2	C	0.45	0/1798	0.63	1/2453 (0.0%)
2	D	0.47	0/1805	0.63	2/2460 (0.1%)
All	All	0.43	0/6718	0.62	4/9168 (0.0%)

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
2	C	0	5
2	D	0	5
All	All	0	11

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	101	ASP	CB-CG-OD1	5.84	123.55	118.30
2	D	99	GLY	N-CA-C	-5.17	100.17	113.10
2	C	102	THR	CA-CB-CG2	-5.14	105.20	112.40
2	D	61	ARG	NE-CZ-NH1	5.00	122.80	120.30

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	183	GLY	Peptide
2	C	101	GLY	Peptide
2	C	132	GLN	Peptide
2	C	133	VAL	Peptide
2	C	140	ALA	Peptide
2	C	238	ASP	Peptide
2	D	101	GLY	Peptide
2	D	106	ILE	Peptide
2	D	140	ALA	Peptide
2	D	146	GLY	Peptide
2	D	147	ALA	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1528	0	0	20	0
1	B	1523	0	7	20	0
2	C	1756	0	19	26	0
2	D	1763	0	19	22	0
3	A	14	0	13	0	0
3	B	14	0	13	4	0
All	All	6598	0	71	83	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 13.

All (83) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:85:THR:CG2	2:C:102:THR:O	2.32	0.77
2:C:105:ASP:OD1	2:C:106:ILE:N	2.21	0.73
2:C:91:GLY:O	1:B:59:ARG:NH2	2.21	0.73
1:A:122:HIS:ND1	1:B:205:SER:OG	2.23	0.71
1:B:182:ARG:CG	1:B:182:ARG:NH1	2.52	0.71
2:C:61:ARG:NH1	2:C:61:ARG:CG	2.54	0.69
1:B:188:GLY:O	1:B:189:VAL:CG1	2.41	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:120:ASP:OD1	1:B:202:LYS:NZ	2.29	0.66
2:C:53:ASN:OD1	2:C:53:ASN:N	2.27	0.65
1:A:120:ASP:OD1	1:A:202:LYS:NZ	2.30	0.65
2:D:53:ASN:N	2:D:53:ASN:OD1	2.29	0.64
2:D:229:ARG:NH1	2:D:230:GLU:O	2.31	0.63
1:B:86:ASN:ND2	3:B:301:NAG:O5	2.30	0.63
2:C:136:GLN:NE2	2:C:242:TYR:O	2.34	0.61
1:A:134:HIS:NE2	1:A:178:SER:OG	2.33	0.61
1:A:181:MET:SD	1:A:208:ILE:CG1	2.90	0.60
1:A:41:SER:OG	1:A:94:LYS:O	2.20	0.60
2:D:90:GLN:NE2	2:D:93:SER:O	2.35	0.59
1:A:40:SER:OG	1:A:43:LEU:O	2.21	0.59
2:D:177:GLU:OE2	2:D:194:LYS:NZ	2.37	0.58
1:B:124:ASP:O	1:B:136:GLU:N	2.35	0.58
2:C:55:HIS:NE2	2:C:241:ASP:OD2	2.37	0.58
1:B:86:ASN:CG	3:B:301:NAG:C1	2.71	0.57
1:A:212:PHE:CZ	1:B:127:GLY:CA	2.87	0.57
1:B:86:ASN:ND2	3:B:301:NAG:C2	2.68	0.57
2:C:218:THR:OG1	2:C:219:SER:N	2.38	0.56
1:A:136:GLU:OE1	1:A:138:ARG:NH1	2.39	0.56
2:C:232:ASP:OD2	2:C:242:TYR:OH	2.24	0.55
2:C:90:GLN:NE2	2:C:93:SER:O	2.39	0.55
1:B:153:ASN:N	1:B:153:ASN:OD1	2.40	0.54
1:A:153:ASN:N	1:A:153:ASN:OD1	2.41	0.54
2:C:65:SER:OG	2:C:66:GLY:N	2.41	0.54
2:C:6:GLN:OE1	2:C:99:GLY:O	2.25	0.53
2:D:65:SER:OG	2:D:66:GLY:N	2.42	0.53
1:A:59:ARG:NH2	2:D:92:HIS:O	2.42	0.53
1:A:101:ASP:OD1	1:A:101:ASP:C	2.49	0.51
1:B:67:ARG:NH2	1:B:91:ASP:OD2	2.44	0.51
