



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 19, 2016 – 11:26 PM GMT

PDB ID : 5E2Z
Title : Crystal structure of H5 hemagglutinin Q226L mutant from the influenza virus
A/duck/Egypt/10185SS/2010 (H5N1) with LSTa
Authors : Zhu, X.; Wilson, I.A.
Deposited on : 2015-10-01
Resolution : 2.62 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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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-20026982

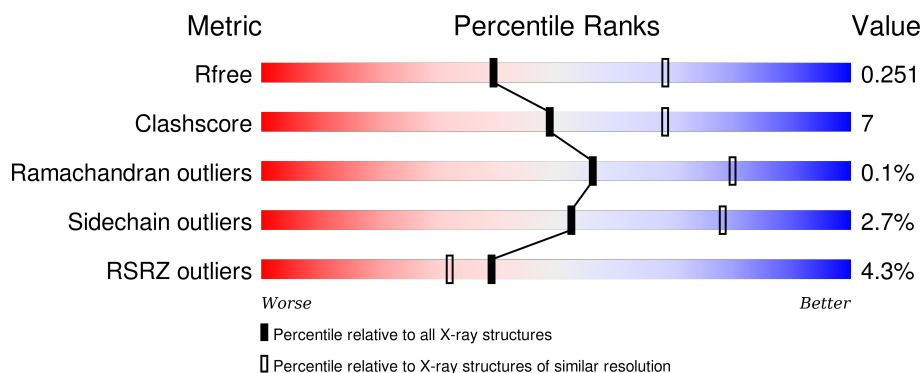
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.62 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}	91344	2700 (2.64-2.60)
Clashscore	102246	3065 (2.64-2.60)
Ramachandran outliers	100387	3015 (2.64-2.60)
Sidechain outliers	100360	3015 (2.64-2.60)
RSRZ outliers	91569	2706 (2.64-2.60)

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>83%</div> <div>12%</div> <div>• •</div> </div>
1	C	333	<div> <div>2%</div> <div>81%</div> <div>16%</div> <div>• •</div> </div>
1	E	333	<div> <div>82%</div> <div>14%</div> <div>• •</div> </div>
2	B	180	<div> <div>10%</div> <div>74%</div> <div>21%</div> <div>• •</div> </div>
2	D	180	<div> <div>15%</div> <div>72%</div> <div>23%</div> <div>• •</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	180	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	SIA	C	1005	-	-	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 12369 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	C	323	Total	C	N	O	S	0	0	0
			2558	1611	443	490	14			
1	A	323	Total	C	N	O	S	0	0	0
			2558	1611	443	490	14			
1	E	323	Total	C	N	O	S	0	0	0
			2558	1611	443	490	14			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	7	ALA	-	expression tag	UNP G8IPF0
C	8	ASP	-	expression tag	UNP G8IPF0
C	9	PRO	-	expression tag	UNP G8IPF0
C	10	GLY	-	expression tag	UNP G8IPF0
C	226	LEU	GLN	engineered mutation	UNP G8IPF0
A	7	ALA	-	expression tag	UNP G8IPF0
A	8	ASP	-	expression tag	UNP G8IPF0
A	9	PRO	-	expression tag	UNP G8IPF0
A	10	GLY	-	expression tag	UNP G8IPF0
A	226	LEU	GLN	engineered mutation	UNP G8IPF0
E	7	ALA	-	expression tag	UNP G8IPF0
E	8	ASP	-	expression tag	UNP G8IPF0
E	9	PRO	-	expression tag	UNP G8IPF0
E	10	GLY	-	expression tag	UNP G8IPF0
E	226	LEU	GLN	engineered mutation	UNP G8IPF0

- Molecule 2 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	175	Total	C	N	O	S	0	0	0
			1418	880	248	282	8			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	175	Total	C	N	O	S	0	0	0
			1418	880	248	282	8			
2	F	175	Total	C	N	O	S	0	0	0
			1418	880	248	282	8			

There are 18 discrepancies between the modelled and reference sequences:

