



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 14, 2017 – 09:05 AM EST

PDB ID : 4XKE
Title : Crystal structure of hemagglutinin from Taiwan (2013) H6N1 influenza virus
in complex with 3'-SLN
Authors : Tzarum, N.; Zhu, X.; Wilson, I.A.
Deposited on : unknown
Resolution : 2.36 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : rb-20030345
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) : rb-20030345

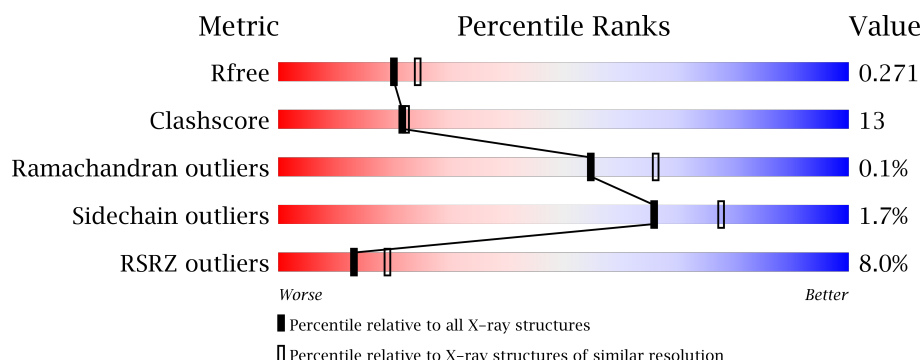
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.36 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	1522 (2.38-2.34)
Clashscore	112137	1626 (2.38-2.34)
Ramachandran outliers	110173	1605 (2.38-2.34)
Sidechain outliers	110143	1606 (2.38-2.34)
RSRZ outliers	101464	1528 (2.38-2.34)

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	333	<div> <div>8%</div> <div>74%</div> <div>22%</div> <div>..</div> </div>
1	C	333	<div> <div>7%</div> <div>75%</div> <div>21%</div> <div>..</div> </div>
1	E	333	<div> <div>6%</div> <div>67%</div> <div>29%</div> <div>..</div> </div>
2	B	180	<div> <div>10%</div> <div>75%</div> <div>21%</div> <div>.</div> </div>
2	D	180	<div> <div>10%</div> <div>77%</div> <div>19%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	180	<div><div>8%</div><div>73%</div><div>23%</div><div>.</div></div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12144 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 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	330	Total	C	N	O	S	0	0	0
			2600	1648	443	496	13			
1	C	326	Total	C	N	O	S	0	0	0
			2569	1629	437	490	13			
1	E	325	Total	C	N	O	S	0	0	0
			2563	1626	437	487	13			

- Molecule 2 is a protein called Hemagglutinin HA2 chain.

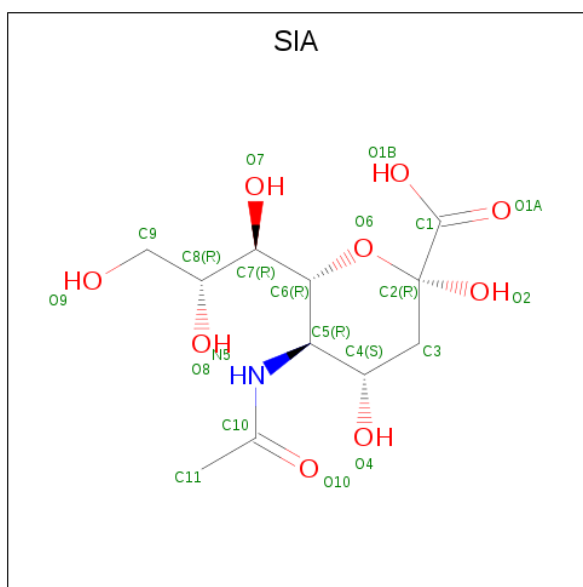
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	173	Total	C	N	O	S	0	0	0
			1393	868	244	274	7			
2	D	173	Total	C	N	O	S	0	0	0
			1393	868	244	274	7			
2	F	172	Total	C	N	O	S	0	0	0
			1385	862	243	273	7			

