



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 07:31 pm GMT

PDB ID : 2WRF  
Title : STRUCTURE OF H2 AVIAN JENA HEMAGGLUTININ WITH HUMAN RECEPTOR  
Authors : Liu, J.; Stevens, D.J.; Haire, L.F.; Walker, P.A.; Coombs, P.J.; Russell, R.J.; Gamblin, S.J.; Skehel, J.J.  
Deposited on : 2009-09-01  
Resolution : 3.10 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](mailto: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.

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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) : trunk28620

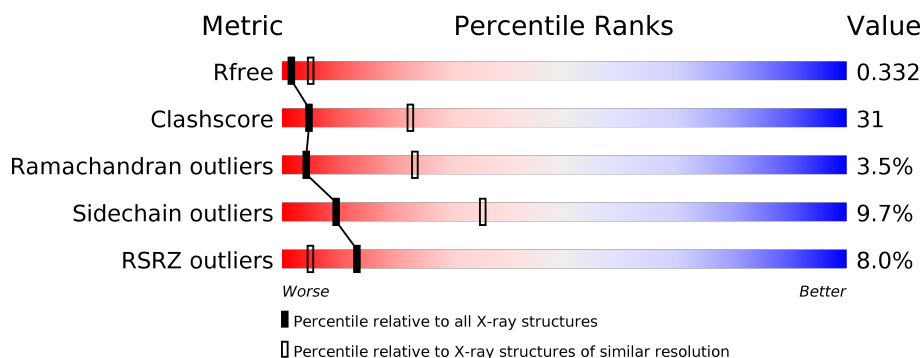
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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	1001 (3.12-3.08)
Clashscore	112137	1099 (3.12-3.08)
Ramachandran outliers	110173	1057 (3.12-3.08)
Sidechain outliers	110143	1057 (3.12-3.08)
RSRZ outliers	101464	1006 (3.12-3.08)

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  $\geq 3$ , 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	507	<div> <div>4%</div> <div> <div>32%</div> <div>48%</div> <div>15%</div> </div> </div>
1	B	507	<div> <div>5%</div> <div> <div>54%</div> <div>37%</div> </div> </div>
1	C	507	<div> <div>6%</div> <div> <div>55%</div> <div>37%</div> </div> </div>
1	D	507	<div> <div>9%</div> <div> <div>37%</div> <div>49%</div> <div>9%</div> </div> </div>
1	E	507	<div> <div>12%</div> <div> <div>53%</div> <div>39%</div> </div> </div>
1	F	507	<div> <div>8%</div> <div> <div>53%</div> <div>39%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	507	<div><div></div><div>9%</div><div>49%</div><div>36%</div><div>9%</div><div></div></div>
1	H	507	<div><div></div><div>10%</div><div>54%</div><div>36%</div><div>5%</div><div></div></div>
1	I	507	<div><div></div><div>7%</div><div>56%</div><div>35%</div><div>5%</div><div></div></div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 34577 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	486	Total	C	N	O	S	0	0	0
			3837	2409	656	748	24			
1	B	486	Total	C	N	O	S	0	0	0
			3837	2409	656	748	24			
1	C	486	Total	C	N	O	S	0	0	0
			3834	2408	655	747	24			
1	D	486	Total	C	N	O	S	0	0	0
			3837	2409	656	748	24			
1	E	486	Total	C	N	O	S	0	0	0
			3837	2409	656	748	24			
1	F	486	Total	C	N	O	S	0	0	0
			3834	2408	655	747	24			
1	G	486	Total	C	N	O	S	0	0	0
			3837	2409	656	748	24			
1	H	486	Total	C	N	O	S	0	0	0
			3837	2409	656	748	24			
1	I	486	Total	C	N	O	S	0	0	0
			3834	2408	655	747	24			

There are 36 discrepancies between the modelled and reference sequences:

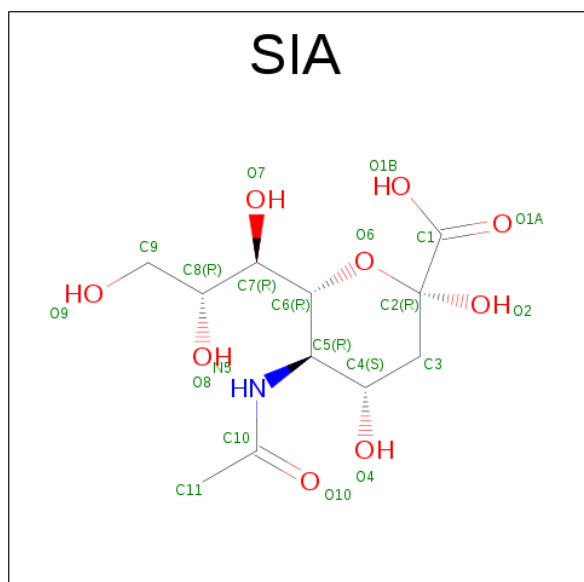
Chain	Residue	Modelled	Actual	Comment	Reference
A	109	ILE	LEU	CONFLICT	UNP Q67326
A	142	ASP	GLY	CONFLICT	UNP Q67326
A	374	PHE	ILE	CONFLICT	UNP Q67326
A	459	VAL	ALA	CONFLICT	UNP Q67326
B	109	ILE	LEU	CONFLICT	UNP Q67326
B	142	ASP	GLY	CONFLICT	UNP Q67326
B	374	PHE	ILE	CONFLICT	UNP Q67326
B	459	VAL	ALA	CONFLICT	UNP Q67326
C	109	ILE	LEU	CONFLICT	UNP Q67326
C	142	ASP	GLY	CONFLICT	UNP Q67326
C	374	PHE	ILE	CONFLICT	UNP Q67326

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Chain	Residue	Modelled	Actual	Comment	Reference
C	459	VAL	ALA	CONFLICT	UNP Q67326
D	109	ILE	LEU	CONFLICT	UNP Q67326
D	142	ASP	GLY	CONFLICT	UNP Q67326
D	374	PHE	ILE	CONFLICT	UNP Q67326
D	459	VAL	ALA	CONFLICT	UNP Q67326
E	109	ILE	LEU	CONFLICT	UNP Q67326
E	142	ASP	GLY	CONFLICT	UNP Q67326
E	374	PHE	ILE	CONFLICT	UNP Q67326
E	459	VAL	ALA	CONFLICT	UNP Q67326
F	109	ILE	LEU	CONFLICT	UNP Q67326
F	142	ASP	GLY	CONFLICT	UNP Q67326
F	374	PHE	ILE	CONFLICT	UNP Q67326
F	459	VAL	ALA	CONFLICT	UNP Q67326
G	109	ILE	LEU	CONFLICT	UNP Q67326
G	142	ASP	GLY	CONFLICT	UNP Q67326
G	374	PHE	ILE	CONFLICT	UNP Q67326
G	459	VAL	ALA	CONFLICT	UNP Q67326
H	109	ILE	LEU	CONFLICT	UNP Q67326
H	142	ASP	GLY	CONFLICT	UNP Q67326
H	374	PHE	ILE	CONFLICT	UNP Q67326
H	459	VAL	ALA	CONFLICT	UNP Q67326
I	109	ILE	LEU	CONFLICT	UNP Q67326
I	142	ASP	GLY	CONFLICT	UNP Q67326
I	374	PHE	ILE	CONFLICT	UNP Q67326
I	459	VAL	ALA	CONFLICT	UNP Q67326

- Molecule 2 is SUGAR (O-SIALIC ACID) (three-letter code: SIA) (formula:  $C_{11}H_{19}NO_9$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	D	1	Total	C	N	O	0	0
			21	11	1	9		

- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	F	2	Total	C	N	O	0	0
			32	17	1	14		

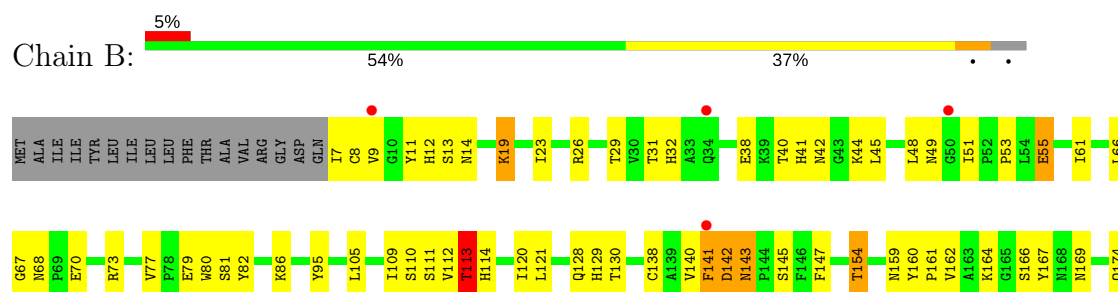
### 3 Residue-property plots [i](#)