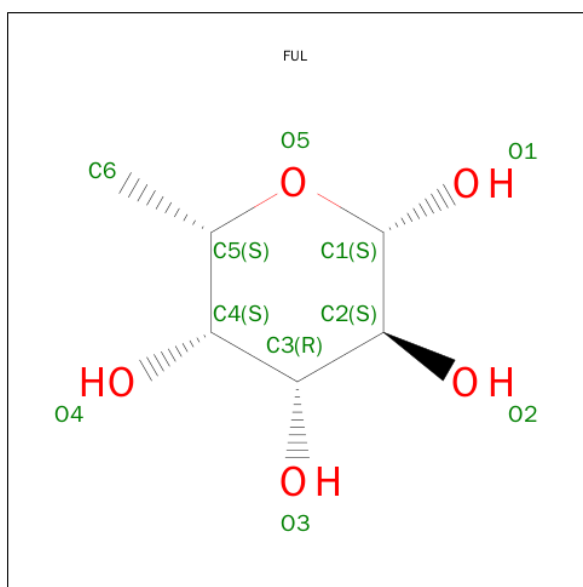
Chain	Residue	Modelled	Actual	Comment	Reference
D	1	GLY	-	expression tag	UNP G8IPF0
D	176	ARG	-	expression tag	UNP G8IPF0
D	177	LEU	-	expression tag	UNP G8IPF0
D	178	VAL	-	expression tag	UNP G8IPF0
D	179	PRO	-	expression tag	UNP G8IPF0
D	180	ARG	-	expression tag	UNP G8IPF0
B	1	GLY	-	expression tag	UNP G8IPF0
B	176	ARG	-	expression tag	UNP G8IPF0
B	177	LEU	-	expression tag	UNP G8IPF0
B	178	VAL	-	expression tag	UNP G8IPF0
B	179	PRO	-	expression tag	UNP G8IPF0
B	180	ARG	-	expression tag	UNP G8IPF0
F	1	GLY	-	expression tag	UNP G8IPF0
F	176	ARG	-	expression tag	UNP G8IPF0
F	177	LEU	-	expression tag	UNP G8IPF0
F	178	VAL	-	expression tag	UNP G8IPF0
F	179	PRO	-	expression tag	UNP G8IPF0
F	180	ARG	-	expression tag	UNP G8IPF0

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



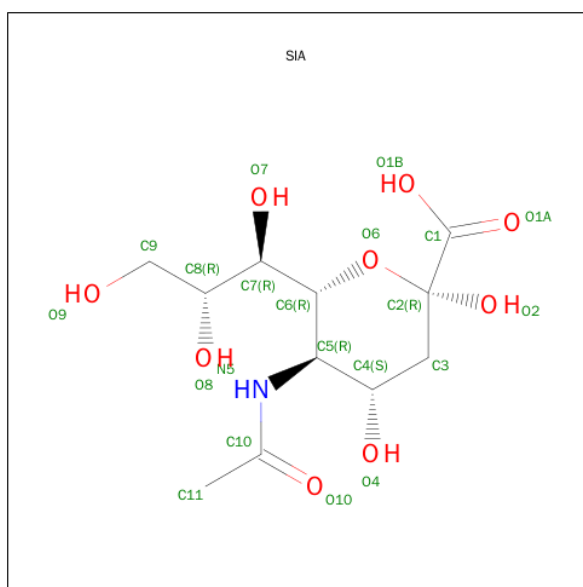
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			15	8	1	6		
3	E	1	Total	C	N	O	0	0
			14	8	1	5		
3	E	1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

- Molecule 4 is BETA-L-FUCOSE (three-letter code: FUL) (formula: C₆H₁₂O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			10	6	4		
4	A	1	Total	C	O	0	0
			10	6	4		
4	E	1	Total	C	O	0	0
			10	6	4		

- Molecule 5 is O-SIALIC ACID (three-letter code: SIA) (formula: $C_{11}H_{19}NO_9$).