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



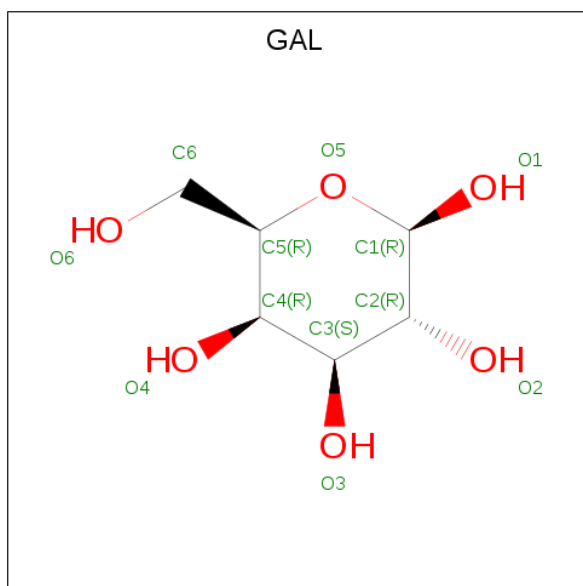
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			15	8	1	6		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		
3	E	1	Total	C	N	O	0	0
			14	8	1	5		
3	E	1	Total	C	N	O	0	0
			14	8	1	5		
3	F	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is O-SIALIC ACID (three-letter code: SIA) (formula: C₁₁H₁₉NO₉).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			20	11	1	8		

- Molecule 5 is BETA-D-GALACTOSE (three-letter code: GAL) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			11	6	5		

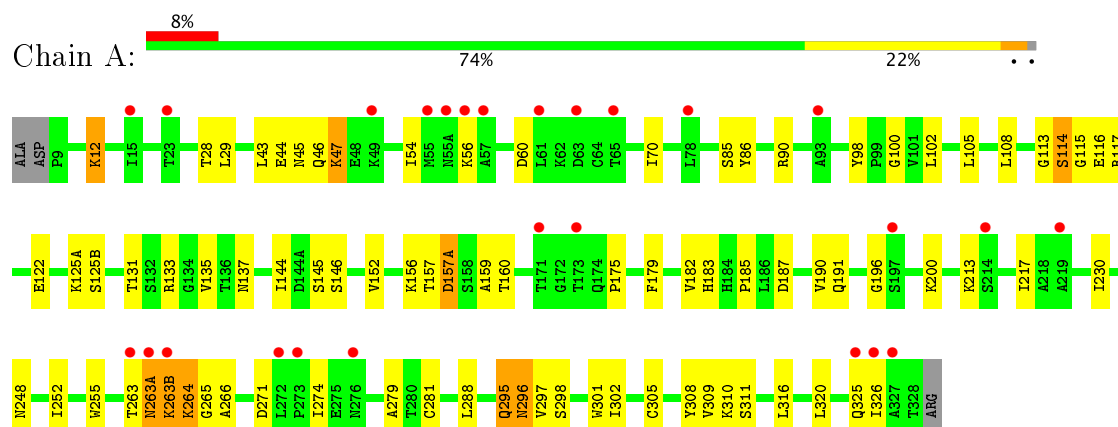
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	27	Total 27	O 27	0	0
6	B	21	Total 21	O 21	0	0
6	C	25	Total 25	O 25	0	0
6	D	12	Total 12	O 12	0	0
6	E	19	Total 19	O 19	0	0
6	F	7	Total 7	O 7	0	0

