



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 01:03 am GMT

PDB ID : 4F23
Title : Influenza A virus hemagglutinin H16 HA0 structure with an alpha-helix con-
formation in the cleavage site: a potential drug target
Authors : Lu, X.; Shi, Y.; Gao, F.; Xiao, H.; Qi, J.; Gao, G.F.
Deposited on : 2012-05-07
Resolution : 1.70 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

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

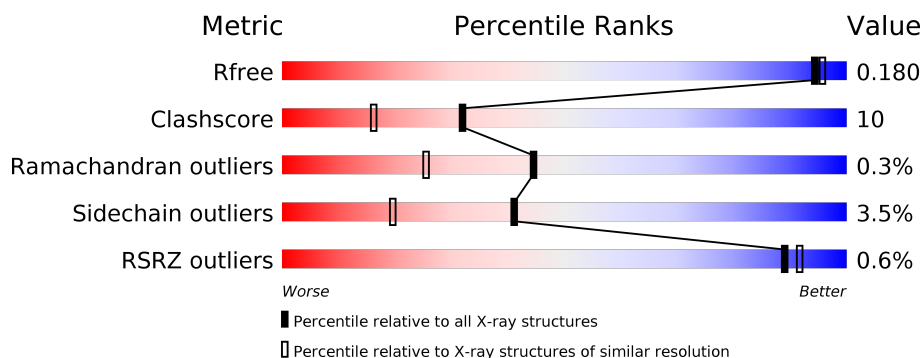
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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}	100719	3453 (1.70-1.70)
Clashscore	112137	3876 (1.70-1.70)
Ramachandran outliers	110173	3815 (1.70-1.70)
Sidechain outliers	110143	3815 (1.70-1.70)
RSRZ outliers	101464	3491 (1.70-1.70)

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. 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	515	<div> <div>80%</div> <div>17%</div> <div>..</div> </div>
1	B	515	<div> <div>%</div> <div>74%</div> <div>22%</div> <div>...</div> </div>
1	C	515	<div> <div>%</div> <div>82%</div> <div>15%</div> <div>..</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14190 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	509	Total	C	N	O	S	0	3	0
			4040	2522	719	781	18			
1	B	509	Total	C	N	O	S	0	1	0
			4025	2513	716	778	18			
1	C	509	Total	C	N	O	S	0	0	0
			4019	2510	715	776	18			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	HIS	-	EXPRESSION TAG	UNP Q5DL24
A	-4	HIS	-	EXPRESSION TAG	UNP Q5DL24
A	-3	HIS	-	EXPRESSION TAG	UNP Q5DL24
A	-2	HIS	-	EXPRESSION TAG	UNP Q5DL24
A	-1	HIS	-	EXPRESSION TAG	UNP Q5DL24
A	0	HIS	-	EXPRESSION TAG	UNP Q5DL24
A	1	ALA	-	SEE REMARK 999	UNP Q5DL24
A	2	ASP	-	SEE REMARK 999	UNP Q5DL24
A	3	GLY	-	SEE REMARK 999	UNP Q5DL24
A	4	ILE	-	SEE REMARK 999	UNP Q5DL24
A	5	GLN	-	SEE REMARK 999	UNP Q5DL24
A	505	ARG	-	SEE REMARK 999	UNP Q5DL24
A	506	LEU	-	SEE REMARK 999	UNP Q5DL24
A	507	VAL	-	SEE REMARK 999	UNP Q5DL24
A	508	PRO	-	SEE REMARK 999	UNP Q5DL24
A	509	ARG	-	SEE REMARK 999	UNP Q5DL24
B	-5	HIS	-	EXPRESSION TAG	UNP Q5DL24
B	-4	HIS	-	EXPRESSION TAG	UNP Q5DL24
B	-3	HIS	-	EXPRESSION TAG	UNP Q5DL24
B	-2	HIS	-	EXPRESSION TAG	UNP Q5DL24
B	-1	HIS	-	EXPRESSION TAG	UNP Q5DL24
B	0	HIS	-	EXPRESSION TAG	UNP Q5DL24
B	1	ALA	-	SEE REMARK 999	UNP Q5DL24

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Chain	Residue	Modelled	Actual	Comment	Reference
B	2	ASP	-	SEE REMARK 999	UNP Q5DL24
B	3	GLY	-	SEE REMARK 999	UNP Q5DL24
B	4	ILE	-	SEE REMARK 999	UNP Q5DL24
B	5	GLN	-	SEE REMARK 999	UNP Q5DL24
B	505	ARG	-	SEE REMARK 999	UNP Q5DL24
B	506	LEU	-	SEE REMARK 999	UNP Q5DL24
B	507	VAL	-	SEE REMARK 999	UNP Q5DL24
B	508	PRO	-	SEE REMARK 999	UNP Q5DL24
B	509	ARG	-	SEE REMARK 999	UNP Q5DL24
C	-5	HIS	-	EXPRESSION TAG	UNP Q5DL24
C	-4	HIS	-	EXPRESSION TAG	UNP Q5DL24
C	-3	HIS	-	EXPRESSION TAG	UNP Q5DL24
C	-2	HIS	-	EXPRESSION TAG	UNP Q5DL24
C	-1	HIS	-	EXPRESSION TAG	UNP Q5DL24
C	0	HIS	-	EXPRESSION TAG	UNP Q5DL24
C	1	ALA	-	SEE REMARK 999	UNP Q5DL24
C	2	ASP	-	SEE REMARK 999	UNP Q5DL24
C	3	GLY	-	SEE REMARK 999	UNP Q5DL24
C	4	ILE	-	SEE REMARK 999	UNP Q5DL24
C	5	GLN	-	SEE REMARK 999	UNP Q5DL24
C	505	ARG	-	SEE REMARK 999	UNP Q5DL24
C	506	LEU	-	SEE REMARK 999	UNP Q5DL24
C	507	VAL	-	SEE REMARK 999	UNP Q5DL24
C	508	PRO	-	SEE REMARK 999	UNP Q5DL24
C	509	ARG	-	SEE REMARK 999	UNP Q5DL24

