



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 08:28 PM GMT

PDB ID : 1KEN
Title : INFLUENZA VIRUS HEMAGGLUTININ COMPLEXED WITH AN AN-
TIBODY THAT PREVENTS THE HEMAGGLUTININ LOW PH FUSO-
GENIC TRANSITION
Authors : Barbey-Martin, C.; Gigant, B.; Bizebard, T.; Calder, L.J.; Wharto, S.A.;
Skehel, J.J.; Knossow, M.
Deposited on : 2001-11-16
Resolution : 3.50 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 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

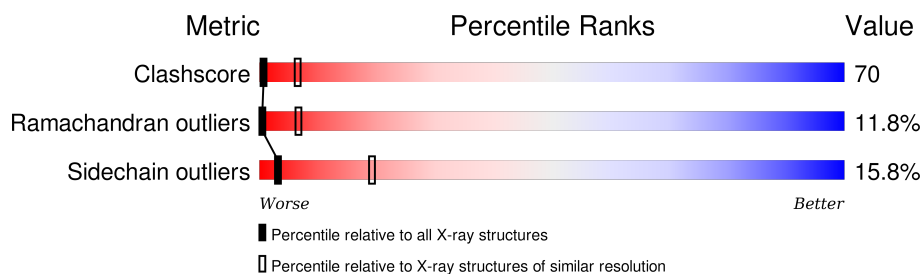
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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))
Clashscore	102246	1157 (3.60-3.40)
Ramachandran outliers	100387	1120 (3.60-3.40)
Sidechain outliers	100360	1121 (3.60-3.40)

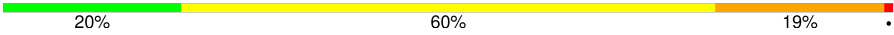
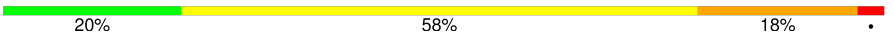
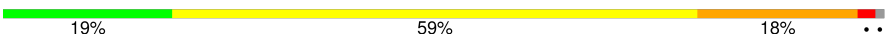
The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	328	
1	C	328	
1	E	328	
2	B	175	
2	D	175	
2	F	175	
3	L	213	

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Mol	Chain	Length	Quality of chain
3	U	213	
4	H	221	
4	T	221	

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	MAN	A	452	X	-	-	-
5	MAN	C	452	X	-	-	-
5	MAN	E	452	X	-	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 18492 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
			2472	1547	434	478	13			
1	C	320	Total	C	N	O	S	0	0	0
			2472	1547	434	478	13			
1	E	320	Total	C	N	O	S	0	0	0
			2472	1547	434	478	13			

- Molecule 2 is a protein called hemagglutinin HA2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	175	Total	C	N	O	S	0	0	0
			1421	882	250	283	6			
2	D	175	Total	C	N	O	S	0	0	0
			1421	882	250	283	6			
2	F	175	Total	C	N	O	S	0	0	0
			1421	882	250	283	6			

- Molecule 3 is a protein called influenza virus infectivity neutralizing antibody (light chain).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	213	Total	C	N	O	S	0	0	0
			1638	1028	272	332	6			
3	U	213	Total	C	N	O	S	0	0	0
			1638	1028	272	332	6			

- Molecule 4 is a protein called influenza virus infectivity neutralizing antibody (heavy chain).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	221	Total	C	N	O	S	0	0	0
			1720	1102	272	340	6			
4	T	219	Total	C	N	O	S	0	0	0
			1700	1092	267	335	6			

- Molecule 5 is a polymer of unknown type called SUGAR (NAG-NAG-MAN).