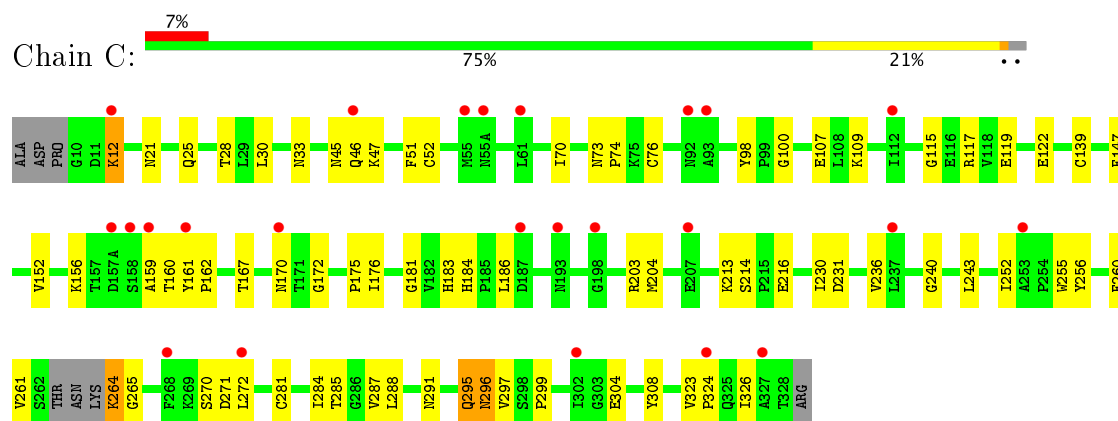
3 Residue-property plots [i](#)

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.