- Molecule 2 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	2	Total	C	N	O	0	0
			28	16	2	10		
2	B	2	Total	C	N	O	0	0
			28	16	2	10		
2	C	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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	C	1	Total	C	N	O	0	0
			14	8	1	5		

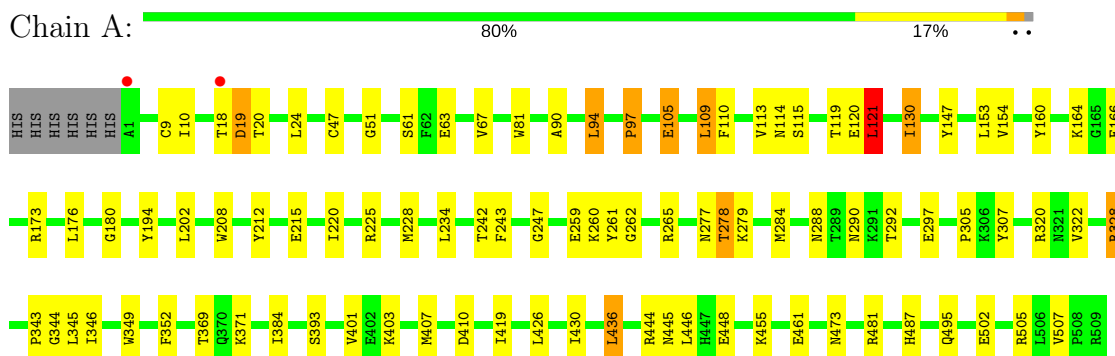
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	676	Total	O	0	0
			676	676		
4	B	650	Total	O	0	0
			650	650		
4	C	654	Total	O	0	0
			654	654		

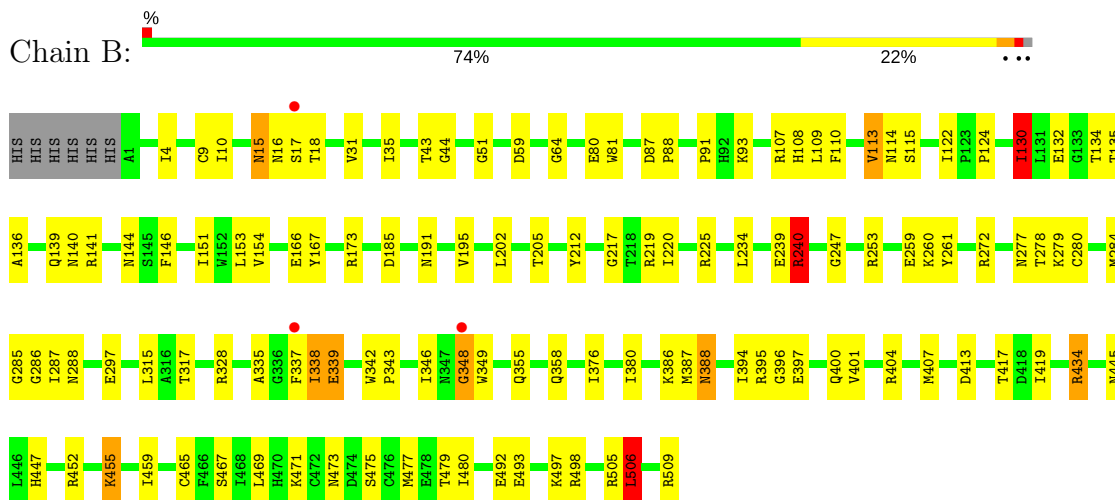
3 Residue-property plots

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

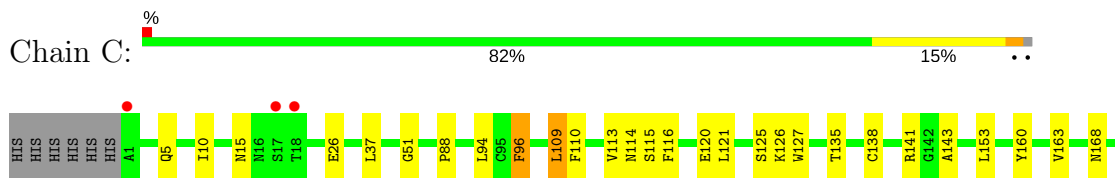
• Molecule 1: Hemagglutinin

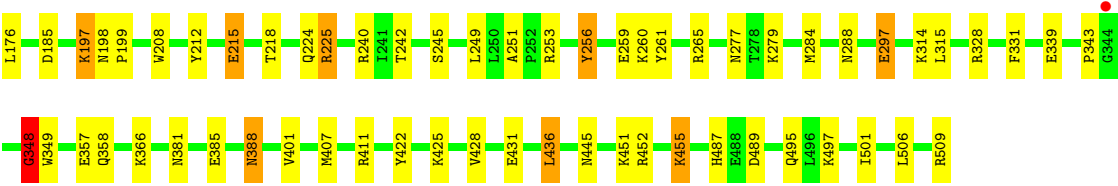


• Molecule 1: Hemagglutinin



• Molecule 1: Hemagglutinin





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	69.33Å 240.94Å 69.67Å 90.00° 119.79° 90.00°	Depositor
Resolution (Å)	25.00 – 1.70 24.15 – 1.71	Depositor EDS
% Data completeness (in resolution range)	97.5 (25.00-1.70) 97.6 (24.15-1.71)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 1.71Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.160 , 0.192 0.154 , 0.180	Depositor DCC
R_{free} test set	10596 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	16.2	Xtriage
Anisotropy	0.759	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 31.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.41$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.217 for -h-l,k,h 0.217 for l,k,-h-l 0.097 for h,-k,-h-l 0.095 for -h-l,-k,l 0.090 for l,-k,h	Xtriage
Reported twinning fraction	0.659 for H, K, L 0.209 for -H-L, K, H 0.132 for L, K, -H-L	Depositor
Outliers	0 of 210913 reflections	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	14190	wwPDB-VP
Average B, all atoms (Å ²)	21.0	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.*