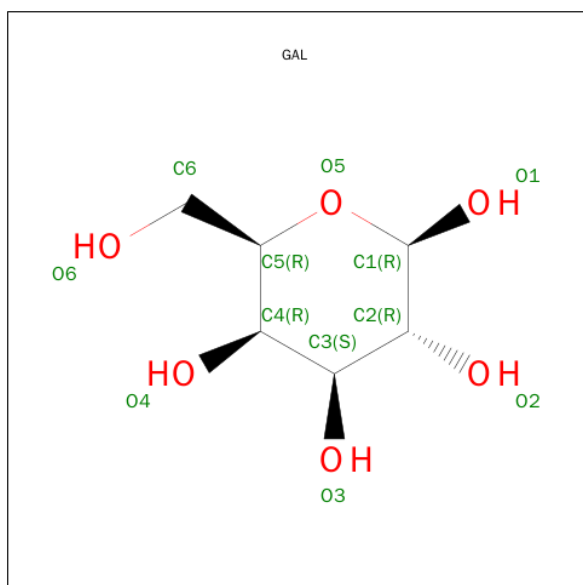
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	C	1	Total	C	N	O	0	0
			20	11	1	8		

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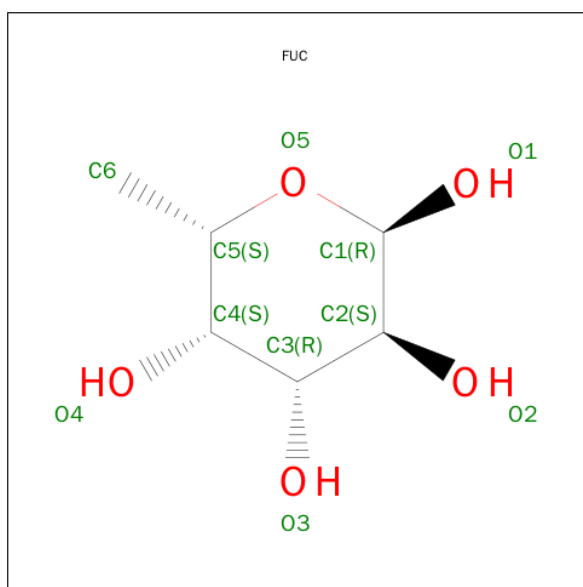
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			20	11	1	8		
5	E	1	Total	C	N	O	0	0
			20	11	1	8		

- Molecule 6 is BETA-D-GALACTOSE (three-letter code: GAL) (formula: C₆H₁₂O₆).



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

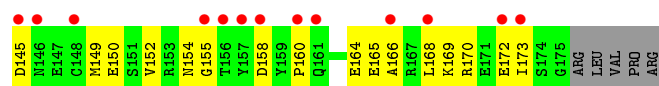
- Molecule 7 is ALPHA-L-FUCOSE (three-letter code: FUC) (formula: C₆H₁₂O₅).



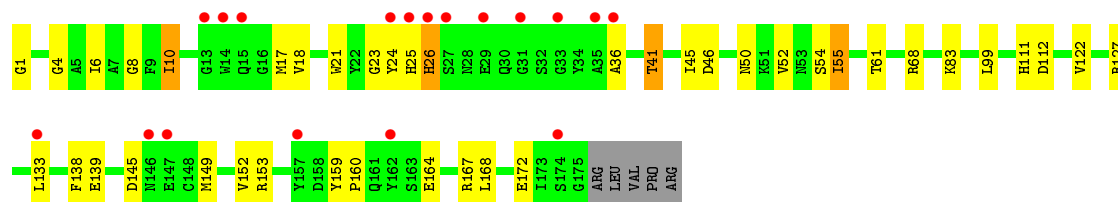
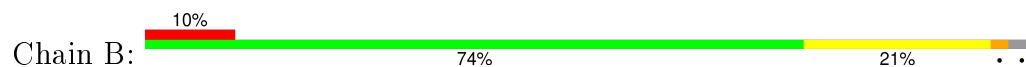
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			10	6	4		

- Molecule 8 is water.