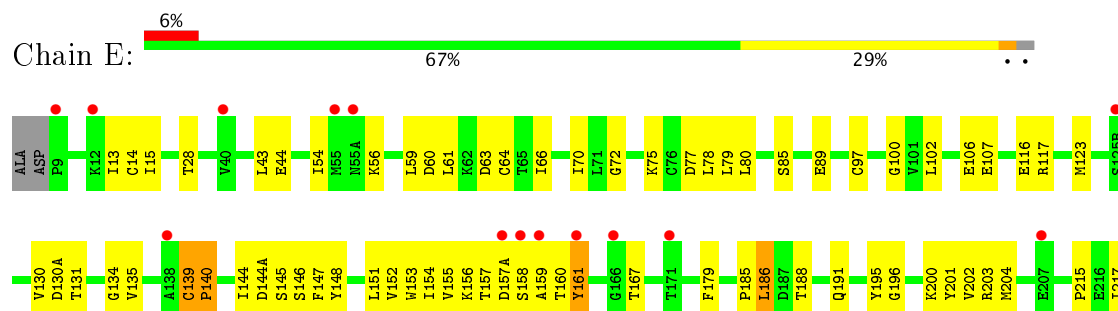
• Molecule 1: Hemagglutinin HA1 chain

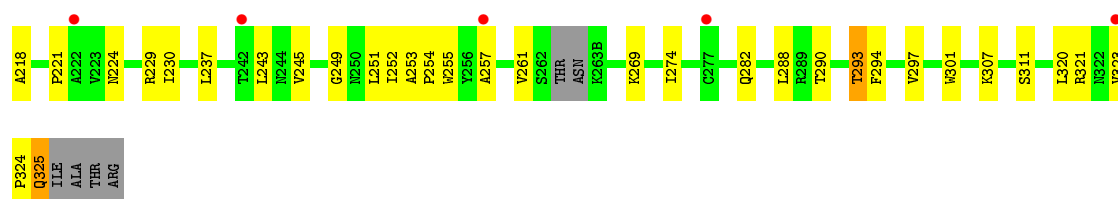


• Molecule 1: Hemagglutinin HA1 chain

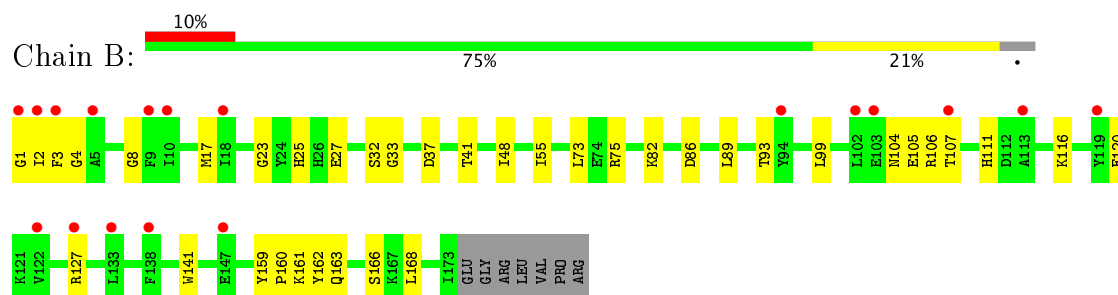


• Molecule 1: Hemagglutinin HA1 chain

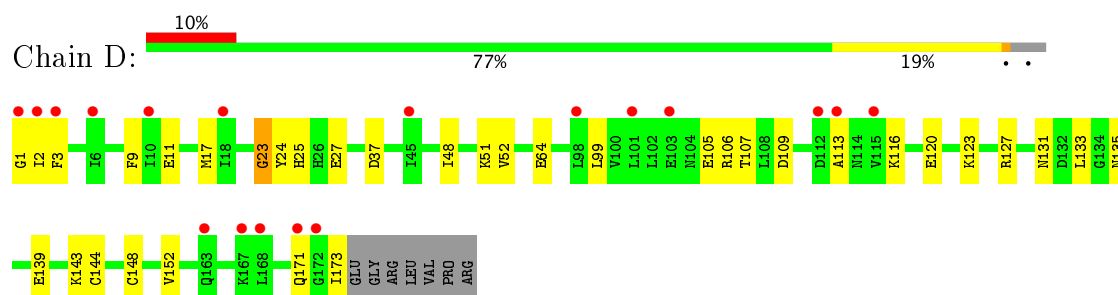




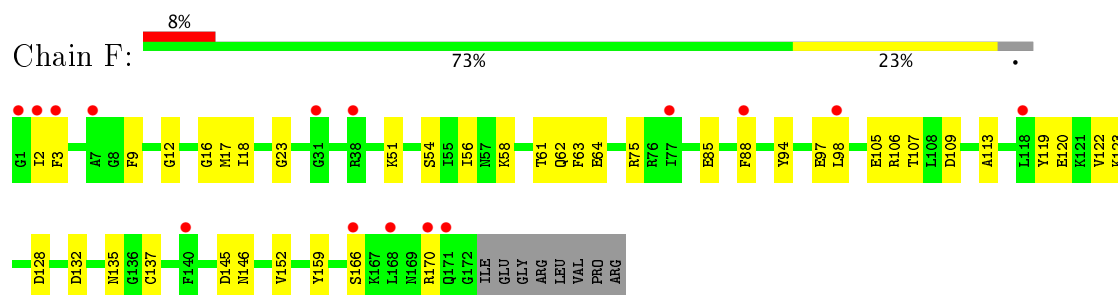
• Molecule 2: Hemagglutinin HA2 chain



• Molecule 2: Hemagglutinin HA2 chain



• Molecule 2: Hemagglutinin HA2 chain



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	185.60Å 99.25Å 133.42Å 90.00° 126.30° 90.00°	Depositor
Resolution (Å)	49.51 – 2.36 49.51 – 2.36	Depositor EDS
% Data completeness (in resolution range)	97.0 (49.51-2.36) 91.9 (49.51-2.36)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.91 (at 2.37Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.230 , 0.272 0.230 , 0.271	Depositor DCC
R_{free} test set	3710 reflections (5.01%)	DCC
Wilson B-factor (Å ²)	50.9	Xtriage
Anisotropy	0.629	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 53.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12144	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.59% 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: SIA, GAL, 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	0.58	1/2662 (0.0%)	0.68	4/3622 (0.1%)
1	C	0.59	2/2629 (0.1%)	0.70	6/3576 (0.2%)
1	E	0.53	1/2624 (0.0%)	0.65	3/3567 (0.1%)
2	B	0.55	0/1421	0.66	1/1913 (0.1%)
2	D	0.49	0/1421	0.65	2/1913 (0.1%)
2	F	0.51	0/1413	0.78	3/1902 (0.2%)
All	All	0.55	4/12170 (0.0%)	0.68	19/16493 (0.1%)