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	1.27	11/4123 (0.3%)	1.03	12/5583 (0.2%)
1	B	1.28	11/4108 (0.3%)	1.04	13/5565 (0.2%)
1	C	1.30	15/4102 (0.4%)	1.00	6/5556 (0.1%)
All	All	1.29	37/12333 (0.3%)	1.02	31/16704 (0.2%)

All (37) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	431	GLU	CB-CG	8.63	1.68	1.52
1	C	348	GLY	N-CA	-7.75	1.34	1.46
1	C	256	TYR	CE1-CZ	-7.22	1.29	1.38
1	A	208	TRP	CE3-CZ3	7.21	1.50	1.38
1	B	493	GLU	CB-CG	6.67	1.64	1.52
1	A	194	TYR	CG-CD2	6.58	1.47	1.39
1	C	143	ALA	CA-CB	-6.36	1.39	1.52
1	B	146	PHE	CE1-CZ	6.10	1.49	1.37
1	B	492	GLU	CD-OE2	6.03	1.32	1.25
1	B	212	TYR	CE1-CZ	6.03	1.46	1.38
1	C	431	GLU	CD-OE2	5.93	1.32	1.25
1	C	138	CYS	CB-SG	5.91	1.92	1.82
1	B	396	GLY	C-O	5.89	1.33	1.23
1	C	208	TRP	CB-CG	5.86	1.60	1.50
1	B	247	GLY	N-CA	5.85	1.54	1.46
1	C	96	PHE	CD2-CE2	-5.80	1.27	1.39
1	B	166	GLU	CB-CG	-5.79	1.41	1.52
1	B	239	GLU	CD-OE1	-5.71	1.19	1.25
1	C	116	PHE	CE1-CZ	5.63	1.48	1.37
1	A	247	GLY	N-CA	5.60	1.54	1.46
1	A	212	TYR	CE2-CZ	-5.58	1.31	1.38
1	B	219	ARG	CZ-NH2	5.43	1.40	1.33
1	A	105	GLU	CD-OE2	-5.42	1.19	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	331	PHE	CD2-CE2	5.37	1.50	1.39
1	C	297	GLU	CB-CG	5.34	1.62	1.52
1	A	322	VAL	CB-CG2	5.34	1.64	1.52
1	C	215	GLU	CD-OE1	-5.28	1.19	1.25
1	A	461	GLU	CD-OE1	5.25	1.31	1.25
1	A	243	PHE	CG-CD1	5.23	1.46	1.38
1	A	120	GLU	CD-OE2	-5.20	1.20	1.25
1	C	212	TYR	CE2-CZ	-5.18	1.31	1.38
1	A	180	GLY	N-CA	5.12	1.53	1.46
1	A	160	TYR	CE1-CZ	5.08	1.45	1.38
1	B	113	VAL	CB-CG2	-5.07	1.42	1.52
1	C	212	TYR	CE1-CZ	5.05	1.45	1.38
1	B	110	PHE	CG-CD1	5.05	1.46	1.38
1	C	509	ARG	CZ-NH2	5.00	1.39	1.33

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	509	ARG	NE-CZ-NH1	10.96	125.78	120.30
1	A	265	ARG	NE-CZ-NH2	-9.77	115.41	120.30
1	A	265	ARG	NE-CZ-NH1	9.27	124.94	120.30
1	C	265	ARG	NE-CZ-NH2	-9.08	115.76	120.30
1	B	509	ARG	NE-CZ-NH2	-8.48	116.06	120.30
1	B	240	ARG	NE-CZ-NH2	-8.40	116.10	120.30
1	B	240	ARG	NE-CZ-NH1	7.99	124.29	120.30
1	A	94	LEU	CB-CG-CD1	7.92	124.46	111.00
1	B	130	ILE	CG1-CB-CG2	7.88	128.75	111.40
1	A	481	ARG	NE-CZ-NH2	-7.85	116.38	120.30
1	C	225	ARG	NE-CZ-NH1	7.82	124.21	120.30
1	C	265	ARG	NE-CZ-NH1	7.64	124.12	120.30
1	A	225	ARG	NE-CZ-NH2	-7.41	116.60	120.30
1	C	411	ARG	NE-CZ-NH1	-7.38	116.61	120.30
1	B	434	ARG	NE-CZ-NH1	7.34	123.97	120.30
1	C	436	LEU	CB-CG-CD1	6.76	122.49	111.00
1	B	506	LEU	CB-CG-CD2	6.55	122.13	111.00
1	B	404	ARG	NE-CZ-NH2	-6.19	117.21	120.30
1	A	121	LEU	CB-CG-CD1	6.18	121.51	111.00
1	A	481	ARG	NE-CZ-NH1	6.17	123.39	120.30
1	B	225	ARG	NE-CZ-NH1	6.02	123.31	120.30
1	A	147	TYR	CB-CG-CD2	-5.99	117.41	121.00
1	B	225	ARG	NE-CZ-NH2	-5.91	117.34	120.30
1	C	109	LEU	CB-CG-CD1	5.35	120.10	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	328	ARG	NE-CZ-NH2	-5.31	117.65	120.30
1	B	395	ARG	NE-CZ-NH1	5.29	122.94	120.30
1	A	410	ASP	CB-CG-OD1	5.27	123.04	118.30
1	A	446	LEU	CB-CG-CD1	-5.25	102.08	111.00
1	A	307	TYR	CB-CG-CD2	-5.16	117.91	121.00
1	B	107	ARG	NE-CZ-NH2	-5.16	117.72	120.30
1	B	167	TYR	CB-CG-CD2	5.13	124.08	121.00

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	4040	0	3923	70	0
1	B	4025	0	3908	107	0
1	C	4019	0	3903	82	0
2	A	28	0	25	0	0
2	B	28	0	25	0	0
2	C	28	0	25	0	0
3	A	14	0	13	0	0
3	B	14	0	13	0	0
3	C	14	0	13	0	0
4	A	676	0	0	30	0
4	B	650	0	0	48	0
4	C	654	0	0	40	0
All	All	14190	0	11848	243	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 10.

