



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:09 PM GMT

PDB ID : 4KPS  
Title : Structure and receptor binding specificity of the hemagglutinin H13 from avian influenza A virus H13N6  
Authors : Lu, X.; Qi, J.; Shi, Y.; Gao, G.  
Deposited on : 2013-05-14  
Resolution : 2.59 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](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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
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) : trunk26865

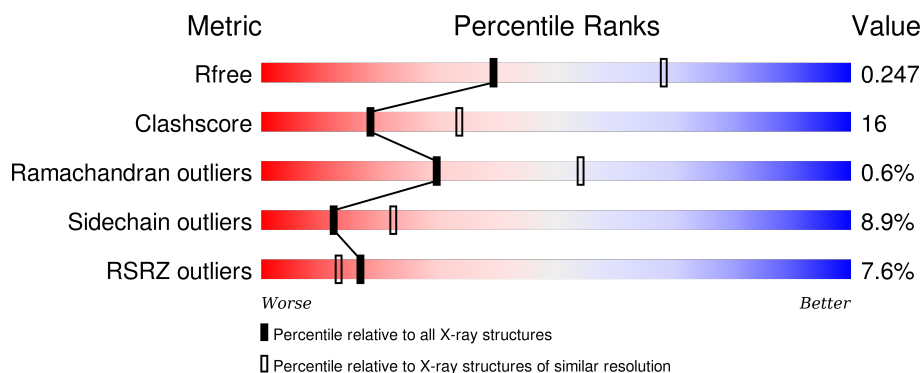
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.59 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	2636 (2.60-2.56)
Clashscore	102246	3003 (2.60-2.56)
Ramachandran outliers	100387	2956 (2.60-2.56)
Sidechain outliers	100360	2956 (2.60-2.56)
RSRZ outliers	91569	2642 (2.60-2.56)

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	324	<div> <div>5%</div> <div>71%</div> <div>25%</div> <div>.</div> </div>
1	C	324	<div> <div>9%</div> <div>73%</div> <div>23%</div> <div>.</div> </div>
1	E	324	<div> <div>4%</div> <div>72%</div> <div>24%</div> <div>.</div> </div>
2	B	165	<div> <div>7%</div> <div>67%</div> <div>30%</div> <div>.</div> </div>
2	D	165	<div> <div>8%</div> <div>73%</div> <div>24%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	165	<div><div></div><div>17%</div><div>72%</div><div>24%</div><div></div></div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 11796 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	324	Total	C	N	O	S	0	0	0
			2555	1610	448	485	12			
1	C	324	Total	C	N	O	S	0	0	0
			2555	1610	448	485	12			
1	E	324	Total	C	N	O	S	0	0	0
			2555	1610	448	485	12			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	4	ILE	-	EXPRESSION TAG	UNP P13103
A	5	GLN	-	EXPRESSION TAG	UNP P13103
C	4	ILE	-	EXPRESSION TAG	UNP P13103
C	5	GLN	-	EXPRESSION TAG	UNP P13103
E	4	ILE	-	EXPRESSION TAG	UNP P13103
E	5	GLN	-	EXPRESSION TAG	UNP P13103

- Molecule 2 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	165	Total	C	N	O	S	0	0	0
			1312	811	229	265	7			
2	D	165	Total	C	N	O	S	0	0	0
			1312	811	229	265	7			
2	F	165	Total	C	N	O	S	0	0	0
			1312	811	229	265	7			

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

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

- Molecule 4 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	E	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	E	3	Total	C	N	O	0	0
			46	25	2	19		

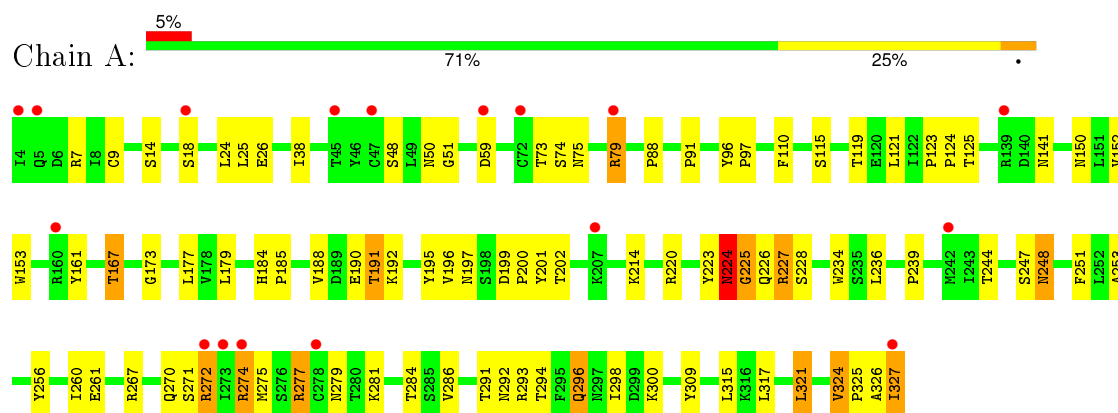
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	15	Total	O	0	0
			15	15		
6	B	19	Total	O	0	0
			19	19		
6	C	20	Total	O	0	0
			20	20		
6	D	13	Total	O	0	0
			13	13		
6	E	25	Total	O	0	0
			25	25		
6	F	11	Total	O	0	0
			11	11		

