



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 9, 2020 – 04:19 PM BST

PDB ID : 4JUK
Title : Crystal structure of H5N1 influenza virus hemagglutinin, clade 2.3.2.1
Authors : DuBois, R.M.; Zaraket, H.; Reddivari, M.; Coop, T.; Heath, R.J.; White, S.W.; Russell, C.J.
Deposited on : 2013-03-25
Resolution : 2.75 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

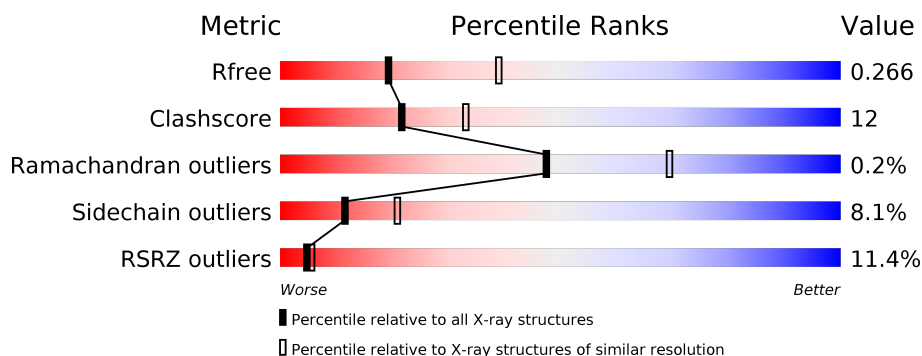
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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	329	<div> <div>3%</div> <div>77%</div> <div>18%</div> <div>...</div> </div>
2	B	182	<div> <div>25%</div> <div>64%</div> <div>25%</div> <div>5%</div> <div>7%</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4020 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 Hemagglutinin HA1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	320	Total	C	N	O	S	0	0	0
			2537	1603	437	483	14			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	5	GLY	-	expression tag	UNP B7NWR4
A	6	SER	-	expression tag	UNP B7NWR4
A	7	ALA	-	expression tag	UNP B7NWR4
A	8	ASP	-	expression tag	UNP B7NWR4
A	9	PRO	-	expression tag	UNP B7NWR4
A	10	GLY	-	expression tag	UNP B7NWR4

- Molecule 2 is a protein called Hemagglutinin HA2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	170	Total	C	N	O	S	0	0	0
			1380	859	241	272	8			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	177	ARG	-	expression tag	UNP B7NWR4
B	178	SER	-	expression tag	UNP B7NWR4
B	179	LEU	-	expression tag	UNP B7NWR4
B	180	VAL	-	expression tag	UNP B7NWR4
B	181	PRO	-	expression tag	UNP B7NWR4
B	182	ARG	-	expression tag	UNP B7NWR4

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

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

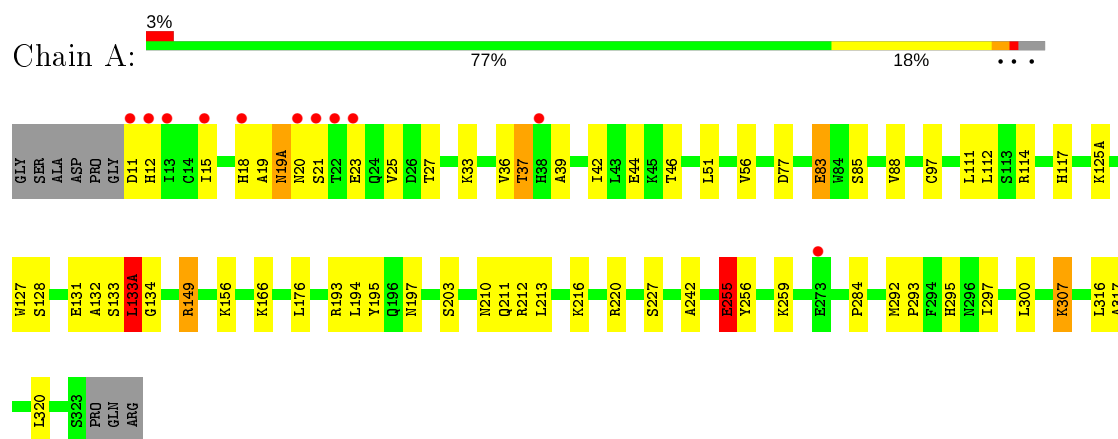
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	49	Total	O	0	0
			49	49		
5	B	7	Total	O	0	0
			7	7		