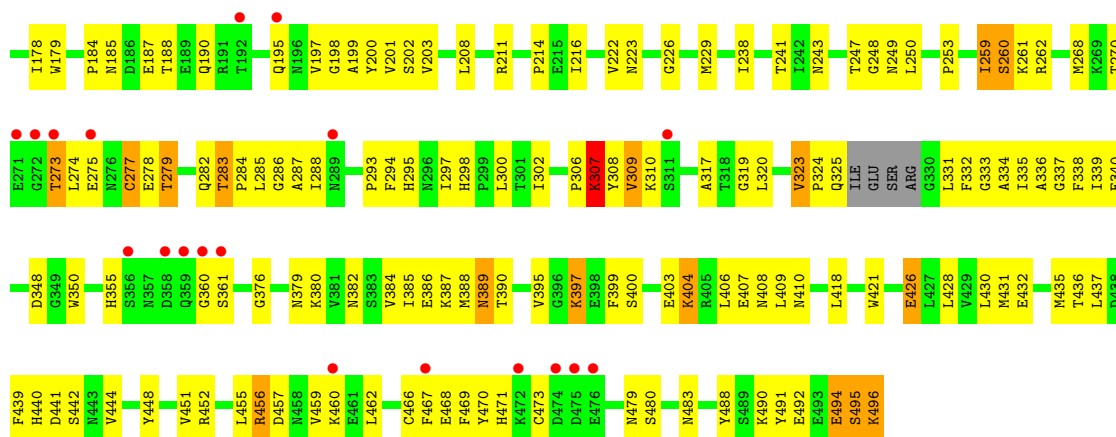
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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