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

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	47	LYS	C-N	9.95	1.56	1.34
1	C	162	PRO	N-CD	5.48	1.55	1.47
1	C	324	PRO	N-CD	5.21	1.55	1.47
1	E	140	PRO	N-CD	5.02	1.54	1.47

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	62	GLN	O-C-N	-12.82	102.19	122.70
2	F	62	GLN	C-N-CA	10.38	147.64	121.70
1	A	12	LYS	CD-CE-NZ	9.26	133.01	111.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	47	LYS	O-C-N	-9.22	107.94	122.70
2	F	62	GLN	CA-C-N	8.80	136.56	117.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	114	SER	Peptide

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	2600	0	2551	100	1
1	C	2569	0	2516	61	0
1	E	2563	0	2506	83	1
2	B	1393	0	1309	37	0
2	D	1393	0	1309	31	0
2	F	1385	0	1297	31	0
3	A	43	0	40	1	0
3	D	14	0	13	5	0
3	E	28	0	26	0	0
3	F	14	0	13	0	0
4	A	20	0	17	2	0
5	A	11	0	9	4	0
6	A	27	0	0	1	0
6	B	21	0	0	1	0
6	C	25	0	0	4	0
6	D	12	0	0	2	0
6	E	19	0	0	5	0
6	F	7	0	0	0	0
All	All	12144	0	11606	314	1

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 13.

The worst 5 of 314 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:137:ASN:HD21	5:A:404:GAL:H4	1.05	1.17
2:F:2:ILE:CG2	2:F:109:ASP:OD1	1.96	1.12
2:F:2:ILE:HG22	2:F:109:ASP:OD1	1.52	1.09
1:A:137:ASN:HD21	5:A:404:GAL:C4	1.67	1.08
1:A:263:THR:HG21	1:A:263(B):LYS:HG2	1.33	1.07

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157(A):ASP:OD1	1:E:188:THR:OG1[2_757]	1.88	0.32

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	328/333 (98%)	314 (96%)	13 (4%)	1 (0%)	44	53
1	C	322/333 (97%)	312 (97%)	10 (3%)	0	100	100
1	E	321/333 (96%)	306 (95%)	15 (5%)	0	100	100
2	B	171/180 (95%)	170 (99%)	1 (1%)	0	100	100
2	D	171/180 (95%)	166 (97%)	5 (3%)	0	100	100
2	F	170/180 (94%)	167 (98%)	3 (2%)	0	100	100
All	All	1483/1539 (96%)	1435 (97%)	47 (3%)	1 (0%)	55	66

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	263(B)	LYS

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	289/291 (99%)	281 (97%)	8 (3%)	49	61
1	C	285/291 (98%)	282 (99%)	3 (1%)	78	87
1	E	284/291 (98%)	275 (97%)	9 (3%)	44	55
2	B	147/153 (96%)	147 (100%)	0	100	100
2	D	147/153 (96%)	146 (99%)	1 (1%)	87	93
2	F	146/153 (95%)	145 (99%)	1 (1%)	87	93
All	All	1298/1332 (97%)	1276 (98%)	22 (2%)	66	77

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	295	GLN
1	E	28	THR
1	E	325	GLN
1	C	296	ASN
2	D	64	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	117	ASN
1	C	325	GLN
1	C	170	ASN
1	A	263(A)	ASN
2	B	163	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