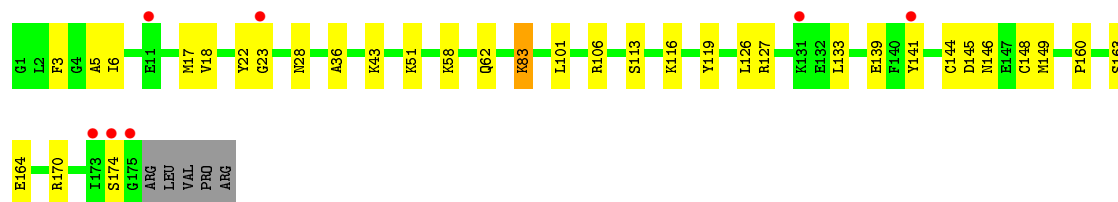
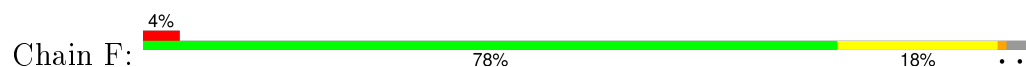
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	C	47	Total	O	0	0
			47	47		
8	D	7	Total	O	0	0
			7	7		
8	A	54	Total	O	0	0
			54	54		
8	B	8	Total	O	0	0
			8	8		
8	E	43	Total	O	0	0
			43	43		
8	F	8	Total	O	0	0
			8	8		



● Molecule 2: Hemagglutinin



● Molecule 2: Hemagglutinin



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.06Å 234.15Å 72.95Å 90.00° 115.49° 90.00°	Depositor
Resolution (Å)	50.00 – 2.62 48.42 – 2.62	Depositor EDS
% Data completeness (in resolution range)	86.8 (50.00-2.62) 86.8 (48.42-2.62)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.89 (at 2.61Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.202 , 0.248 0.209 , 0.251	Depositor DCC
R_{free} test set	2919 reflections (5.38%)	DCC
Wilson B-factor (Å ²)	54.6	Xtriage
Anisotropy	0.303	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 53.8	EDS
Estimated twinning fraction	0.027 for l,-k,h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 57145 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12369	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.65% 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, 0.375 respectively for untwinned datasets, and 0.333, 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, FUL, FUC

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	0.57	0/2619	0.68	1/3559 (0.0%)
1	C	0.55	0/2619	0.66	0/3559
1	E	0.49	0/2619	0.61	0/3559
2	B	0.45	0/1445	0.56	0/1942
2	D	0.46	0/1445	0.60	1/1942 (0.1%)
2	F	0.44	0/1445	0.55	0/1942
All	All	0.51	0/12192	0.62	2/16503 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	213	LEU	CA-CB-CG	5.50	127.94	115.30
2	D	80	LEU	CA-CB-CG	5.34	127.58	115.30

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	2558	0	2492	32	0
1	C	2558	0	2492	36	0
1	E	2558	0	2492	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1418	0	1322	32	0
2	D	1418	0	1322	37	0
2	F	1418	0	1322	22	0
3	A	57	0	50	6	0
3	C	42	0	37	0	0
3	E	42	0	37	0	0
4	A	10	0	10	1	0
4	C	10	0	10	0	0
4	E	10	0	10	0	0
5	A	20	0	17	0	0
5	C	20	0	17	1	0
5	E	20	0	17	0	0
6	A	11	0	9	0	0
6	C	11	0	9	0	0
6	E	11	0	9	0	0
7	A	10	0	10	2	0
8	A	54	0	0	3	0
8	B	8	0	0	0	0
8	C	47	0	0	0	0
8	D	7	0	0	0	0
8	E	43	0	0	1	0
8	F	8	0	0	0	0
All	All	12369	0	11684	172	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 7.

The worst 5 of 172 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:C:206:THR:HG22	1:C:208:THR:H	1.38	0.85
1:E:206:THR:HG22	1:E:209:LEU:H	1.43	0.83
1:E:28:THR:HG22	1:E:30:MET:H	1.45	0.81
2:D:125:GLN:HE22	2:D:155:GLY:HA2	1.47	0.78
1:A:222:LYS:NZ	3:A:1008:NAG:H82	2.04	0.73

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	321/333 (96%)	309 (96%)	12 (4%)	0	100	100
1	C	321/333 (96%)	308 (96%)	13 (4%)	0	100	100
1	E	321/333 (96%)	309 (96%)	12 (4%)	0	100	100
2	B	173/180 (96%)	160 (92%)	13 (8%)	0	100	100
2	D	173/180 (96%)	160 (92%)	12 (7%)	1 (1%)	30	54
2	F	173/180 (96%)	158 (91%)	15 (9%)	0	100	100
All	All	1482/1539 (96%)	1404 (95%)	77 (5%)	1 (0%)	56	80