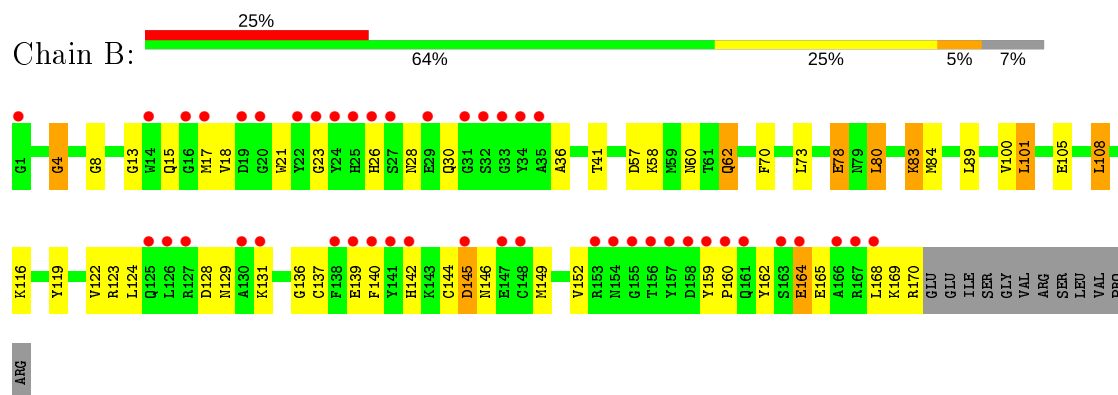
3 Residue-property plots [i](#)

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: Hemagglutinin HA1



• Molecule 2: Hemagglutinin HA2



4 Data and refinement statistics

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α , β , γ	116.36Å 116.36Å 134.60Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	47.19 – 2.75 47.19 – 2.75	Depositor EDS
% Data completeness (in resolution range)	99.4 (47.19-2.75) 99.4 (47.19-2.75)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.76 (at 2.77Å)	Xtriage
Refinement program	PHENIX 1.8_1069	Depositor
R, R_{free}	0.229 , 0.264 0.233 , 0.266	Depositor DCC
R_{free} test set	1397 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	60.6	Xtriage
Anisotropy	0.067	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 41.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.042 for -h,-k,l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4020	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.15% 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, SO4

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	0.58	0/2599	0.67	2/3532 (0.1%)
2	B	0.61	2/1407 (0.1%)	0.59	1/1891 (0.1%)
All	All	0.59	2/4006 (0.0%)	0.64	3/5423 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	78	GLU	CB-CG	-5.93	1.40	1.52
2	B	78	GLU	CG-CD	-5.59	1.43	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	255	GLU	N-CA-CB	5.57	120.62	110.60
2	B	80	LEU	CA-CB-CG	5.42	127.78	115.30
1	A	133(A)	LEU	N-CA-C	5.14	124.89	111.00