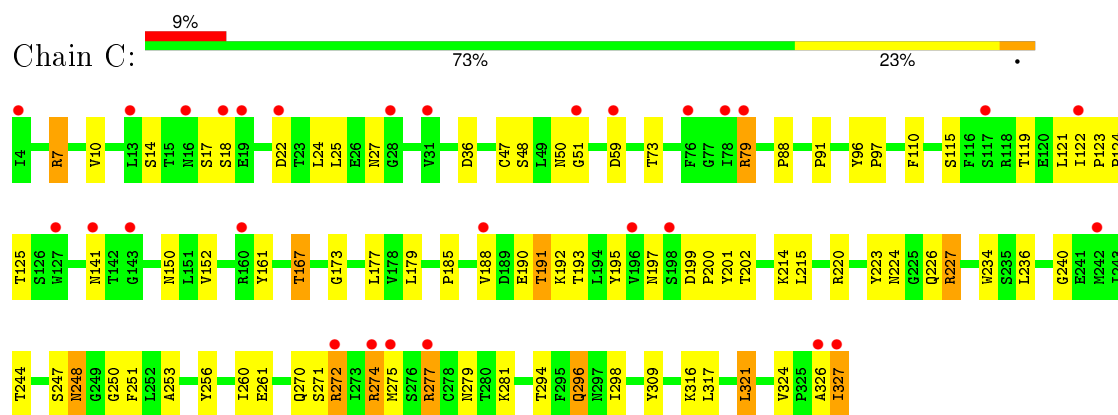
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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 ( $\text{RSRZ} > 2$ ). 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.

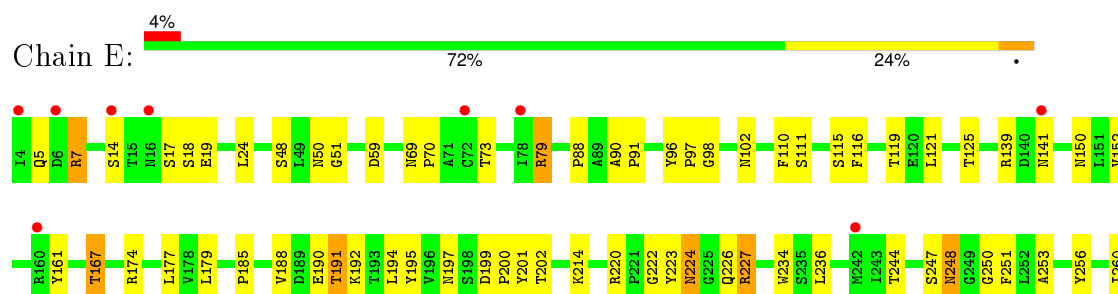
#### • Molecule 1: Hemagglutinin



#### • Molecule 1: Hemagglutinin



#### • Molecule 1: Hemagglutinin

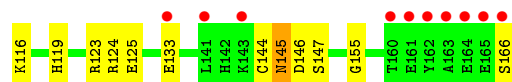
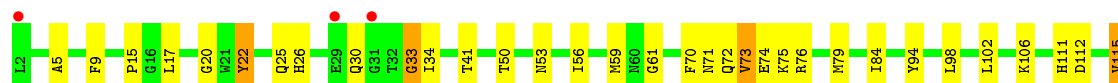
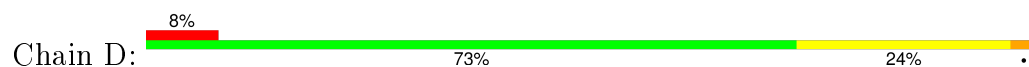