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	145	ASP

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	290/298 (97%)	279 (96%)	11 (4%)	40	68
1	C	290/298 (97%)	287 (99%)	3 (1%)	82	93
1	E	290/298 (97%)	285 (98%)	5 (2%)	68	87
2	B	149/154 (97%)	143 (96%)	6 (4%)	38	66
2	D	149/154 (97%)	146 (98%)	3 (2%)	63	85
2	F	149/154 (97%)	142 (95%)	7 (5%)	32	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1317/1356 (97%)	1282 (97%)	35 (3%)	52 78

5 of 35 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	283	THR
2	B	26	HIS
2	F	101	LEU
1	A	291	SER
2	B	10	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	25	HIS
2	F	142	HIS
2	B	26	HIS
2	D	125	GLN
2	B	125	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

20 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	1001	1	14,14,15	0.77	1 (7%)	15,19,21	0.47	0
3	NAG	A	1002	1,3,4,7	14,14,15	0.46	0	15,19,21	0.59	0
7	FUC	A	1003	3	10,10,11	1.27	1 (10%)	13,14,16	1.77	3 (23%)
4	FUL	A	1004	3	10,10,11	1.26	2 (20%)	13,14,16	1.48	2 (15%)
3	NAG	A	1005	3	14,14,15	0.57	0	15,19,21	0.41	0
5	SIA	A	1006	6	17,20,21	0.75	0	18,28,31	1.17	1 (5%)
6	GAL	A	1007	3,5	11,11,12	1.32	2 (18%)	15,15,17	1.88	2 (13%)
3	NAG	A	1008	6	15,15,15	0.69	1 (6%)	17,21,21	0.73	0
3	NAG	C	1001	1	14,14,15	0.37	0	15,19,21	0.41	0
3	NAG	C	1002	1,3,4	14,14,15	0.68	1 (7%)	15,19,21	0.98	0
4	FUL	C	1003	3	10,10,11	1.35	1 (10%)	13,14,16	1.64	4 (30%)
3	NAG	C	1004	3	14,14,15	0.44	0	15,19,21	0.29	0
5	SIA	C	1005	6	17,20,21	0.57	0	18,28,31	1.41	2 (11%)
6	GAL	C	1006	5	11,11,12	1.82	3 (27%)	15,15,17	1.12	1 (6%)
3	NAG	E	1001	1	14,14,15	0.49	0	15,19,21	0.51	0
3	NAG	E	1002	1,3,4	14,14,15	0.68	1 (7%)	15,19,21	0.64	0
4	FUL	E	1003	3	10,10,11	1.07	1 (10%)	13,14,16	0.82	0
3	NAG	E	1004	3	14,14,15	0.30	0	15,19,21	0.28	0
5	SIA	E	1005	6	17,20,21	0.63	0	18,28,31	1.02	1 (5%)
6	GAL	E	1006	5	11,11,12	1.80	3 (27%)	15,15,17	1.30	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	1001	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1002	1,3,4,7	-	0/6/23/26	0/1/1/1
7	FUC	A	1003	3	-	0/0/17/20	0/1/1/1
4	FUL	A	1004	3	-	0/0/17/20	0/1/1/1
3	NAG	A	1005	3	-	0/6/23/26	0/1/1/1
5	SIA	A	1006	6	-	0/14/34/38	0/1/1/1
6	GAL	A	1007	3,5	-	0/2/19/22	0/1/1/1
3	NAG	A	1008	6	-	0/6/26/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	C	1001	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1002	1,3,4	-	0/6/23/26	0/1/1/1
4	FUL	C	1003	3	-	0/0/17/20	0/1/1/1
3	NAG	C	1004	3	-	0/6/23/26	0/1/1/1
5	SIA	C	1005	6	-	0/14/34/38	0/1/1/1
6	GAL	C	1006	5	-	0/2/19/22	0/1/1/1
3	NAG	E	1001	1	-	0/6/23/26	0/1/1/1
3	NAG	E	1002	1,3,4	-	0/6/23/26	0/1/1/1
4	FUL	E	1003	3	-	0/0/17/20	0/1/1/1
3	NAG	E	1004	3	-	0/6/23/26	0/1/1/1
5	SIA	E	1005	6	-	0/14/34/38	0/1/1/1
6	GAL	E	1006	5	-	0/2/19/22	0/1/1/1