All (243) 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:480:ILE:HD12	4:B:1261:HOH:O	1.25	1.27

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:ALA:HB3	4:A:1086:HOH:O	1.42	1.20
1:B:467:SER:HB2	4:B:872:HOH:O	1.58	1.04
1:B:459:ILE:HB	4:B:872:HOH:O	1.58	1.03
1:A:202:LEU:HB3	4:A:1211:HOH:O	1.60	1.00
1:C:501:ILE:HD11	4:C:1338:HOH:O	1.63	0.98
1:B:253:ARG:HG3	4:B:1271:HOH:O	1.65	0.96
1:A:130:ILE:HA	4:A:1017:HOH:O	1.70	0.91
1:B:80:GLU:HA	4:B:1330:HOH:O	1.71	0.91
1:A:328:ARG:HA	1:C:445:ASN:HD21	1.35	0.90
1:C:253:ARG:HG2	4:C:1076:HOH:O	1.71	0.89
1:A:228:MET:HB2	4:A:1292:HOH:O	1.70	0.89
1:B:278:THR:HG22	1:B:280:CYS:H	1.35	0.88
1:B:445:ASN:HD21	1:C:328:ARG:HA	1.40	0.85
1:A:352:PHE:HD1	4:A:1175:HOH:O	1.58	0.85
1:B:317:THR:O	4:B:1101:HOH:O	1.94	0.85
1:C:51:GLY:H	1:C:277:ASN:HD21	1.24	0.84
1:B:15:ASN:HD22	1:B:16:ASN:H	1.20	0.84
1:C:113:VAL:HA	4:C:1278:HOH:O	1.77	0.84
1:B:64:GLY:HA3	4:B:1113:HOH:O	1.78	0.83
1:B:286:GLY:N	4:B:1062:HOH:O	2.10	0.82
1:C:260:LYS:O	4:C:1278:HOH:O	1.97	0.82
1:C:218:THR:HG21	1:C:225:ARG:NH2	1.94	0.82
1:B:144:ASN:HB3	4:B:992:HOH:O	1.80	0.82
1:C:261:TYR:HA	4:C:1278:HOH:O	1.78	0.81
4:A:972:HOH:O	1:B:220:ILE:HG12	1.79	0.81
1:B:346:ILE:HG13	1:B:348:GLY:HA2	1.62	0.81
1:C:160:TYR:HE2	4:C:1056:HOH:O	1.64	0.80
1:B:51:GLY:H	1:B:277:ASN:HD21	1.29	0.79
1:C:343:PRO:HD2	1:C:348:GLY:CA	2.13	0.79
1:B:477:MET:SD	4:B:1261:HOH:O	2.40	0.79
1:A:352:PHE:CD1	4:A:1175:HOH:O	2.31	0.79
4:A:920:HOH:O	1:B:506:LEU:HD12	1.82	0.78
1:B:447:HIS:HB2	4:B:1069:HOH:O	1.84	0.77
1:C:163:VAL:HG22	4:C:1056:HOH:O	1.84	0.77
1:A:51:GLY:H	1:A:277:ASN:HD21	1.33	0.76
1:C:452:ARG:O	1:C:455:LYS:HD2	1.86	0.74
1:C:489:ASP:OD2	4:C:1299:HOH:O	2.06	0.73
1:C:245:SER:O	4:C:1056:HOH:O	2.06	0.73
1:C:5:GLN:NE2	4:C:1338:HOH:O	2.20	0.73
1:A:110:PHE:CE2	1:A:176:LEU:HD22	2.24	0.72
1:C:160:TYR:CE2	4:C:1056:HOH:O	2.40	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:9:CYS:O	4:A:1175:HOH:O	2.06	0.71
1:C:199:PRO:HA	4:C:1295:HOH:O	1.89	0.71
1:C:197:LYS:HG3	4:C:1267:HOH:O	1.91	0.71
1:B:343:PRO:HD2	1:B:348:GLY:HA3	1.71	0.71
1:A:114:ASN:HB3	1:A:260[B]:LYS:HB2	1.72	0.70
1:C:120:GLU:HG3	4:C:1076:HOH:O	1.91	0.70
1:B:413:ASP:HA	4:B:1122:HOH:O	1.91	0.70
1:A:445:ASN:HD21	1:B:328:ARG:HA	1.57	0.70
1:B:130:ILE:HG21	1:B:153:LEU:HD22	1.75	0.69
1:B:376:ILE:HG13	4:B:1101:HOH:O	1.91	0.69
1:B:15:ASN:ND2	1:B:16:ASN:H	1.90	0.68
1:C:218:THR:CG2	1:C:225:ARG:NH2	2.56	0.68
1:B:497:LYS:HG2	4:B:1234:HOH:O	1.94	0.68
1:B:388:ASN:HD22	1:B:388:ASN:H	1.41	0.68
1:C:489:ASP:HB3	4:C:1243:HOH:O	1.93	0.67
1:A:284:MET:HG3	1:A:297:GLU:HB2	1.76	0.67
1:B:108:HIS:HD1	1:B:397:GLU:H	1.41	0.66
1:C:51:GLY:H	1:C:277:ASN:ND2	1.92	0.66
1:C:15:ASN:OD1	4:C:995:HOH:O	2.14	0.65
1:C:153:LEU:HD12	4:C:1280:HOH:O	1.96	0.65
1:B:417:THR:HG22	4:B:966:HOH:O	1.96	0.65
1:B:15:ASN:HD22	1:B:16:ASN:N	1.93	0.64
1:B:122:ILE:O	4:B:1271:HOH:O	2.15	0.64
1:C:115:SER:HB3	1:C:259:GLU:HB3	1.80	0.63
1:A:164:LYS:HE3	4:A:1310:HOH:O	1.99	0.62
1:B:477:MET:HA	4:B:1261:HOH:O	1.98	0.62
1:B:394:ILE:HD12	4:B:1122:HOH:O	2.00	0.62
1:B:285:GLY:CA	4:B:1062:HOH:O	2.47	0.62
1:B:285:GLY:HA3	4:B:1062:HOH:O	2.00	0.62
1:C:163:VAL:HG13	4:C:1056:HOH:O	2.01	0.61
1:B:278:THR:HG22	1:B:280:CYS:N	2.14	0.61
1:C:114:ASN:HB2	1:C:260:LYS:HD2	1.82	0.61
1:B:115:SER:HB3	1:B:259:GLU:HB3	1.83	0.60
1:C:224:GLN:NE2	4:C:1268:HOH:O	2.35	0.60
1:B:337:PHE:CZ	1:B:339:GLU:HG2	2.36	0.60
1:B:387:MET:HG3	1:C:422:TYR:CE1	2.36	0.60
1:C:168:ASN:OD1	1:C:240:ARG:HG3	2.00	0.60
1:C:343:PRO:HD2	1:C:348:GLY:HA2	1.83	0.60
1:B:51:GLY:H	1:B:277:ASN:ND2	2.00	0.59
1:B:15:ASN:HB2	4:B:1151:HOH:O	2.01	0.59