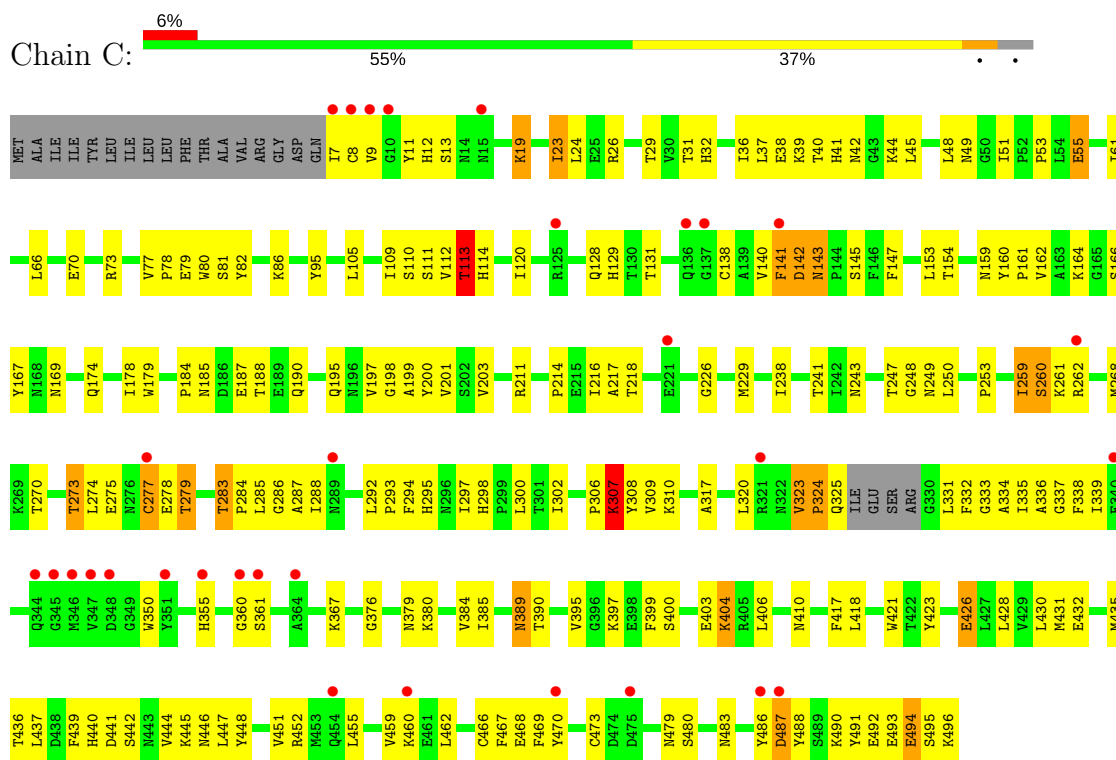


#### • Molecule 1: HEMAGGLUTININ

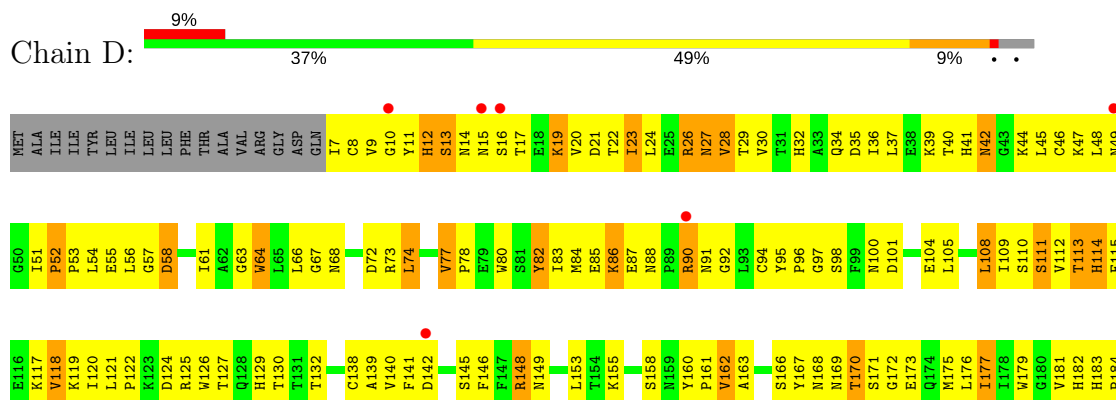




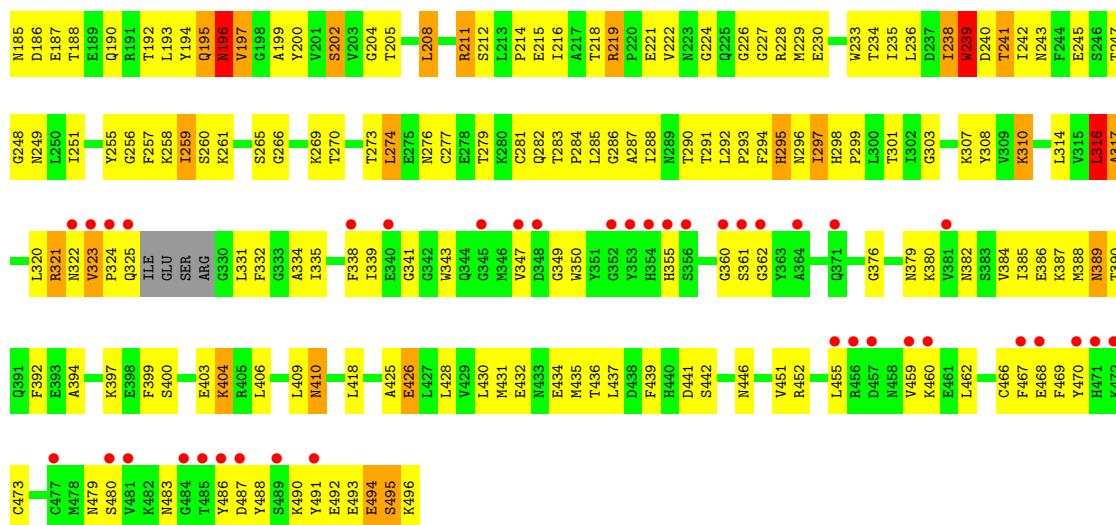
• Molecule 1: HEMAGGLUTININ



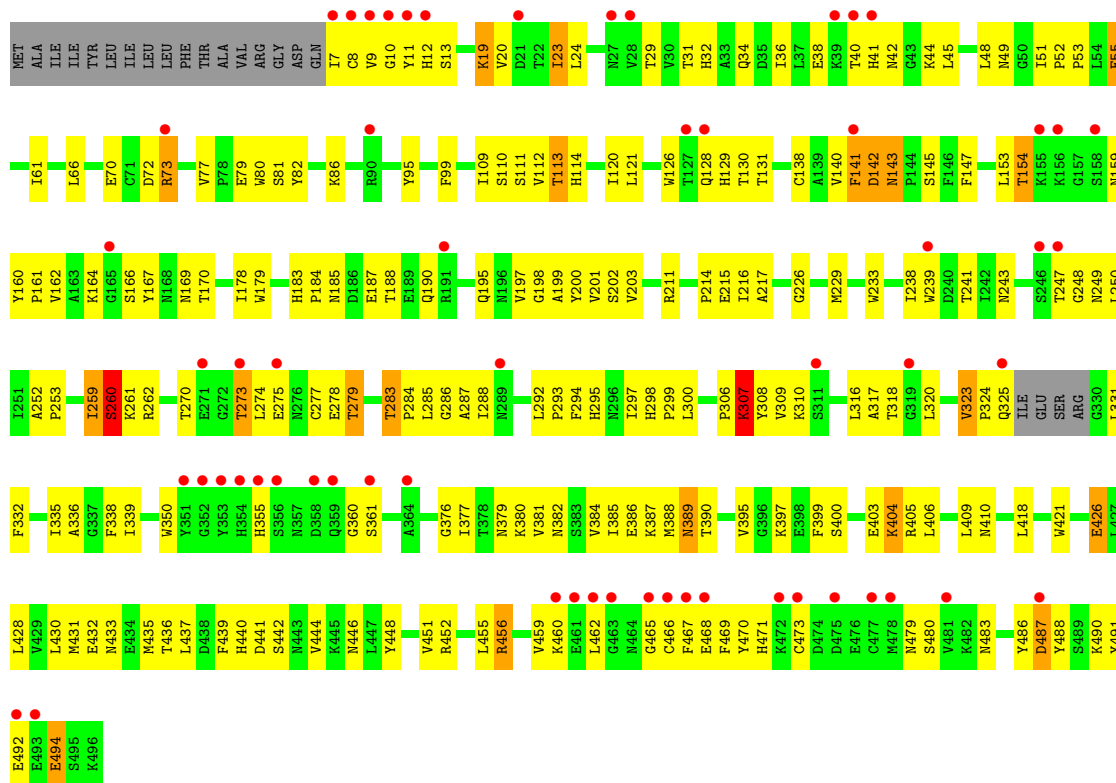
• Molecule 1: HEMAGGLUTININ



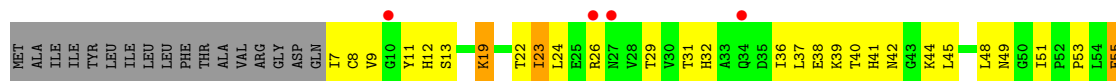


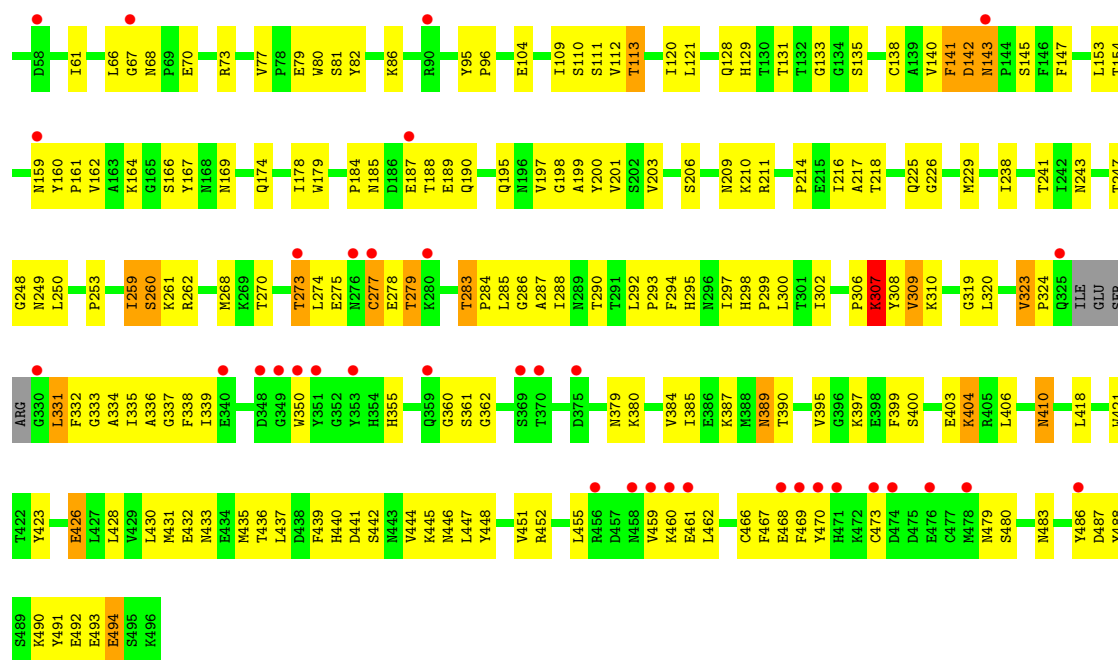


### • Molecule 1: HEMAGGLUTININ

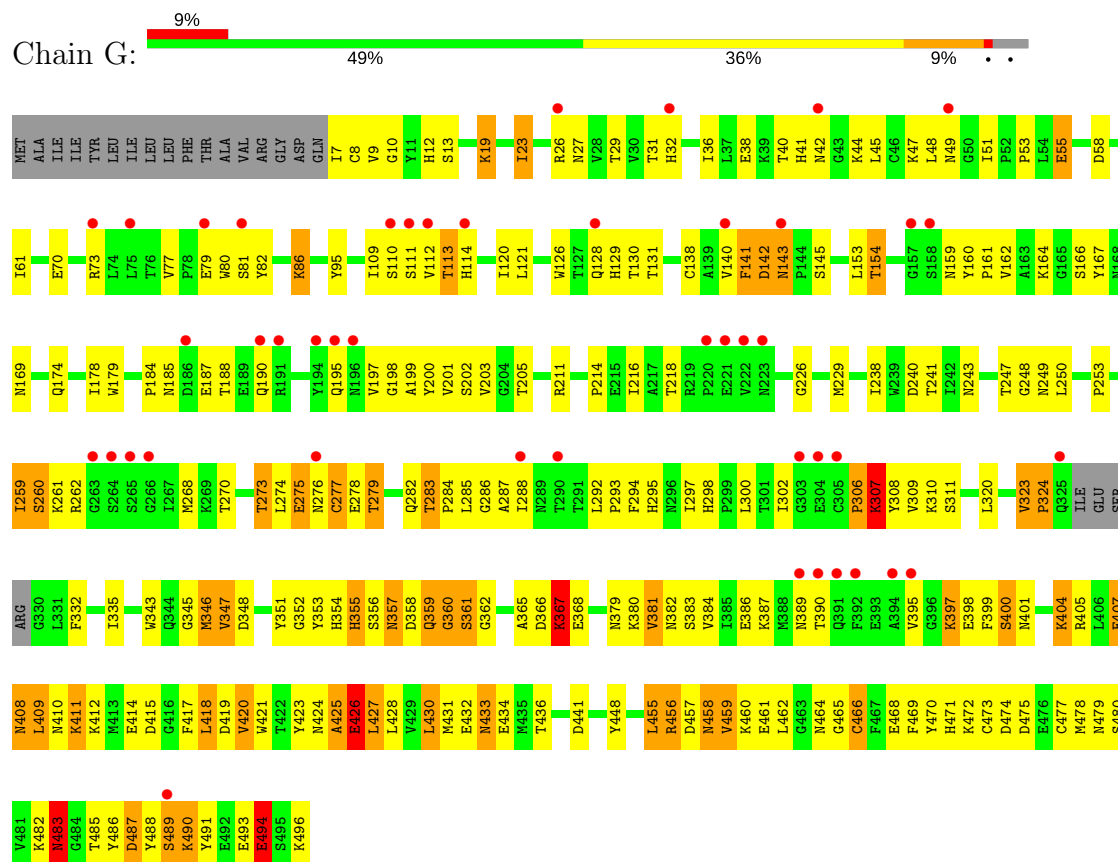


### • Molecule 1: HEMAGGLUTININ



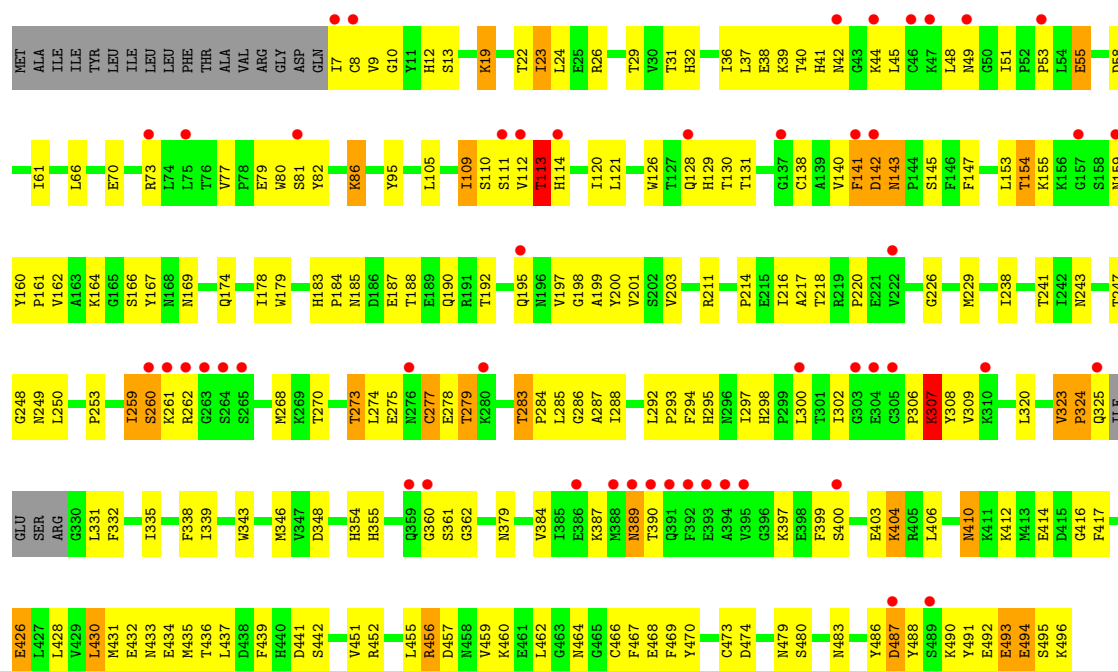


### • Molecule 1: HEMAGGLUTININ

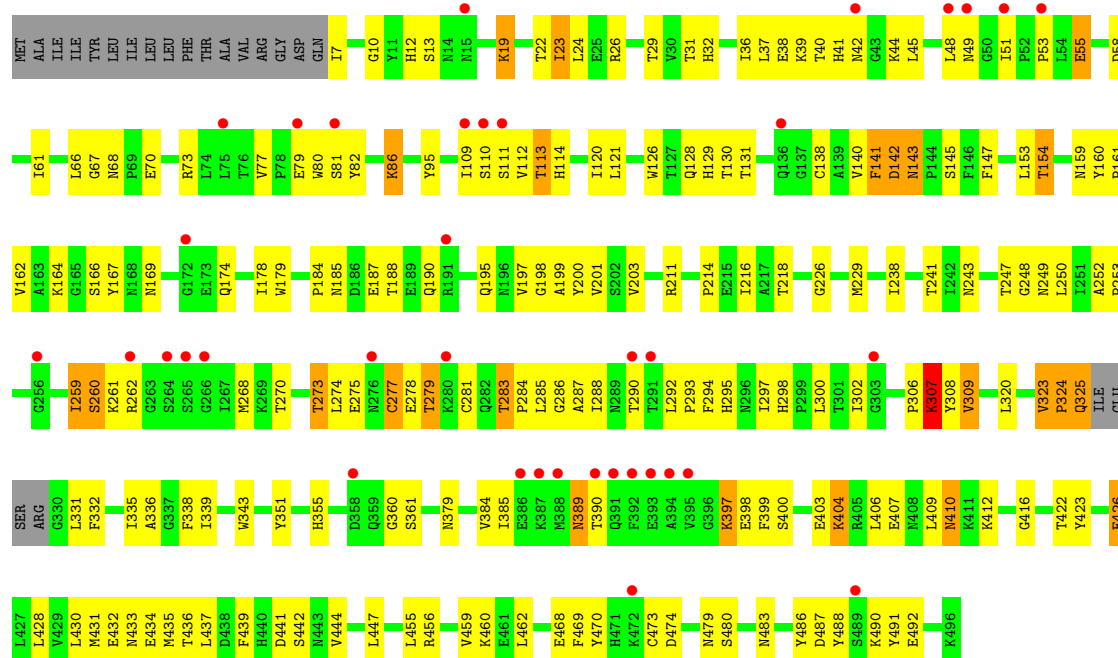