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1002	NAG	O5-C1	-2.28	1.40	1.43
3	E	1002	NAG	O5-C1	-2.19	1.40	1.43
4	E	1003	FUL	C2-C3	2.02	1.55	1.52
3	A	1001	NAG	O5-C1	2.08	1.47	1.43
4	A	1004	FUL	C4-C5	2.11	1.57	1.53

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1004	FUL	C1-C2-C3	-3.44	105.38	109.55
4	C	1003	FUL	C2-C3-C4	-2.98	105.85	111.05
5	C	1005	SIA	C7-C6-C5	-2.12	111.14	114.06
4	C	1003	FUL	C3-C4-C5	-2.09	106.55	109.66
6	E	1006	GAL	C1-C2-C3	2.11	112.10	109.55

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	1003	FUC	2	0
4	A	1004	FUL	1	0
3	A	1005	NAG	3	0
3	A	1008	NAG	3	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	1005	SIA	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 [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	323/333 (96%)	-0.34	2 (0%) 90 88	18, 40, 92, 124	0
1	C	323/333 (96%)	-0.41	7 (2%) 65 59	22, 42, 77, 128	0
1	E	323/333 (96%)	-0.39	3 (0%) 85 83	27, 51, 76, 119	0
2	B	175/180 (97%)	0.48	18 (10%) 9 5	24, 87, 110, 115	0
2	D	175/180 (97%)	0.71	27 (15%) 3 1	26, 89, 130, 134	0
2	F	175/180 (97%)	0.19	7 (4%) 42 35	23, 77, 106, 122	0
All	All	1494/1539 (97%)	-0.09	64 (4%) 39 32	18, 52, 110, 134	0

The worst 5 of 64 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	175	GLY	7.7
2	D	138	PHE	4.7
2	F	173	ILE	4.4
2	D	168	LEU	4.2
2	D	32	SER	4.1

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 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
5	SIA	C	1005	20/21	0.90	0.30	3.46	50,68,78,79	0
3	NAG	A	1002	14/15	0.89	0.16	0.92	52,69,76,81	0
3	NAG	E	1002	14/15	0.91	0.14	0.48	52,72,84,87	0
3	NAG	C	1002	14/15	0.94	0.14	0.05	50,61,71,75	0
5	SIA	E	1005	20/21	0.92	0.14	0.02	42,57,68,70	0
5	SIA	A	1006	20/21	0.97	0.10	-2.06	25,36,42,45	0
4	FUL	C	1003	10/11	0.86	0.17	-	72,77,83,86	0
3	NAG	C	1001	14/15	0.88	0.17	-	83,90,92,94	0
4	FUL	E	1003	10/11	0.85	0.35	-	90,96,103,108	0
6	GAL	A	1007	11/12	0.91	0.16	-	51,58,70,73	0
3	NAG	E	1004	14/15	0.89	0.30	-	89,97,103,107	0
3	NAG	E	1001	14/15	0.84	0.23	-	95,101,103,105	0
4	FUL	A	1004	10/11	0.83	0.29	-	78,85,87,90	0
7	FUC	A	1003	10/11	0.91	0.32	-	59,69,78,81	0
3	NAG	C	1004	14/15	0.88	0.22	-	74,81,87,87	0
3	NAG	A	1008	15/15	0.79	0.27	-	85,94,101,104	0
3	NAG	A	1001	14/15	0.85	0.16	-	90,103,107,107	0
6	GAL	C	1006	11/12	0.80	0.43	-	76,80,87,90	0
3	NAG	A	1005	14/15	0.82	0.28	-	78,86,93,94	0
6	GAL	E	1006	11/12	0.87	0.29	-	60,74,83,85	0

6.5 Other polymers ⓘ

There are no such residues in this entry.