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	2537	0	2465	57	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1380	0	1291	46	0
3	A	5	0	0	0	0
4	A	42	0	39	4	0
5	A	49	0	0	5	0
5	B	7	0	0	0	0
All	All	4020	0	3795	92	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 (92) 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)
2:B:123:ARG:HH21	2:B:124:LEU:HD13	1.15	1.05
1:A:211:GLN:HE21	1:A:213:LEU:HD21	1.23	1.02
1:A:131:GLU:HG3	5:A:535:HOH:O	1.62	1.00
1:A:255:GLU:HG2	1:A:256:TYR:CD2	2.01	0.95
2:B:123:ARG:NH2	2:B:124:LEU:HD13	1.88	0.89
1:A:255:GLU:HG2	1:A:256:TYR:CE2	2.10	0.87
2:B:142:HIS:ND1	2:B:162:TYR:HD1	1.74	0.85
1:A:211:GLN:NE2	1:A:213:LEU:HD21	1.91	0.84
1:A:12:HIS:CE1	2:B:137:CYS:HB3	2.19	0.77
2:B:142:HIS:ND1	2:B:162:TYR:CD1	2.54	0.76
2:B:142:HIS:HD1	2:B:162:TYR:HD1	1.34	0.76
1:A:211:GLN:HE21	1:A:213:LEU:CD2	1.98	0.76
2:B:170:ARG:HG2	2:B:170:ARG:HH11	1.53	0.73
1:A:131:GLU:HG2	1:A:133(A):LEU:HD22	1.71	0.71
1:A:11:ASP:O	2:B:140:PHE:HD2	1.74	0.71
1:A:36:VAL:HG22	1:A:37:THR:N	2.07	0.69
2:B:28:ASN:OD1	2:B:146:ASN:ND2	2.25	0.69
1:A:27:THR:HB	2:B:105:GLU:HG3	1.75	0.69
1:A:295:HIS:HD2	1:A:297:ILE:H	1.42	0.65
1:A:19(A):ASN:HD22	1:A:19(A):ASN:C	2.00	0.64
2:B:28:ASN:HD21	2:B:146:ASN:HD22	1.44	0.64
2:B:159:TYR:HB3	2:B:160:PRO:HD3	1.81	0.62
2:B:142:HIS:CE1	2:B:162:TYR:CD1	2.88	0.62
2:B:70:PHE:CD2	2:B:78:GLU:HG3	2.33	0.62
1:A:216:LYS:O	1:A:220:ARG:NH2	2.33	0.62
2:B:57:ASP:O	2:B:60:ASN:ND2	2.33	0.62
2:B:30:GLN:NE2	2:B:145:ASP:OD2	2.32	0.62
1:A:307:LYS:HD3	2:B:62:GLN:HG2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:19(A):ASN:HD21	1:A:21:SER:HB3	1.67	0.59
1:A:149:ARG:NH2	5:A:546:HOH:O	2.34	0.59
1:A:19(A):ASN:HD21	1:A:21:SER:CB	2.17	0.58
1:A:11:ASP:O	2:B:140:PHE:CD2	2.56	0.58
1:A:156:LYS:HE2	1:A:193:ARG:O	2.05	0.57
2:B:170:ARG:HH11	2:B:170:ARG:CG	2.18	0.56
1:A:56:VAL:HB	1:A:85:SER:HB3	1.88	0.56
1:A:133:SER:O	1:A:133(A):LEU:HD12	2.06	0.56
1:A:36:VAL:CG2	1:A:37:THR:N	2.69	0.55
2:B:21:TRP:HB2	2:B:41:THR:HG23	1.90	0.54
2:B:28:ASN:HD21	2:B:146:ASN:ND2	2.05	0.54
1:A:216:LYS:NZ	5:A:526:HOH:O	2.41	0.53
1:A:25:VAL:HG11	1:A:317:ALA:HB2	1.91	0.53
1:A:242:ALA:CB	4:A:402:NAG:H82	2.38	0.53
1:A:255:GLU:HG3	1:A:255:GLU:O	2.08	0.52
1:A:133:SER:HA	5:A:524:HOH:O	2.09	0.52
2:B:28:ASN:ND2	2:B:146:ASN:HD22	2.07	0.52
1:A:133(A):LEU:N	1:A:134:GLY:HA3	2.24	0.52
1:A:242:ALA:HB3	4:A:402:NAG:H82	1.93	0.51
2:B:30:GLN:NE2	2:B:145:ASP:HA	2.26	0.51
1:A:18:HIS:HE1	2:B:18:VAL:HG13	1.75	0.50
1:A:33:LYS:HB2	4:A:403:NAG:H82	1.91	0.50
1:A:19(A):ASN:ND2	1:A:21:SER:CB	2.74	0.49
2:B:131:LYS:HB2	2:B:139:GLU:HB3	1.94	0.49
1:A:36:VAL:HG22	1:A:37:THR:H	1.78	0.49
1:A:51:LEU:HD13	1:A:88:VAL:HG21	1.95	0.49
1:A:242:ALA:HB3	4:A:402:NAG:C8	2.42	0.49
1:A:127:TRP:CH2	1:A:166:LYS:HD3	2.48	0.49
1:A:36:VAL:CG2	1:A:37:THR:H	2.26	0.48
1:A:19(A):ASN:ND2	1:A:19(A):ASN:C	2.66	0.48
2:B:128:ASP:OD1	2:B:128:ASP:N	2.44	0.48
1:A:27:THR:HB	2:B:105:GLU:CG	2.44	0.47
2:B:119:TYR:CE1	2:B:136:GLY:HA2	2.49	0.47
2:B:4:GLY:O	2:B:8:GLY:HA3	2.15	0.47
1:A:83:GLU:HB2	1:A:117:HIS:HB2	1.97	0.47
1:A:176:LEU:HD12	1:A:259:LYS:HA	1.97	0.46
1:A:125(A):LYS:HE3	1:A:132:ALA:O	2.14	0.46
1:A:19:ALA:HB2	2:B:13:GLY:HA3	1.97	0.46
1:A:195:TYR:O	1:A:197:ASN:N	2.47	0.46
2:B:170:ARG:CG	2:B:170:ARG:NH1	2.76	0.46
1:A:284:PRO:HD3	1:A:300:LEU:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:ASP:HB2	5:A:507:HOH:O	2.16	0.46
1:A:23:GLU:OE1	1:A:39:ALA:HB3	2.16	0.45
1:A:42:ILE:O	1:A:293:PRO:HD2	2.17	0.45
1:A:19(A):ASN:ND2	1:A:21:SER:HB2	2.32	0.45
1:A:316:LEU:HD13	2:B:100:VAL:HG22	1.98	0.45
2:B:119:TYR:HE1	2:B:136:GLY:HA2	1.81	0.45
2:B:28:ASN:ND2	2:B:146:ASN:ND2	2.63	0.45
1:A:133:SER:O	1:A:133(A):LEU:CD1	2.65	0.44
2:B:23:GLY:HA3	2:B:36:ALA:HA	2.00	0.44
1:A:20:ASN:OD1	2:B:15:GLN:NE2	2.51	0.44
2:B:101:LEU:HA	2:B:101:LEU:HD12	1.80	0.44
1:A:44:GLU:OE2	1:A:46:THR:HG22	2.17	0.44
2:B:146:ASN:HD22	2:B:146:ASN:HA	1.59	0.43
2:B:70:PHE:HD2	2:B:78:GLU:HG3	1.79	0.43
1:A:15:ILE:HD11	2:B:122:VAL:HG21	2.00	0.42
2:B:108:LEU:HA	2:B:108:LEU:HD12	1.91	0.42
2:B:58:LYS:HD3	2:B:58:LYS:HA	1.84	0.42
1:A:131:GLU:CG	1:A:133(A):LEU:HD22	2.47	0.42
1:A:220:ARG:HD2	1:A:227:SER:O	2.19	0.41
2:B:164:GLU:OE2	2:B:165:GLU:HG2	2.21	0.41
2:B:83:LYS:HE2	2:B:83:LYS:HB3	1.81	0.40
2:B:129:ASN:HD22	2:B:129:ASN:N	2.19	0.40
2:B:73:LEU:HD23	2:B:73:LEU:HA	1.99	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	318/329 (97%)	308 (97%)	10 (3%)	0	100	100
2	B	168/182 (92%)	160 (95%)	7 (4%)	1 (1%)	25	42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	486/511 (95%)	468 (96%)	17 (4%)	1 (0%)	47 69