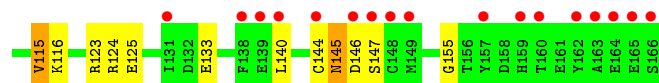
• Molecule 2: Hemagglutinin



• Molecule 2: Hemagglutinin



• Molecule 2: Hemagglutinin



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	75.64Å 76.80Å 76.38Å 85.60° 82.67° 87.52°	Depositor
Resolution (Å)	42.45 – 2.59 42.46 – 2.59	Depositor EDS
% Data completeness (in resolution range)	90.3 (42.45-2.59) 93.2 (42.46-2.59)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.12 (at 2.58Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, $R_{free}$	0.216 , 0.255 0.209 , 0.247	Depositor DCC
$R_{free}$ test set	2573 reflections (5.10%)	DCC
Wilson B-factor (Å <sup>2</sup> )	49.8	Xtriage
Anisotropy	0.510	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 50.9	EDS
Estimated twinning fraction	0.010 for -l,-k,-h	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 50524 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	11796	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% 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, 0.375 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

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	0.37	0/2619	0.46	0/3560
1	C	0.27	0/2619	0.43	0/3560
1	E	0.36	0/2619	0.44	0/3560
2	B	0.35	0/1333	0.43	0/1798
2	D	0.24	0/1333	0.42	0/1798
2	F	0.23	0/1333	0.42	0/1798
All	All	0.32	0/11856	0.44	0/16074

There are no bond length outliers.

There are no bond angle outliers.

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	2555	0	2476	85	0
1	C	2555	0	2476	76	0
1	E	2555	0	2474	81	0
2	B	1312	0	1240	67	0
2	D	1312	0	1240	37	0
2	F	1312	0	1240	40	0
3	A	32	0	27	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	14	0	13	0	0
5	E	46	0	39	2	0
6	A	15	0	0	24	0
6	B	19	0	0	37	0
6	C	20	0	0	22	0
6	D	13	0	0	3	0
6	E	25	0	0	21	0
6	F	11	0	0	11	0
All	All	11796	0	11225	356	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 16.