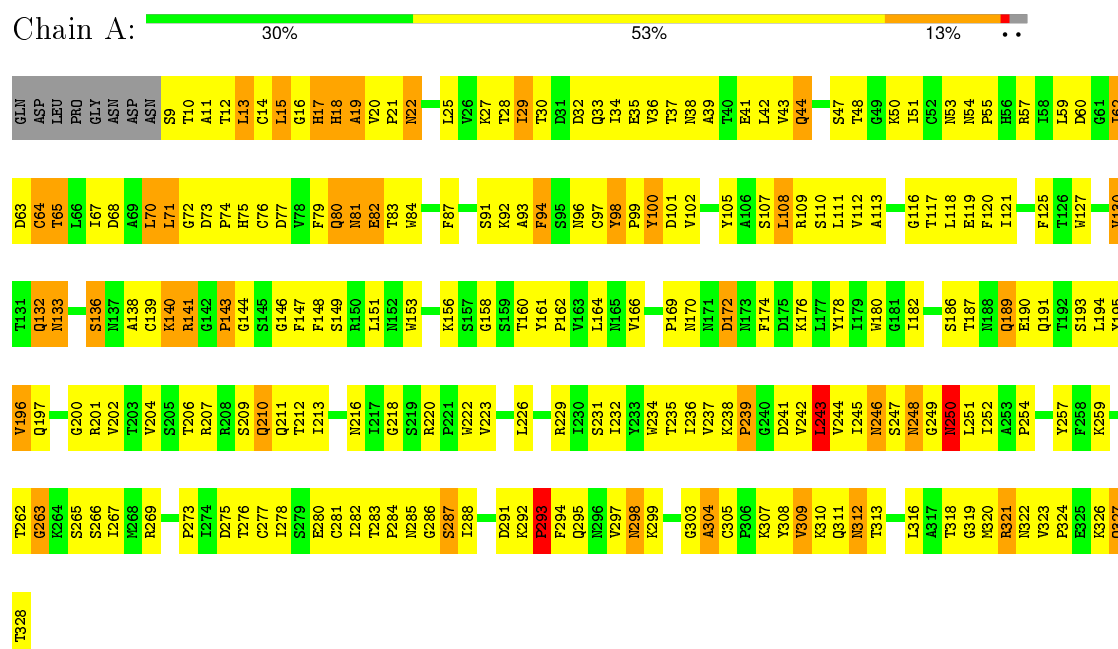
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	3	Total	C	N	O	0	0
			39	22	2	15		
5	C	3	Total	C	N	O	0	0
			39	22	2	15		
5	E	3	Total	C	N	O	0	0
			39	22	2	15		

3 Residue-property plots

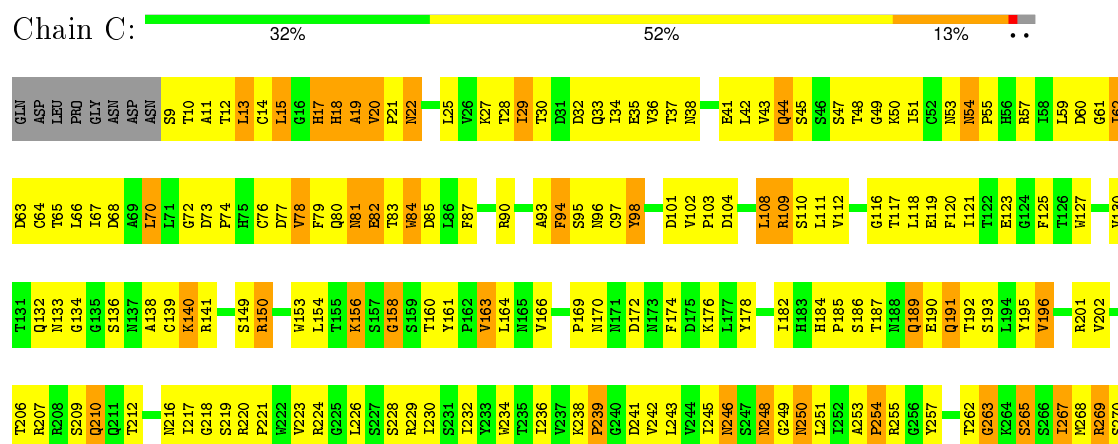
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

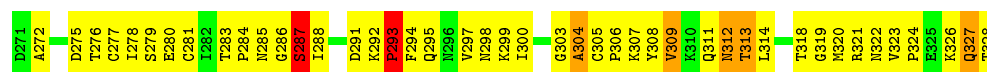
Note EDS was not executed.