2:D:229:ARG:O	2:D:241:ASP:N	2.44	0.51
1:B:116:ALA:N	1:B:143:TYR:O	2.45	0.50
1:A:206:ILE:CG1	1:A:207:SER:N	2.75	0.50
1:A:67:ARG:NH2	1:A:91:ASP:OD2	2.44	0.49
2:D:50:ARG:CG	2:D:50:ARG:NH1	2.74	0.49
2:D:241:ASP:OD1	2:D:242:TYR:N	2.45	0.49
2:D:232:ASP:OD2	2:D:242:TYR:OH	2.31	0.49
2:C:32:TRP:CE3	2:C:238:ASP:OD1	2.65	0.49
1:A:116:ALA:N	1:A:143:TYR:O	2.47	0.47
2:D:226:TYR:CD1	2:D:246:GLY:CA	2.98	0.47
2:C:106:ILE:O	2:C:107:LYS:O	2.32	0.47
2:C:67:SER:OG	2:C:68:ALA:N	2.48	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:216:SER:OG	2:C:216:SER:O	2.33	0.46
2:D:49:TYR:O	2:D:50:ARG:CB	2.63	0.46
2:C:49:TYR:O	2:C:50:ARG:CB	2.64	0.46
2:C:241:ASP:OD1	2:C:242:TYR:N	2.49	0.45
2:C:198:LYS:NZ	2:C:221:ASP:OD2	2.49	0.45
1:A:181:MET:O	1:A:213:PHE:CE1	2.70	0.45
1:B:129:LYS:CE	1:B:134:HIS:ND1	2.80	0.45
2:D:153:CYS:O	2:D:209:THR:CG2	2.64	0.45
2:D:221:ASP:O	2:D:225:TYR:OH	2.35	0.45
2:C:106:ILE:C	2:C:107:LYS:O	2.52	0.45
1:A:95:TYR:N	1:A:110:VAL:O	2.50	0.45
2:D:218:THR:OG1	2:D:219:SER:N	2.48	0.44
2:D:7:SER:O	2:D:22:THR:N	2.50	0.44
2:D:204:ASP:OD1	2:D:207:SER:N	2.51	0.44
2:D:96:TYR:CD1	2:D:96:TYR:N	2.86	0.44
1:A:119:SER:N	1:A:140:THR:O	2.51	0.43
1:B:20:ASP:OD2	1:B:83:ARG:NH2	2.51	0.43
1:B:95:TYR:N	1:B:110:VAL:O	2.51	0.43
2:D:226:TYR:CE1	2:D:246:GLY:CA	3.02	0.43
1:A:20:ASP:OD2	1:A:83:ARG:NH2	2.52	0.43
2:C:183:ASN:ND2	1:B:62:ALA:O	2.52	0.43
2:C:13:ALA:O	2:C:106:ILE:HA	2.19	0.42
2:C:7:SER:O	2:C:22:THR:N	2.52	0.42
1:B:119:SER:N	1:B:140:THR:O	2.52	0.42
2:D:198:LYS:NZ	2:D:221:ASP:OD2	2.52	0.42
2:C:204:ASP:OD1	2:C:207:SER:N	2.52	0.42
2:D:252:SER:OG	2:D:254:ALA:O	2.37	0.42
2:D:216:SER:O	2:D:216:SER:OG	2.38	0.41
2:C:218:THR:OG1	2:C:220:GLU:N	2.53	0.41
2:C:102:THR:CG2	2:C:103:LYS:N	2.74	0.41
1:A:103:ASP:N	1:A:103:ASP:OD1	2.52	0.41
1:B:188:GLY:C	1:B:189:VAL:CG1	2.89	0.41
1:A:46:VAL:O	1:A:61:SER:OG	2.39	0.41
1:B:86:ASN:OD1	3:B:301:NAG:N2	2.54	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	212/220 (96%)	210 (99%)	2 (1%)	0	100	100
1	B	211/220 (96%)	205 (97%)	6 (3%)	0	100	100
2	C	228/259 (88%)	209 (92%)	19 (8%)	0	100	100
2	D	228/259 (88%)	214 (94%)	14 (6%)	0	100	100
All	All	879/958 (92%)	838 (95%)	41 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	149/178 (84%)	124 (83%)	25 (17%)	3	13
1	B	146/178 (82%)	114 (78%)	32 (22%)	1	7
2	C	188/204 (92%)	149 (79%)	39 (21%)	2	8
2	D	189/204 (93%)	149 (79%)	40 (21%)	1	8
All	All	672/764 (88%)	536 (80%)	136 (20%)	2	9

All (136) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	MET
1	A	38	TRP
1	A	40	SER
1	A	43	LEU
1	A	44	ARG