All (356) 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:47:CYS:HB2	6:C:409:HOH:O	1.14	1.32
2:B:106:LYS:HB2	6:B:218:HOH:O	1.15	1.29
2:B:30:GLN:HG2	6:B:207:HOH:O	1.30	1.25
6:A:903:HOH:O	2:D:50:THR:HG21	1.38	1.24
2:B:147:SER:HB3	6:B:215:HOH:O	1.42	1.19
1:A:25:LEU:C	6:A:903:HOH:O	1.85	1.15
1:C:316:LYS:HG2	6:C:412:HOH:O	1.46	1.13
2:B:148:CYS:N	6:B:215:HOH:O	1.82	1.11
2:B:109:ASP:CA	6:B:206:HOH:O	1.98	1.11
1:C:274:ARG:NH1	6:C:408:HOH:O	1.86	1.09
2:B:30:GLN:N	6:B:207:HOH:O	1.83	1.09
1:E:277:ARG:N	6:E:716:HOH:O	1.86	1.08
6:A:903:HOH:O	2:D:50:THR:CG2	1.93	1.08
1:E:277:ARG:CB	6:E:716:HOH:O	2.06	1.04
1:A:296:GLN:NE2	6:A:908:HOH:O	1.91	1.04
2:B:147:SER:CB	6:B:215:HOH:O	2.02	1.03
2:B:147:SER:CA	6:B:215:HOH:O	2.06	1.02
2:B:109:ASP:N	6:B:206:HOH:O	1.91	1.02
1:A:150:ASN:HD22	1:A:256:TYR:HB2	1.26	1.01
1:A:293:ARG:CD	6:A:907:HOH:O	2.08	1.00
1:E:277:ARG:CA	6:E:716:HOH:O	2.09	1.00
2:B:30:GLN:CG	6:B:207:HOH:O	1.94	0.99
1:E:150:ASN:HD22	1:E:256:TYR:HB2	1.25	0.98
1:C:150:ASN:HD22	1:C:256:TYR:HB2	1.25	0.98
1:A:293:ARG:HD3	6:A:907:HOH:O	1.61	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224:ASN:N	1:A:224:ASN:HD22	1.58	0.96
2:B:110:MET:N	6:B:206:HOH:O	1.98	0.95
2:B:109:ASP:HB2	6:B:206:HOH:O	1.64	0.94
1:C:48:SER:O	6:C:409:HOH:O	1.86	0.93
2:B:164:GLU:O	6:B:208:HOH:O	1.85	0.93
2:F:47:GLN:NE2	6:F:201:HOH:O	2.03	0.92
1:E:277:ARG:HB2	6:E:716:HOH:O	1.68	0.92
2:D:61:GLY:O	6:D:205:HOH:O	1.86	0.92
1:A:38:ILE:C	6:A:907:HOH:O	2.07	0.91
1:A:239:PRO:O	6:A:912:HOH:O	1.88	0.91
1:C:240:GLY:O	6:C:411:HOH:O	1.89	0.90
1:A:25:LEU:O	6:A:903:HOH:O	1.85	0.90
1:A:296:GLN:OE1	6:A:908:HOH:O	1.90	0.89
1:E:167:THR:HB	1:E:244:THR:HG22	1.56	0.89
1:C:27:ASN:OD1	6:C:418:HOH:O	1.91	0.88
6:A:903:HOH:O	2:D:50:THR:CB	2.17	0.88
1:C:294:THR:OG1	6:C:410:HOH:O	1.83	0.88
1:E:307:PRO:O	6:E:703:HOH:O	1.90	0.88
1:C:193:THR:OG1	6:C:405:HOH:O	1.91	0.87
1:A:167:THR:HB	1:A:244:THR:HG22	1.55	0.87
1:E:98:GLY:O	6:E:707:HOH:O	1.92	0.87
1:C:167:THR:HB	1:C:244:THR:HG22	1.57	0.87
2:B:88:VAL:O	6:B:211:HOH:O	1.94	0.86
2:B:69:GLU:OE2	6:B:214:HOH:O	1.92	0.85
1:C:122:ILE:O	6:C:403:HOH:O	1.93	0.85
1:E:102:ASN:OD1	6:E:705:HOH:O	1.93	0.84
1:A:296:GLN:CD	6:A:908:HOH:O	2.13	0.81
2:B:109:ASP:CB	6:B:206:HOH:O	2.13	0.80
1:C:22:ASP:HB3	6:C:418:HOH:O	1.81	0.79
2:B:87:ALA:O	6:B:211:HOH:O	2.00	0.78
1:E:59:ASP:OD1	6:E:723:HOH:O	2.01	0.78
2:B:88:VAL:C	6:B:211:HOH:O	2.21	0.78
1:A:224:ASN:HD22	1:A:224:ASN:H	1.30	0.78
1:A:224:ASN:N	1:A:224:ASN:ND2	2.30	0.78
1:C:200:PRO:O	6:C:413:HOH:O	2.02	0.78
1:E:19:GLU:OE1	6:E:712:HOH:O	2.02	0.78
2:B:147:SER:C	6:B:215:HOH:O	2.05	0.77
2:D:166:SER:N	6:D:203:HOH:O	2.18	0.77
2:B:30:GLN:CB	6:B:207:HOH:O	2.25	0.76
1:C:240:GLY:C	6:C:411:HOH:O	2.24	0.76
2:F:74:GLU:OE2	6:F:205:HOH:O	2.05	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:51:GLY:H	1:C:279:ASN:HD21	1.35	0.75
1:A:38:ILE:O	6:A:907:HOH:O	2.04	0.75
1:C:79:ARG:NH1	1:C:79:ARG:HB3	2.02	0.74
1:A:79:ARG:HB3	1:A:79:ARG:NH1	2.03	0.74
1:E:59:ASP:OD2	6:E:723:HOH:O	2.05	0.74
2:B:106:LYS:N	6:B:218:HOH:O	1.82	0.73