• Molecule 1: hemagglutinin HA1



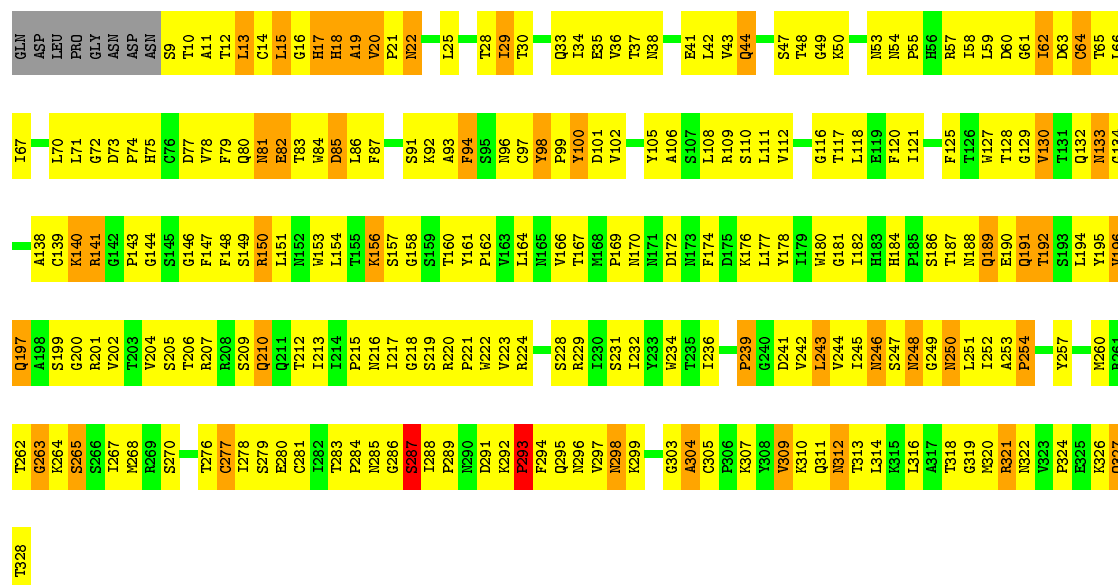
• Molecule 1: hemagglutinin HA1





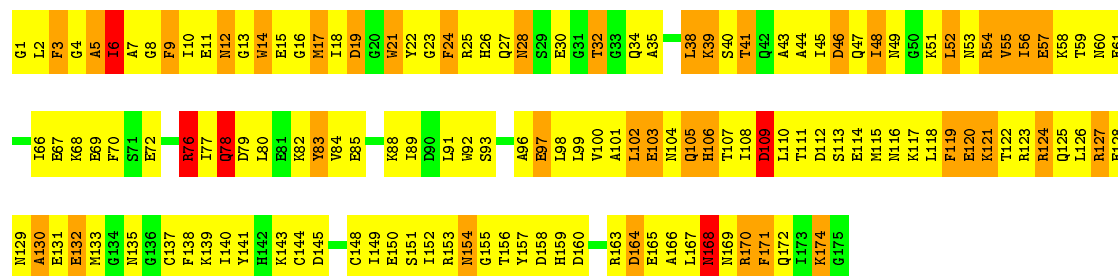
• Molecule 1: hemagglutinin HA1

Chain E: 27% 57% 13% ..