1:A:344:GLY:O	4:A:1371:HOH:O	2.16	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:358:GLN:HG3	4:C:1260:HOH:O	2.03	0.59
1:B:43:THR:OG1	4:B:1062:HOH:O	2.16	0.59
1:A:292:THR:HG21	4:A:1169:HOH:O	2.01	0.59
1:B:342:TRP:NE1	4:B:1151:HOH:O	2.29	0.59
1:A:444:ARG:HG2	4:A:1120:HOH:O	2.02	0.58
1:C:245:SER:HB3	4:C:1280:HOH:O	2.02	0.58
1:A:10:ILE:HD12	4:A:1175:HOH:O	2.02	0.58
1:A:110:PHE:CZ	1:A:176:LEU:HD22	2.37	0.58
1:A:401:VAL:HG12	1:A:401:VAL:O	2.03	0.58
1:B:284:MET:HG3	1:B:297:GLU:HB2	1.84	0.58
1:B:337:PHE:CE2	1:B:338:ILE:O	2.57	0.58
1:A:47:CYS:HB2	1:A:278:THR:HG22	1.84	0.58
1:A:18:THR:O	1:A:19:ASP:HB2	2.03	0.57
1:B:467:SER:CB	4:B:872:HOH:O	2.31	0.57
1:C:388:ASN:HD22	1:C:388:ASN:H	1.52	0.57
1:A:130:ILE:HG21	1:A:153:LEU:HD22	1.86	0.57
1:A:130:ILE:HG12	1:A:153:LEU:HB3	1.86	0.57
1:B:355:GLN:NE2	4:B:1034:HOH:O	2.36	0.57
1:C:185:ASP:OD1	1:C:225:ARG:NH1	2.37	0.57
1:A:202:LEU:HD22	1:B:217:GLY:HA3	1.88	0.56
1:A:130:ILE:HG13	1:A:154:VAL:O	2.05	0.56
1:C:343:PRO:HD2	1:C:348:GLY:HA3	1.86	0.56
1:A:290:ASN:HA	4:A:1294:HOH:O	2.05	0.56
1:B:467:SER:O	4:B:872:HOH:O	2.17	0.56
1:B:132:GLU:HG2	1:B:151:ILE:CG2	2.36	0.55
1:C:88:PRO:HG2	4:C:1285:HOH:O	2.06	0.55
1:C:215:GLU:HA	4:C:1273:HOH:O	2.05	0.55
1:B:434:ARG:HD2	4:B:883:HOH:O	2.05	0.55
1:C:37:LEU:HD12	1:C:428:VAL:HG21	1.88	0.55
1:A:345:LEU:N	4:A:921:HOH:O	2.39	0.54
1:B:338:ILE:HG23	1:B:339:GLU:H	1.71	0.54
1:B:144:ASN:ND2	4:B:992:HOH:O	2.37	0.54
1:B:93:LYS:HA	4:B:1113:HOH:O	2.08	0.54
1:B:387:MET:HG3	1:C:422:TYR:CD1	2.42	0.54
1:C:357:GLU:HB2	4:C:1288:HOH:O	2.07	0.53
1:C:455:LYS:HD3	1:C:487:HIS:CD2	2.43	0.53
1:A:202:LEU:HD23	4:A:1211:HOH:O	2.09	0.53
1:B:278:THR:HG23	1:B:287:ILE:O	2.09	0.53
1:C:197:LYS:HD2	4:C:1178:HOH:O	2.09	0.52
1:B:467:SER:CA	4:B:872:HOH:O	2.56	0.52
1:B:140:ASN:OD1	1:B:141:ARG:HD2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:386:LYS:HD3	1:C:425:LYS:HD3	1.91	0.52
1:A:115:SER:HB3	1:A:259:GLU:HB3	1.91	0.52
1:A:166:GLU:HB2	4:A:1012:HOH:O	2.09	0.52
1:A:403:LYS:O	1:A:407:MET:HG3	2.10	0.51
1:B:278:THR:CG2	1:B:280:CYS:H	2.16	0.51
1:A:215:GLU:CD	4:A:1100:HOH:O	2.49	0.51
1:A:61:SER:N	4:A:1086:HOH:O	2.42	0.51
1:C:366:LYS:HD2	4:C:1261:HOH:O	2.11	0.51
1:A:119:THR:HG23	1:A:121:LEU:HD13	1.91	0.51
1:A:114:ASN:HB3	1:A:260[A]:LYS:HB3	1.93	0.51
1:C:126:LYS:HD3	1:C:126:LYS:O	2.11	0.51
1:A:51:GLY:H	1:A:277:ASN:ND2	2.05	0.51
1:B:114:ASN:C	4:B:1330:HOH:O	2.49	0.50
1:B:195:VAL:HG12	4:B:1162:HOH:O	2.10	0.50
1:C:114:ASN:ND2	4:C:1323:HOH:O	2.44	0.50
1:C:366:LYS:HD3	4:C:1027:HOH:O	2.09	0.50
1:A:242:THR:HG21	1:B:220:ILE:HG21	1.94	0.50
1:B:401:VAL:HG12	1:B:401:VAL:O	2.10	0.50
1:C:197:LYS:HG2	1:C:197:LYS:O	2.12	0.50
1:C:96:PHE:CE1	4:C:1268:HOH:O	2.64	0.50
1:B:130:ILE:HG13	1:B:154:VAL:O	2.12	0.49
1:B:452:ARG:O	1:B:455:LYS:HE3	2.12	0.49
1:B:144:ASN:CB	4:B:992:HOH:O	2.52	0.49
1:B:455:LYS:HE2	4:B:1243:HOH:O	2.11	0.49
1:C:249:LEU:HB3	4:C:1280:HOH:O	2.12	0.49
1:A:220:ILE:HG21	1:C:242:THR:HG21	1.94	0.49
1:A:384:ILE:HA	4:A:1169:HOH:O	2.11	0.49
1:B:317:THR:CG2	1:B:380:ILE:HD11	2.43	0.49
1:B:445:ASN:ND2	1:C:328:ARG:HA	2.20	0.49
1:A:234:LEU:HB3	4:A:1355:HOH:O	2.12	0.49
1:A:328:ARG:HA	1:C:445:ASN:ND2	2.17	0.49
1:B:10:ILE:HB	4:B:1069:HOH:O	2.13	0.49
1:B:475:SER:O	1:B:479:THR:HG23	2.13	0.49
1:C:198:ASN:N	1:C:199:PRO:HD3	2.28	0.48
1:B:343:PRO:HD3	1:B:349:TRP:CE2	2.48	0.48
1:B:113:VAL:O	4:B:1330:HOH:O	2.20	0.48
1:B:335:ALA:O	1:B:342:TRP:HZ2	1.97	0.48
1:B:44:GLY:N	4:B:1062:HOH:O	2.47	0.48
1:A:455:LYS:HD3	1:A:487:HIS:NE2	2.29	0.48
1:C:163:VAL:HG21	4:C:1280:HOH:O	2.14	0.48
1:C:110:PHE:CZ	1:C:176:LEU:HD22	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:497:LYS:HD2	4:C:1338:HOH:O	2.14	0.47