### • Molecule 1: HEMAGGLUTININ





• Molecule 1: HEMAGGLUTININ



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	134.17Å 113.28Å 184.67Å 90.00° 92.20° 90.00°	Depositor
Resolution (Å)	29.92 – 3.10 29.92 – 3.10	Depositor EDS
% Data completeness (in resolution range)	92.8 (29.92-3.10) 99.6 (29.92-3.10)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.14 (at 3.11Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.273 , 0.337 0.269 , 0.332	Depositor DCC
$R_{free}$ test set	4990 reflections (4.99%)	DCC
Wilson B-factor (Å <sup>2</sup> )	68.7	Xtriage
Anisotropy	0.586	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 53.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.019 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.87	EDS
Total number of atoms	34577	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.73% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

### 5.1 Standard geometry

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

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	0.47	0/3923	0.68	1/5309 (0.0%)
1	B	0.40	0/3923	0.53	0/5309
1	C	0.38	0/3920	0.51	0/5305
1	D	0.44	0/3923	0.63	1/5309 (0.0%)
1	E	0.35	0/3923	0.50	0/5309
1	F	0.34	0/3920	0.49	0/5305
1	G	0.47	0/3923	0.63	0/5309
1	H	0.41	0/3923	0.53	0/5309
1	I	0.40	0/3920	0.52	0/5305
All	All	0.41	0/35298	0.56	2/47769 (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	314	LEU	CA-CB-CG	5.74	128.51	115.30
1	D	251	ILE	N-CA-C	-5.12	97.19	111.00

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	3837	0	3674	344	0
1	B	3837	0	3672	205	0
1	C	3834	0	3666	211	0
1	D	3837	0	3672	308	0
1	E	3837	0	3672	264	0
1	F	3834	0	3666	234	0
1	G	3837	0	3672	289	0
1	H	3837	0	3672	216	0
1	I	3834	0	3666	185	0
2	D	21	0	18	1	0
3	F	32	0	28	7	0
All	All	34577	0	33078	2079	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 31.