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	4	GLY

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	286/292 (98%)	268 (94%)	18 (6%)	18 31
2	B	145/156 (93%)	128 (88%)	17 (12%)	5 8
All	All	431/448 (96%)	396 (92%)	35 (8%)	11 21

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19(A)	ASN
1	A	37	THR
1	A	83	GLU
1	A	97	CYS
1	A	111	LEU
1	A	112	LEU
1	A	114	ARG
1	A	128	SER
1	A	133(A)	LEU
1	A	149	ARG
1	A	194	LEU
1	A	203	SER
1	A	210	ASN
1	A	212	ARG
1	A	255	GLU
1	A	292	MET
1	A	307	LYS

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Mol	Chain	Res	Type
1	A	320	LEU
2	B	17	MET
2	B	26	HIS
2	B	62	GLN
2	B	80	LEU
2	B	83	LYS
2	B	84	MET
2	B	89	LEU
2	B	101	LEU
2	B	108	LEU
2	B	116	LYS
2	B	144	CYS
2	B	145	ASP
2	B	149	MET
2	B	152	VAL
2	B	164	GLU
2	B	168	LEU
2	B	169	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	HIS
1	A	19(A)	ASN
1	A	81	ASN
1	A	210	ASN
1	A	211	GLN
1	A	226	GLN
1	A	295	HIS
2	B	26	HIS
2	B	28	ASN
2	B	30	GLN
2	B	60	ASN
2	B	95	ASN
2	B	114	ASN
2	B	117	ASN
2	B	129	ASN
2	B	146	ASN