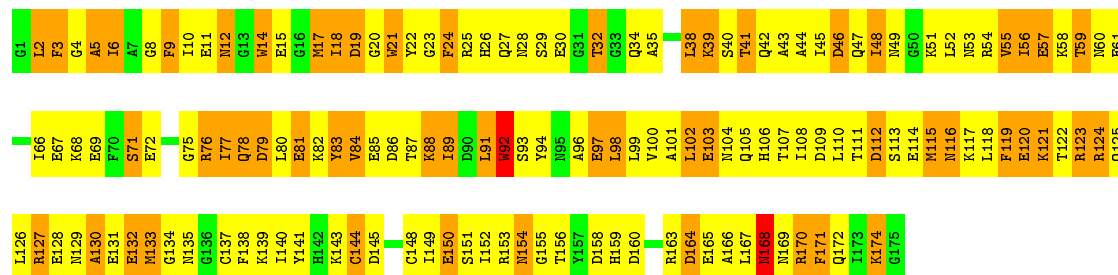
• Molecule 2: hemagglutinin HA2

Chain B: 18% 57% 22% •

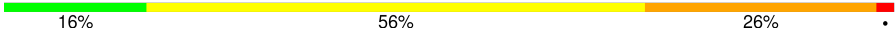


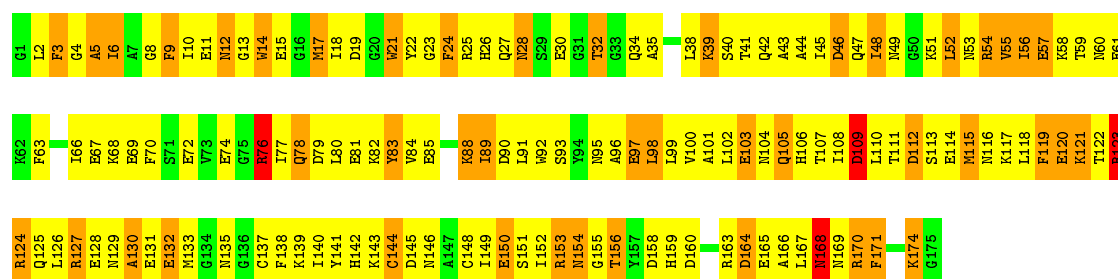
• Molecule 2: hemagglutinin HA2

Chain D: 15% 51% 32% •

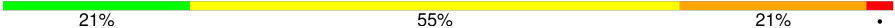


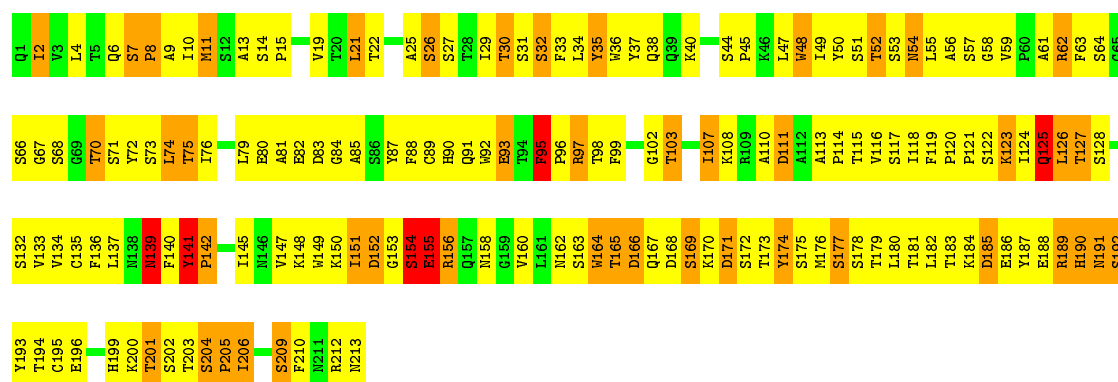
• Molecule 2: hemagglutinin HA2

Chain F:  16% 56% 26%

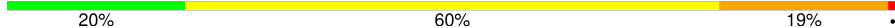


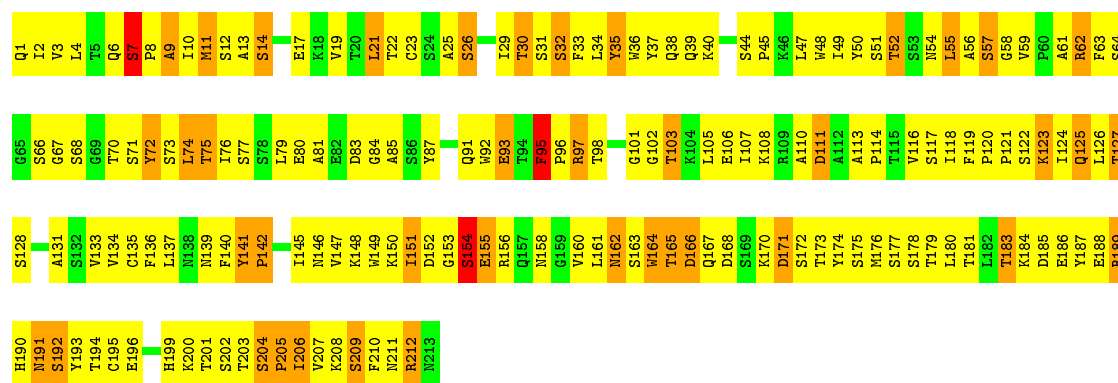
- Molecule 3: influenza virus infectivity neutralizing antibody (light chain)