1:B:43:THR:N	4:B:1062:HOH:O	2.46	0.47
1:B:358:GLN:OE1	1:B:473:ASN:HB2	2.15	0.47
1:C:451:LYS:NZ	4:C:1210:HOH:O	2.47	0.47
1:A:260[A]:LYS:O	1:A:260[A]:LYS:HG2	2.16	0.46
1:A:24:LEU:HD22	1:A:430:ILE:HG12	1.96	0.46
1:B:205:THR:HA	1:B:240:ARG:O	2.16	0.46
1:A:10:ILE:CD1	4:A:1175:HOH:O	2.62	0.46
1:A:320:ARG:HB2	1:A:436:LEU:HG	1.97	0.46
4:A:1316:HOH:O	1:C:455:LYS:HE3	2.16	0.46
1:C:284:MET:HG3	1:C:297:GLU:HB2	1.97	0.46
1:A:495:GLN:NE2	1:B:505:ARG:HH22	2.14	0.45
1:B:202:LEU:HD23	4:B:854:HOH:O	2.15	0.45
1:B:185:ASP:HA	1:B:217:GLY:O	2.17	0.45
1:A:473:ASN:ND2	4:A:906:HOH:O	2.49	0.44
1:B:81:TRP:CZ2	1:B:113:VAL:HG13	2.52	0.44
1:B:35:ILE:HD13	1:B:380:ILE:HD13	1.99	0.44
1:A:10:ILE:N	1:A:10:ILE:HD12	2.33	0.44
4:B:1051:HOH:O	1:C:407:MET:SD	2.62	0.44
1:C:110:PHE:CE2	1:C:176:LEU:HD22	2.52	0.44
1:A:220:ILE:HD13	1:C:242:THR:HG23	1.99	0.44
1:C:366:LYS:NZ	4:C:989:HOH:O	2.48	0.44
1:A:81:TRP:CZ2	1:A:113:VAL:HG13	2.53	0.44
1:A:346:ILE:HD11	1:A:369:THR:HG23	1.99	0.44
1:A:401:VAL:HG13	4:C:1223:HOH:O	2.18	0.44
1:A:61:SER:HB3	4:A:1086:HOH:O	2.17	0.44
1:A:97:PRO:O	4:A:1292:HOH:O	2.21	0.43
1:C:10:ILE:HD12	1:C:10:ILE:N	2.32	0.43
1:A:305:PRO:HD3	4:A:842:HOH:O	2.18	0.43
1:B:113:VAL:HB	1:B:261:TYR:HB3	2.00	0.43
1:A:455:LYS:HD3	1:A:487:HIS:CD2	2.53	0.43
1:B:240:ARG:NH2	4:B:1204:HOH:O	2.52	0.43
1:B:191:ASN:OD1	4:B:1209:HOH:O	2.21	0.43
1:B:343:PRO:HG2	1:B:348:GLY:O	2.19	0.43
1:B:278:THR:HG21	1:B:287:ILE:N	2.34	0.43
1:C:381:ASN:O	1:C:385:GLU:HB2	2.19	0.43
1:B:17:SER:HA	4:B:925:HOH:O	2.19	0.43
1:B:328:ARG:HD2	4:B:972:HOH:O	2.17	0.43
1:B:471:LYS:HE2	1:B:473:ASN:HB3	2.00	0.43
1:C:314:LYS:NZ	4:C:1245:HOH:O	2.52	0.43
1:A:63:GLU:O	1:A:67:VAL:HG22	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:317:THR:HG22	1:B:380:ILE:HD11	2.02	0.42
1:A:505:ARG:HH22	1:C:495:GLN:NE2	2.17	0.42
1:B:220:ILE:HG23	4:B:1110:HOH:O	2.19	0.42
1:C:127:TRP:CZ2	1:C:251:ALA:HB1	2.55	0.42
1:B:260:LYS:HE2	1:B:260:LYS:HB3	1.86	0.42
1:C:388:ASN:ND2	4:C:1225:HOH:O	2.51	0.42
1:A:502:GLU:HG3	4:A:1303:HOH:O	2.19	0.42
1:B:87:ASP:HA	1:B:88:PRO:HD3	1.95	0.42
1:C:125:SER:HB3	4:C:1281:HOH:O	2.19	0.42
1:A:110:PHE:HE2	1:A:176:LEU:HD22	1.80	0.41
1:A:262:GLY:O	1:B:407:MET:HE1	2.20	0.41
1:C:497:LYS:HD3	1:C:497:LYS:HA	1.75	0.41
1:A:401:VAL:CG1	1:A:401:VAL:O	2.68	0.41
1:B:394:ILE:HB	4:B:1122:HOH:O	2.21	0.41
1:B:9:CYS:HA	1:B:465:CYS:HA	2.02	0.41
1:C:37:LEU:HD12	1:C:428:VAL:CG2	2.49	0.41
1:B:328:ARG:HH11	1:B:328:ARG:HD2	1.71	0.41
1:B:136:ALA:O	1:B:139:GLN:HG3	2.21	0.41
1:B:17:SER:HB2	1:B:31:VAL:O	2.21	0.41
1:C:176:LEU:HD23	1:C:256:TYR:HD2	1.85	0.41
1:C:218:THR:HG22	1:C:225:ARG:CZ	2.51	0.41
1:B:134:THR:C	4:B:992:HOH:O	2.59	0.41
1:B:59:ASP:O	1:B:91:PRO:HD2	2.20	0.41
1:C:96:PHE:CD1	4:C:1268:HOH:O	2.57	0.41
1:A:343:PRO:HD3	1:A:349:TRP:CE2	2.56	0.41
1:A:444:ARG:O	1:A:448:GLU:HG2	2.21	0.41
1:C:114:ASN:CB	1:C:260:LYS:HD2	2.49	0.40
1:C:343:PRO:HD3	1:C:349:TRP:CE2	2.57	0.40
1:A:419:ILE:HG21	1:B:419:ILE:HD13	2.04	0.40
1:B:337:PHE:HZ	1:B:339:GLU:HG2	1.82	0.40
1:C:215:GLU:HG2	4:C:1273:HOH:O	2.21	0.40
1:C:401:VAL:HG22	1:C:401:VAL:O	2.22	0.40
1:A:113:VAL:HB	1:A:261:TYR:HB3	2.03	0.40
1:A:105:GLU:O	1:A:109:LEU:HD13	2.22	0.40
1:A:279:LYS:NZ	4:A:1294:HOH:O	2.48	0.40
1:B:124:PRO:HD3	4:B:1271:HOH:O	2.21	0.40
1:B:469:LEU:HD13	1:B:498:ARG:HB2	2.02	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	510/515 (99%)	495 (97%)	14 (3%)	1 (0%)	51	31
1	B	508/515 (99%)	488 (96%)	17 (3%)	3 (1%)	28	12
1	C	507/515 (98%)	488 (96%)	18 (4%)	1 (0%)	51	31
All	All	1525/1545 (99%)	1471 (96%)	49 (3%)	5 (0%)	44	25