The worst 5 of 2079 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:471:HIS:HB3	1:B:494:GLU:HG2	1.19	1.18
1:E:11:TYR:CE2	1:E:335:ILE:HA	1.83	1.14
1:G:7:ILE:HD11	1:G:482:LYS:HE3	1.15	1.12
1:C:9:VAL:HG21	1:C:448:TYR:HA	1.31	1.11
1:G:459:VAL:HG12	1:G:469:PHE:HA	1.22	1.11

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	482/507 (95%)	371 (77%)	80 (17%)	31 (6%)	1	9
1	B	482/507 (95%)	408 (85%)	62 (13%)	12 (2%)	6	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	482/507 (95%)	407 (84%)	63 (13%)	12 (2%)	6	31
1	D	482/507 (95%)	384 (80%)	74 (15%)	24 (5%)	2	16
1	E	482/507 (95%)	411 (85%)	60 (12%)	11 (2%)	7	33
1	F	482/507 (95%)	407 (84%)	63 (13%)	12 (2%)	6	31
1	G	482/507 (95%)	393 (82%)	61 (13%)	28 (6%)	2	12
1	H	482/507 (95%)	406 (84%)	64 (13%)	12 (2%)	6	31
1	I	482/507 (95%)	403 (84%)	69 (14%)	10 (2%)	8	36
All	All	4338/4563 (95%)	3590 (83%)	596 (14%)	152 (4%)	4	23

5 of 152 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	30	VAL
1	A	155	LYS
1	A	196	ASN
1	A	276	ASN
1	A	306	PRO

### 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	422/444 (95%)	347 (82%)	75 (18%)	2	9
1	B	422/444 (95%)	389 (92%)	33 (8%)	15	48
1	C	421/444 (95%)	392 (93%)	29 (7%)	18	53
1	D	422/444 (95%)	361 (86%)	61 (14%)	4	16
1	E	422/444 (95%)	391 (93%)	31 (7%)	16	50
1	F	421/444 (95%)	391 (93%)	30 (7%)	17	52
1	G	422/444 (95%)	374 (89%)	48 (11%)	7	27
1	H	422/444 (95%)	391 (93%)	31 (7%)	16	50
1	I	421/444 (95%)	389 (92%)	32 (8%)	15	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	3795/3996 (95%)	3425 (90%)	370 (10%)	9 35

5 of 370 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	195	GLN
1	E	141	PHE
1	I	61	ILE
1	D	211	ARG
1	D	321	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 147 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	371	GLN
1	E	371	GLN
1	I	185	ASN
1	D	389	ASN
1	E	159	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 ⓘ

2 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
3	SIA	F	1497	3	17,20,21	0.43	0	19,28,31	1.53	3 (15%)
3	GAL	F	1498	3	12,12,12	0.52	0	17,17,17	1.21	2 (11%)

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	SIA	F	1497	3	-	0/14/34/38	0/1/1/1
3	GAL	F	1498	3	-	0/2/22/22	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	1497	SIA	C8-C7-C6	-3.37	106.49	113.04
3	F	1497	SIA	C3-C4-C5	-2.79	108.09	111.46
3	F	1498	GAL	O5-C1-C2	2.38	113.98	110.04
3	F	1498	GAL	C1-C2-C3	2.68	115.49	110.65
3	F	1497	SIA	C6-C5-N5	3.33	116.87	111.00

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	1497	SIA	7	0

## 5.6 Ligand geometry [i](#)

1 ligand is 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	SIA	D	1497	-	18,21,21	0.67	0	19,31,31	0.94	0

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	SIA	D	1497	-	-	0/14/38/38	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1497	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	486/507 (95%)	-0.09	20 (4%) 38 18	23, 64, 148, 275	0
1	B	486/507 (95%)	0.09	23 (4%) 32 14	27, 66, 148, 278	0
1	C	486/507 (95%)	0.19	31 (6%) 20 7	24, 78, 160, 298	0
1	D	486/507 (95%)	0.22	45 (9%) 9 3	26, 71, 222, 378	0
1	E	486/507 (95%)	0.50	59 (12%) 5 2	31, 94, 232, 308	0
1	F	486/507 (95%)	0.40	40 (8%) 12 5	40, 96, 188, 258	0
1	G	486/507 (95%)	0.24	45 (9%) 9 3	20, 70, 182, 365	0
1	H	486/507 (95%)	0.51	50 (10%) 7 2	20, 73, 179, 367	0
1	I	486/507 (95%)	0.32	37 (7%) 15 5	26, 73, 195, 376	0
All	All	4374/4563 (95%)	0.27	350 (8%) 13 5	20, 76, 188, 378	0

The worst 5 of 350 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	263	GLY	14.8
1	G	265	SER	13.0
1	I	391	GLN	10.4
1	H	75	LEU	10.0
1	D	486	TYR	9.3

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	SIA	F	1497	20/21	0.90	0.16	-0.98	89,89,89,89	0
3	GAL	F	1498	12/12	0.87	0.17	-	89,89,89,89	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	SIA	D	1497	21/21	0.92	0.17	0.23	52,52,52,52	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.