Chain L:  21% 55% 21%

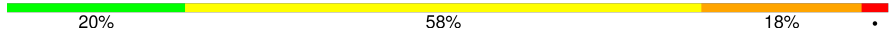


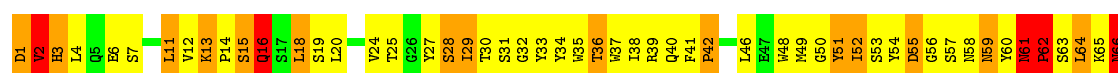
- Molecule 3: influenza virus infectivity neutralizing antibody (light chain)

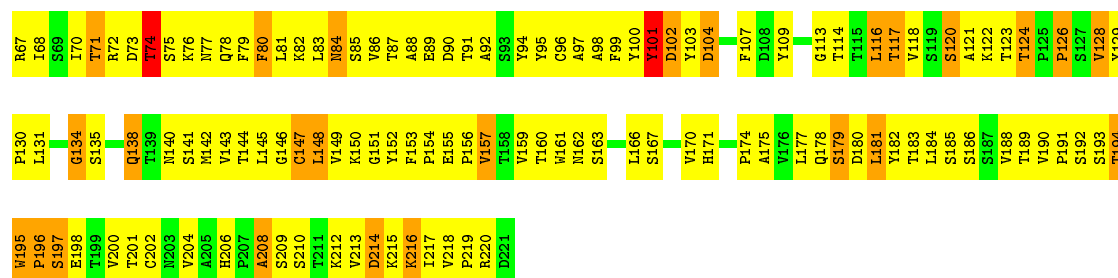
Chain U:  20% 60% 19%



- Molecule 4: influenza virus infectivity neutralizing antibody (heavy chain)

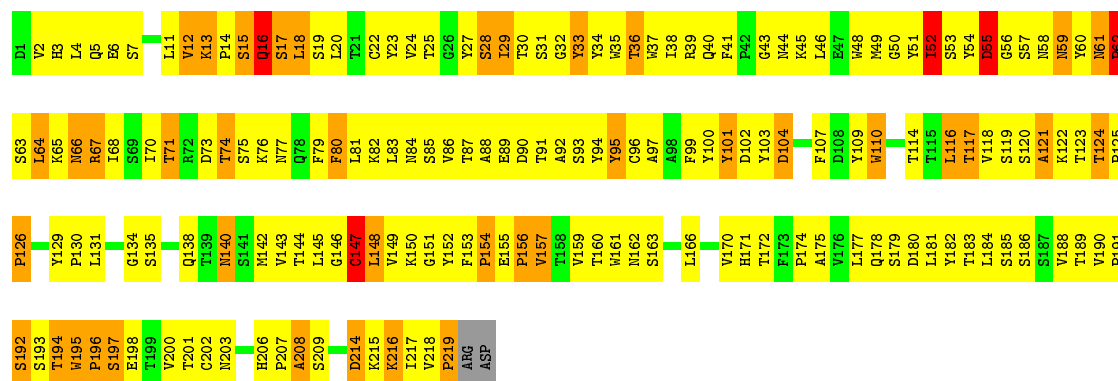
Chain H:  20% 58% 18%





- Molecule 4: influenza virus infectivity neutralizing antibody (heavy chain)

Chain T: 19% 59% 18% ..