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	19	ASP
1	B	339	GLU
1	C	348	GLY
1	B	348	GLY
1	B	338	ILE

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	442/445 (99%)	428 (97%)	14 (3%)	44	22
1	B	440/445 (99%)	423 (96%)	17 (4%)	37	15
1	C	439/445 (99%)	424 (97%)	15 (3%)	42	20
All	All	1321/1335 (99%)	1275 (96%)	46 (4%)	41	19

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	THR
1	A	94	LEU
1	A	97	PRO
1	A	109	LEU
1	A	121	LEU
1	A	130	ILE
1	A	173	ARG
1	A	278	THR
1	A	288	ASN
1	A	371	LYS
1	A	393	SER
1	A	426	LEU
1	A	436	LEU
1	A	507	VAL
1	B	4	ILE
1	B	15	ASN
1	B	18	THR
1	B	109	LEU
1	B	130	ILE
1	B	135	THR
1	B	173	ARG
1	B	234	LEU
1	B	240	ARG
1	B	272	ARG
1	B	279	LYS
1	B	288	ASN
1	B	315	LEU
1	B	388	ASN
1	B	400	GLN
1	B	455	LYS
1	B	506	LEU
1	C	26	GLU
1	C	94	LEU
1	C	109	LEU
1	C	121	LEU
1	C	135	THR
1	C	141	ARG
1	C	197	LYS
1	C	279	LYS
1	C	288	ASN
1	C	315	LEU
1	C	339	GLU
1	C	388	ASN