5.3.3 RNA ⓘ

There are no RNA molecules 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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

4 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$
4	NAG	A	402	1	14,14,15	0.96	1 (7%)	17,19,21	1.80	3 (17%)
3	SO4	A	401	-	4,4,4	0.11	0	6,6,6	0.18	0
4	NAG	A	404	1	14,14,15	0.55	0	17,19,21	1.05	1 (5%)
4	NAG	A	403	1	14,14,15	0.60	0	17,19,21	0.93	1 (5%)

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
4	NAG	A	402	1	-	2/6/23/26	0/1/1/1
4	NAG	A	404	1	-	0/6/23/26	0/1/1/1
4	NAG	A	403	1	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	402	NAG	O5-C1	-2.37	1.39	1.43

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	402	NAG	C1-O5-C5	-4.56	106.02	112.19
4	A	402	NAG	O5-C1-C2	-4.40	104.34	111.29
4	A	404	NAG	O5-C1-C2	-2.57	107.23	111.29
4	A	402	NAG	O4-C4-C3	-2.29	105.06	110.35
4	A	403	NAG	C3-C4-C5	2.02	113.85	110.24

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	403	NAG	O5-C5-C6-O6
4	A	403	NAG	C4-C5-C6-O6
4	A	402	NAG	C4-C5-C6-O6
4	A	402	NAG	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	402	NAG	3	0
4	A	403	NAG	1	0

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	320/329 (97%)	0.07	11 (3%) 45 53	4, 18, 66, 108	0
2	B	170/182 (93%)	1.25	45 (26%) 0 0	6, 72, 110, 119	0
All	All	490/511 (95%)	0.48	56 (11%) 5 5	4, 25, 104, 119	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	138	PHE	7.6
2	B	160	PRO	6.9
2	B	35	ALA	6.5
2	B	158	ASP	6.3
2	B	27	SER	6.2
2	B	161	GLN	5.3
2	B	29	GLU	4.9
2	B	19	ASP	4.8
2	B	156	THR	4.7
2	B	141	TYR	4.6
2	B	34	TYR	4.5
1	A	13	ILE	4.3
2	B	31	GLY	4.1
1	A	22	THR	4.1
2	B	25	HIS	4.0
2	B	17	MET	3.9
2	B	145	ASP	3.9
2	B	140	PHE	3.9
2	B	23	GLY	3.7
2	B	131	LYS	3.7
2	B	26	HIS	3.6
2	B	142	HIS	3.5
2	B	154	ASN	3.5
2	B	1	GLY	3.5

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Mol	Chain	Res	Type	RSRZ
2	B	33	GLY	3.5
2	B	166	ALA	3.4
2	B	168	LEU	3.2
1	A	12	HIS	3.2
2	B	164	GLU	3.2
2	B	163	SER	3.1
2	B	127	ARG	3.1
2	B	126	LEU	3.0
1	A	21	SER	3.0
2	B	157	TYR	3.0
2	B	148	CYS	2.9
2	B	159	TYR	2.9
1	A	20	ASN	2.8
2	B	139	GLU	2.7
2	B	155	GLY	2.7
2	B	147	GLU	2.7
2	B	24	TYR	2.7
2	B	16	GLY	2.6
2	B	14	TRP	2.6
1	A	15	ILE	2.6
2	B	130	ALA	2.6
2	B	167	ARG	2.5
2	B	125	GLN	2.5
1	A	11	ASP	2.5
1	A	23	GLU	2.4
1	A	18	HIS	2.4
2	B	32	SER	2.4
2	B	22	TYR	2.4
2	B	153	ARG	2.3
1	A	273	GLU	2.2
1	A	38	HIS	2.2
2	B	20	GLY	2.1

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
4	NAG	A	404	14/15	0.75	0.38	71,81,89,99	0
4	NAG	A	403	14/15	0.83	0.33	69,78,83,86	0
4	NAG	A	402	14/15	0.88	0.21	16,32,46,55	0
3	SO4	A	401	5/5	0.98	0.08	30,34,43,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.