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	143.04Å 315.59Å 97.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 3.50	Depositor
% Data completeness (in resolution range)	91.8 (25.00-3.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.255 , 0.323	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	18492	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, MAN

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	0.71	0/2528	0.91	3/3443 (0.1%)
1	C	0.77	1/2528 (0.0%)	0.96	2/3443 (0.1%)
1	E	0.71	0/2528	0.93	2/3443 (0.1%)
2	B	0.74	0/1445	0.86	0/1939
2	D	0.77	1/1445 (0.1%)	0.89	3/1939 (0.2%)
2	F	0.73	0/1445	0.84	0/1939
3	L	0.82	2/1679 (0.1%)	1.05	7/2281 (0.3%)
3	U	0.76	0/1679	0.97	3/2281 (0.1%)
4	H	0.85	2/1774 (0.1%)	1.00	2/2431 (0.1%)
4	T	0.78	1/1754 (0.1%)	1.00	2/2406 (0.1%)
All	All	0.76	7/18805 (0.0%)	0.95	24/25545 (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
3	L	0	1
3	U	0	1
4	H	0	1
4	T	0	2
5	A	1	0
5	C	1	0
5	E	1	0
All	All	3	5

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	1	ASP	CB-CG	7.47	1.67	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	155	GLU	CB-CG	7.10	1.65	1.52
3	L	155	GLU	CG-CD	6.60	1.61	1.51
4	H	61	ASN	CB-CG	5.86	1.64	1.51
2	D	92	TRP	CB-CG	-5.42	1.40	1.50

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	T	64	LEU	CA-CB-CG	-10.84	90.37	115.30
3	L	111	ASP	N-CA-C	-9.85	84.40	111.00
4	H	64	LEU	CA-CB-CG	-7.90	97.13	115.30
3	U	111	ASP	N-CA-C	-7.69	90.24	111.00
2	D	79	ASP	CB-CG-OD2	7.20	124.78	118.30

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	A	452	MAN	C1
5	C	452	MAN	C1
5	E	452	MAN	C1

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	H	101	TYR	Sidechain
3	L	141	TYR	Sidechain
4	T	33	TYR	Sidechain
4	T	95	TYR	Sidechain
3	U	72	TYR	Sidechain

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	2472	0	2424	336	0
1	C	2472	0	2424	328	0
1	E	2472	0	2424	334	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1421	0	1346	259	0
2	D	1421	0	1346	273	0
2	F	1421	0	1346	276	0
3	L	1638	0	1578	232	0
3	U	1638	0	1578	260	0
4	H	1720	0	1639	264	0
4	T	1700	0	1622	276	0
5	A	39	0	34	3	0
5	C	39	0	34	4	0
5	E	39	0	34	0	0
All	All	18492	0	17829	2549	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 70.

The worst 5 of 2549 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:74:PRO:HA	1:A:141:ARG:HH12	1.11	1.16
3:U:199:HIS:HB3	3:U:201:THR:HG22	1.28	1.11
3:U:134:VAL:HG22	3:U:179:THR:HG23	1.30	1.11
1:C:77:ASP:O	1:C:80:GLN:HG2	1.47	1.10
1:C:96:ASN:HD21	1:C:140:LYS:HE2	1.10	1.10

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	318/328 (97%)	247 (78%)	43 (14%)	28 (9%)	1	12
1	C	318/328 (97%)	241 (76%)	53 (17%)	24 (8%)	1	15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	318/328 (97%)	250 (79%)	41 (13%)	27 (8%)	1	13
2	B	173/175 (99%)	96 (56%)	44 (25%)	33 (19%)	0	2
2	D	173/175 (99%)	89 (51%)	48 (28%)	36 (21%)	0	1
2	F	173/175 (99%)	89 (51%)	49 (28%)	35 (20%)	0	1
3	L	211/213 (99%)	141 (67%)	46 (22%)	24 (11%)	0	7
3	U	211/213 (99%)	139 (66%)	51 (24%)	21 (10%)	1	9
4	H	219/221 (99%)	158 (72%)	38 (17%)	23 (10%)	1	8
4	T	217/221 (98%)	147 (68%)	47 (22%)	23 (11%)	0	8
All	All	2331/2377 (98%)	1597 (68%)	460 (20%)	274 (12%)	0	7