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Mol	Chain	Res	Type
1	C	436	LEU
1	C	455	LYS
1	C	506	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	A	92	HIS
1	A	114	ASN
1	A	268	GLN
1	A	277	ASN
1	A	288	ASN
1	A	445	ASN
1	A	495	GLN
1	B	15	ASN
1	B	41	ASN
1	B	92	HIS
1	B	277	ASN
1	B	388	ASN
1	B	445	ASN
1	B	495	GLN
1	C	114	ASN
1	C	139	GLN
1	C	277	ASN
1	C	288	ASN
1	C	388	ASN
1	C	445	ASN
1	C	495	GLN

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

6 carbohydrates 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	A	601	1,2	14,14,15	0.77	0	15,19,21	0.78	1 (6%)
2	NAG	A	602	2	14,14,15	1.28	2 (14%)	15,19,21	1.62	4 (26%)
2	NAG	B	601	1,2	14,14,15	0.55	0	15,19,21	1.76	6 (40%)
2	NAG	B	602	2	14,14,15	0.62	0	15,19,21	1.45	3 (20%)
2	NAG	C	601	1,2	14,14,15	0.87	0	15,19,21	0.92	0
2	NAG	C	602	2	14,14,15	0.63	0	15,19,21	1.37	2 (13%)

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	A	601	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	602	2	-	0/6/23/26	0/1/1/1
2	NAG	B	601	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	602	2	-	0/6/23/26	0/1/1/1
2	NAG	C	601	1,2	-	0/6/23/26	0/1/1/1
2	NAG	C	602	2	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	602	NAG	O4-C4	2.20	1.48	1.43
2	A	602	NAG	C1-C2	2.61	1.56	1.52

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	602	NAG	C3-C4-C5	-2.85	105.20	110.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	NAG	C1-C2-N2	-2.80	105.70	110.49
2	A	602	NAG	C2-N2-C7	-2.51	119.28	122.94
2	B	601	NAG	O6-C6-C5	-2.45	103.11	111.34
2	B	601	NAG	O7-C7-C8	-2.34	117.79	122.06
2	A	601	NAG	C3-C4-C5	-2.11	106.51	110.22
2	A	602	NAG	C6-C5-C4	-2.10	108.08	113.00
2	B	602	NAG	C1-C2-N2	2.03	113.95	110.49
2	C	602	NAG	C1-C2-N2	2.03	113.96	110.49
2	C	602	NAG	C2-N2-C7	2.20	126.16	122.94
2	B	602	NAG	C4-C3-C2	2.26	114.33	111.02
2	B	601	NAG	C8-C7-N2	2.29	120.25	116.11
2	B	601	NAG	C1-O5-C5	2.75	115.96	112.17
2	B	601	NAG	O5-C1-C2	2.83	115.42	111.47
2	A	602	NAG	C1-O5-C5	3.10	116.43	112.17
2	B	602	NAG	C2-N2-C7	3.75	128.41	122.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.6 Ligand geometry

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	$\# Z > 2$
3	NAG	A	603	1	14,14,15	1.84	1 (7%)	15,19,21	1.32	2 (13%)
3	NAG	B	603	1	14,14,15	1.04	1 (7%)	15,19,21	1.15	2 (13%)
3	NAG	C	603	1	14,14,15	1.09	1 (7%)	15,19,21	1.60	2 (13%)

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	603	1	-	0/6/23/26	0/1/1/1
3	NAG	B	603	1	-	0/6/23/26	0/1/1/1
3	NAG	C	603	1	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	603	NAG	C1-C2	2.73	1.56	1.52
3	B	603	NAG	C1-C2	3.08	1.56	1.52
3	A	603	NAG	C1-C2	6.05	1.60	1.52

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	603	NAG	C4-C3-C2	-2.91	106.76	111.02
3	B	603	NAG	C2-N2-C7	-2.35	119.51	122.94
3	B	603	NAG	C1-O5-C5	2.40	115.47	112.17
3	A	603	NAG	O3-C3-C4	2.51	115.83	110.36
3	C	603	NAG	O5-C1-C2	2.55	115.03	111.47
3	C	603	NAG	C1-O5-C5	5.06	119.15	112.17

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	509/515 (98%)	-0.16	2 (0%) 92 93	9, 18, 28, 44	0
1	B	509/515 (98%)	-0.18	3 (0%) 89 91	9, 19, 30, 45	0
1	C	509/515 (98%)	-0.19	4 (0%) 86 88	9, 19, 29, 42	0
All	All	1527/1545 (98%)	-0.18	9 (0%) 89 91	9, 19, 29, 45	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	18	THR	5.6
1	A	1	ALA	5.6
1	C	1	ALA	4.1
1	B	17	SER	3.0
1	C	17	SER	3.0
1	C	18	THR	3.0
1	C	344	GLY	2.7
1	B	337	PHE	2.6
1	B	348	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](#)

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	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	NAG	C	601	14/15	0.84	0.12	0.67	22,32,35,35	0
2	NAG	B	601	14/15	0.92	0.09	-1.23	26,29,33,36	0
2	NAG	A	602	14/15	0.76	0.19	-	27,31,37,39	0
2	NAG	B	602	14/15	0.88	0.14	-	34,37,40,40	0
2	NAG	A	601	14/15	0.95	0.08	-	19,22,27,31	0
2	NAG	C	602	14/15	0.88	0.14	-	31,35,41,44	0

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. 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	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	NAG	A	603	14/15	0.89	0.13	-	26,29,33,37	0
3	NAG	C	603	14/15	0.88	0.18	-	32,36,39,41	0
3	NAG	B	603	14/15	0.82	0.15	-	30,34,36,38	0

6.5 Other polymers [i](#)

There are no such residues in this entry.