9 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	401	1	14,14,15	0.53	0	15,19,21	0.79	0
3	NAG	A	402	1	14,14,15	0.42	0	15,19,21	0.48	0
4	SIA	A	403	5	17,20,21	0.68	0	19,28,31	1.19	2 (10%)
5	GAL	A	404	3,4	11,11,12	1.59	2 (18%)	13,15,17	1.56	4 (30%)
3	NAG	A	405	5	15,15,15	0.65	0	21,21,21	1.71	4 (19%)
3	NAG	D	201	2	14,14,15	0.58	0	15,19,21	2.58	5 (33%)
3	NAG	E	401	1	14,14,15	0.44	0	15,19,21	1.44	3 (20%)
3	NAG	E	402	1	14,14,15	0.71	0	15,19,21	1.77	3 (20%)
3	NAG	F	201	2	14,14,15	0.53	0	15,19,21	1.22	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	401	1	-	0/6/23/26	0/1/1/1
3	NAG	A	402	1	-	0/6/23/26	0/1/1/1
4	SIA	A	403	5	-	0/14/34/38	0/1/1/1
5	GAL	A	404	3,4	-	0/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	A	405	5	-	0/6/26/26	0/1/1/1
3	NAG	D	201	2	-	0/6/23/26	0/1/1/1
3	NAG	E	401	1	-	0/6/23/26	0/1/1/1
3	NAG	E	402	1	-	0/6/23/26	0/1/1/1
3	NAG	F	201	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)
5	A	404	GAL	O5-C1	-3.65	1.37	1.43
5	A	404	GAL	C1-C2	3.15	1.59	1.52

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	201	NAG	C1-C2-N2	-7.81	97.14	110.49
3	E	402	NAG	C1-C2-N2	-4.64	102.56	110.49
3	A	405	NAG	O5-C1-C2	-4.01	105.48	109.52
3	D	201	NAG	C6-C5-C4	-3.64	104.49	113.00
3	A	405	NAG	O4-C4-C3	-3.62	102.48	110.36

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	403	SIA	2	0
5	A	404	GAL	4	0
3	A	405	NAG	1	0
3	D	201	NAG	5	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 [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	330/333 (99%)	0.67	26 (7%)	13 20	48, 64, 81, 96	0
1	C	326/333 (97%)	0.65	24 (7%)	15 22	49, 62, 80, 99	0
1	E	325/333 (97%)	0.65	19 (5%)	24 34	50, 63, 79, 98	0
2	B	173/180 (96%)	0.83	18 (10%)	7 11	47, 58, 72, 85	0
2	D	173/180 (96%)	0.84	18 (10%)	7 11	49, 62, 78, 91	0
2	F	172/180 (95%)	0.87	15 (8%)	11 16	48, 62, 78, 95	0
All	All	1499/1539 (97%)	0.72	120 (8%)	13 19	47, 62, 79, 99	0

The worst 5 of 120 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	1	GLY	8.8
2	F	1	GLY	7.7
2	B	1	GLY	7.5
2	F	38	ARG	5.3
1	A	55	MET	4.8

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 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	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	NAG	F	201	14/15	0.73	0.21	1.27	85,89,95,98	0
3	NAG	A	405	15/15	0.84	0.20	0.49	83,87,99,105	0
4	SIA	A	403	20/21	0.83	0.17	0.25	62,69,74,75	1
3	NAG	A	402	14/15	0.84	0.16	-0.55	76,84,88,88	0
3	NAG	E	402	14/15	0.86	0.19	-	91,97,103,108	0
3	NAG	D	201	14/15	0.65	0.25	-	91,100,105,110	0
3	NAG	E	401	14/15	0.69	0.47	-	102,111,118,118	0
5	GAL	A	404	11/12	0.94	0.09	-	72,76,78,81	0
3	NAG	A	401	14/15	0.65	0.24	-	89,96,104,105	0

6.5 Other polymers

There are no such residues in this entry.