5 of 274 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	29	ILE
1	A	81	ASN
1	A	210	GLN
1	A	263	GLY
1	A	287	SER

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	282/289 (98%)	252 (89%)	30 (11%)	8	38
1	C	282/289 (98%)	249 (88%)	33 (12%)	7	32
1	E	282/289 (98%)	248 (88%)	34 (12%)	6	30
2	B	149/149 (100%)	120 (80%)	29 (20%)	2	10
2	D	149/149 (100%)	116 (78%)	33 (22%)	1	6
2	F	149/149 (100%)	118 (79%)	31 (21%)	1	8
3	L	187/187 (100%)	147 (79%)	40 (21%)	1	7
3	U	187/187 (100%)	152 (81%)	35 (19%)	2	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	H	196/196 (100%)	163 (83%)	33 (17%)	2	15
4	T	194/196 (99%)	167 (86%)	27 (14%)	4	25
All	All	2057/2080 (99%)	1732 (84%)	325 (16%)	3	19

5 of 325 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	239	PRO
2	F	123	ARG
4	T	16	GLN
1	E	250	ASN
2	F	21	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 102 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	28	ASN
1	E	80	GLN
4	T	58	ASN
2	D	49	ASN
2	D	154	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 ⓘ

9 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	$\# Z > 2$
5	NAG	A	450	1,5	14,14,15	0.68	0	15,19,21	1.53	2 (13%)
5	NAG	A	451	5	14,14,15	0.51	0	15,19,21	0.97	1 (6%)
5	MAN	A	452	5	11,11,12	0.96	1 (9%)	14,15,17	0.97	1 (7%)
5	NAG	C	450	1,5	14,14,15	0.67	0	15,19,21	1.12	2 (13%)
5	NAG	C	451	5	14,14,15	0.73	0	15,19,21	0.94	1 (6%)
5	MAN	C	452	5	11,11,12	1.11	1 (9%)	14,15,17	1.05	1 (7%)
5	NAG	E	450	1,5	14,14,15	0.78	0	15,19,21	1.22	2 (13%)
5	NAG	E	451	5	14,14,15	1.24	1 (7%)	15,19,21	1.20	2 (13%)
5	MAN	E	452	5	11,11,12	0.85	0	14,15,17	1.13	1 (7%)

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
5	NAG	A	450	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	451	5	-	0/6/23/26	0/1/1/1
5	MAN	A	452	5	1/1/4/5	0/2/19/22	0/1/1/1
5	NAG	C	450	1,5	-	0/6/23/26	0/1/1/1
5	NAG	C	451	5	-	0/6/23/26	0/1/1/1
5	MAN	C	452	5	1/1/4/5	0/2/19/22	0/1/1/1
5	NAG	E	450	1,5	-	0/6/23/26	0/1/1/1
5	NAG	E	451	5	-	0/6/23/26	0/1/1/1
5	MAN	E	452	5	1/1/4/5	0/2/19/22	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	451	NAG	C1-C2	-3.37	1.47	1.52
5	C	452	MAN	C4-C5	2.04	1.57	1.53
5	A	452	MAN	C4-C5	2.16	1.57	1.53

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	450	NAG	C2-N2-C7	-4.25	117.58	123.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	450	NAG	C4-C3-C2	-3.16	106.31	111.23
5	E	451	NAG	C2-N2-C7	-2.92	119.29	123.04
5	C	451	NAG	C2-N2-C7	-2.91	119.30	123.04
5	A	451	NAG	C2-N2-C7	-2.78	119.46	123.04

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	E	452	MAN	C1
5	A	452	MAN	C1
5	C	452	MAN	C1

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	451	NAG	3	0
5	C	450	NAG	2	0
5	C	451	NAG	2	0

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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](#)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.