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Mol	Chain	Res	Type
1	A	56	VAL
1	A	59	ARG
1	A	68	THR
1	A	76	THR
1	A	90	SER
1	A	96	LEU
1	A	106	GLU
1	A	151	SER
1	A	158	ILE
1	A	160	THR
1	A	161	VAL
1	A	170	VAL
1	A	175	VAL
1	A	178	SER
1	A	179	VAL
1	A	190	SER
1	A	192	THR
1	A	195	SER
1	A	197	LEU
1	A	208	ILE
2	D	1	ASP
2	D	5	THR
2	D	6	GLN
2	D	10	SER
2	D	14	SER
2	D	15	LEU
2	D	19	ILE
2	D	26	SER
2	D	27	GLN
2	D	31	LEU
2	D	43	ILE
2	D	50	ARG
2	D	53	ASN
2	D	56	THR
2	D	61	ARG
2	D	69	THR
2	D	76	SER
2	D	79	GLN
2	D	97	THR
2	D	105	ASP
2	D	135	LEU
2	D	137	GLU

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Mol	Chain	Res	Type
2	D	142	LEU
2	D	143	VAL
2	D	149	VAL
2	D	156	SER
2	D	182	ILE
2	D	191	PHE
2	D	200	THR
2	D	202	THR
2	D	203	VAL
2	D	206	SER
2	D	215	SER
2	D	218	THR
2	D	228	SER
2	D	229	ARG
2	D	232	ASP
2	D	236	THR
2	D	240	MET
2	D	250	THR
2	C	5	THR
2	C	6	GLN
2	C	10	SER
2	C	14	SER
2	C	15	LEU
2	C	19	ILE
2	C	26	SER
2	C	27	GLN
2	C	31	LEU
2	C	43	ILE
2	C	53	ASN
2	C	56	THR
2	C	61	ARG
2	C	69	THR
2	C	76	SER
2	C	79	GLN
2	C	102	THR
2	C	104	LEU
2	C	133	VAL
2	C	135	LEU
2	C	136	GLN
2	C	142	LEU
2	C	143	VAL
2	C	148	SER

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Mol	Chain	Res	Type
2	C	149	VAL
2	C	151	LEU
2	C	156	SER
2	C	159	THR
2	C	165	LEU
2	C	186	ASN
2	C	191	PHE
2	C	200	THR
2	C	203	VAL
2	C	215	SER
2	C	218	THR
2	C	228	SER
2	C	229	ARG
2	C	245	GLN
2	C	253	SER
1	B	8	SER
1	B	29	MET
1	B	32	GLU
1	B	38	TRP
1	B	43	LEU
1	B	56	VAL
1	B	59	ARG
1	B	68	THR
1	B	76	THR
1	B	90	SER
1	B	96	LEU
1	B	101	ASP
1	B	106	GLU
1	B	128	TYR
1	B	130	ASP
1	B	151	SER
1	B	158	ILE
1	B	160	THR
1	B	161	VAL
1	B	170	VAL
1	B	175	VAL
1	B	178	SER
1	B	179	VAL
1	B	181	MET
1	B	182	ARG
1	B	190	SER
1	B	192	THR

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Mol	Chain	Res	Type
1	B	195	SER
1	B	198	LEU
1	B	206	ILE
1	B	208	ILE
1	B	210	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains 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	$\# Z > 2$
3	NAG	A	301	1	12,14,15	0.64	0	15,19,21	0.89	1 (6%)
3	NAG	B	301	1	12,14,15	0.63	0	15,19,21	0.95	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
3	NAG	A	301	1	-	0/6/23/26	0/1/1/1
3	NAG	B	301	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	301	NAG	O5-C5-C6	2.74	109.85	106.98
3	B	301	NAG	O5-C5-C6	2.38	109.48	106.98

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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	214/220 (97%)	0.15	1 (0%) 88 42	55, 95, 157, 220	0
1	B	213/220 (96%)	0.09	0 100 100	53, 96, 150, 210	0
2	C	232/259 (89%)	-0.17	0 100 100	46, 74, 106, 131	0
2	D	232/259 (89%)	-0.17	0 100 100	36, 66, 100, 144	0
All	All	891/958 (93%)	-0.03	1 (0%) 93 72	36, 81, 143, 220	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	32	GLU	2.1

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	NAG	A	301	14/15	0.28	2.02	79,122,136,137	0
3	NAG	B	301	14/15	0.30	1.75	83,118,145,160	0

6.5 Other polymers ⓘ

There are no such residues in this entry.