1:E:51:GLY:H	1:E:279:ASN:HD21	1.35	0.73
1:C:201:TYR:H	1:C:248:ASN:HD21	1.37	0.73
1:A:201:TYR:H	1:A:248:ASN:HD21	1.37	0.73
1:A:173:GLY:HA2	6:A:915:HOH:O	1.88	0.73
1:A:51:GLY:H	1:A:279:ASN:HD21	1.36	0.72
1:A:96:TYR:CE1	1:A:226:GLN:HG3	2.24	0.72
2:B:106:LYS:O	6:B:206:HOH:O	2.06	0.72
1:E:277:ARG:CD	6:E:716:HOH:O	2.37	0.72
1:C:47:CYS:CB	6:C:409:HOH:O	1.91	0.72
1:A:293:ARG:HD2	6:A:907:HOH:O	1.80	0.72
1:E:59:ASP:CG	6:E:723:HOH:O	2.28	0.72
1:E:227:ARG:HH11	1:E:227:ARG:HG2	1.55	0.72
1:E:322:ARG:O	6:E:713:HOH:O	2.07	0.71
1:C:96:TYR:CE1	1:C:226:GLN:HG3	2.25	0.71
1:E:272:ARG:HD2	1:E:272:ARG:H	1.56	0.71
1:A:326:ALA:HB2	2:B:15:PRO:HD3	1.73	0.71
1:A:274:ARG:HG3	1:A:275:MET:N	2.06	0.70
1:A:79:ARG:HH11	1:A:79:ARG:HB3	1.55	0.70
6:A:903:HOH:O	2:D:50:THR:HB	1.86	0.70
1:E:96:TYR:CE1	1:E:226:GLN:HG3	2.26	0.70
1:C:79:ARG:HB3	1:C:79:ARG:HH11	1.56	0.70
2:B:91:ILE:HB	6:B:211:HOH:O	1.90	0.70
1:C:272:ARG:H	1:C:272:ARG:HD2	1.55	0.70
1:E:201:TYR:H	1:E:248:ASN:HD21	1.38	0.70
1:A:97:PRO:HA	1:A:223:TYR:CZ	2.27	0.69
1:C:215:LEU:HG	6:C:413:HOH:O	1.93	0.68
1:C:240:GLY:HA3	6:C:411:HOH:O	1.93	0.68
1:A:236:LEU:HD21	1:A:260:ILE:HD11	1.76	0.68
1:C:236:LEU:HD21	1:C:260:ILE:HD11	1.76	0.67
1:A:272:ARG:HD2	1:A:272:ARG:H	1.59	0.67
2:F:2:LEU:N	6:F:202:HOH:O	2.26	0.67
1:E:236:LEU:HD21	1:E:260:ILE:HD11	1.78	0.65
1:A:150:ASN:ND2	1:A:256:TYR:HB2	2.07	0.64
2:B:69:GLU:CD	6:B:214:HOH:O	2.35	0.64
1:C:17:SER:N	6:C:420:HOH:O	2.17	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:224:ASN:N	1:E:224:ASN:HD22	1.93	0.64
1:E:227:ARG:NH1	1:E:227:ARG:HG2	2.09	0.63
1:C:274:ARG:HG3	1:C:275:MET:N	2.11	0.63
1:C:240:GLY:CA	6:C:411:HOH:O	2.45	0.63
1:A:173:GLY:N	6:A:915:HOH:O	2.31	0.63
1:E:97:PRO:HA	1:E:223:TYR:CZ	2.34	0.63
1:E:194:LEU:HD21	5:E:602:SIA:O10	1.99	0.62
1:A:24:LEU:HD22	2:B:102:LEU:HD23	1.81	0.62
1:E:150:ASN:ND2	1:E:256:TYR:HB2	2.08	0.62
2:B:91:ILE:N	6:B:211:HOH:O	1.91	0.62
2:B:106:LYS:CB	6:B:218:HOH:O	1.85	0.62
1:C:272:ARG:N	1:C:272:ARG:HD2	2.16	0.61
1:E:326:ALA:HB2	2:F:15:PRO:HD3	1.82	0.61
1:C:201:TYR:H	1:C:248:ASN:ND2	1.97	0.61
1:C:47:CYS:C	6:C:409:HOH:O	2.39	0.61
1:A:201:TYR:H	1:A:248:ASN:ND2	1.97	0.60
1:E:201:TYR:H	1:E:248:ASN:ND2	1.99	0.60
1:E:294:THR:N	6:E:715:HOH:O	2.18	0.60
1:E:327:ILE:H	1:E:327:ILE:HD12	1.66	0.60
2:F:70:PHE:HB3	2:F:74:GLU:HG3	1.84	0.60
1:C:327:ILE:H	1:C:327:ILE:HD12	1.67	0.60
2:B:106:LYS:CA	6:B:218:HOH:O	2.15	0.60
1:A:327:ILE:H	1:A:327:ILE:HD12	1.67	0.60
1:C:48:SER:HB2	1:C:279:ASN:HD22	1.67	0.59
1:E:272:ARG:HD2	1:E:272:ARG:N	2.16	0.59
1:A:272:ARG:HD2	1:A:272:ARG:N	2.18	0.59
1:A:48:SER:HB2	1:A:279:ASN:HD22	1.66	0.59
1:C:36:ASP:OD1	6:C:412:HOH:O	2.16	0.59
1:A:74:SER:HA	6:A:914:HOH:O	2.02	0.59
1:C:150:ASN:ND2	1:C:256:TYR:HB2	2.08	0.58
5:E:602:SIA:O1B	5:E:602:SIA:H6	2.02	0.58
1:E:174:ARG:HD3	6:E:706:HOH:O	2.03	0.58
1:A:173:GLY:CA	6:A:915:HOH:O	2.47	0.58
1:A:195:TYR:O	1:A:196:VAL:HB	2.04	0.58
2:B:70:PHE:HB3	2:B:74:GLU:HG3	1.85	0.58
2:B:166:SER:C	6:B:208:HOH:O	2.41	0.58
2:B:145:ASN:CB	6:B:215:HOH:O	2.52	0.57
2:B:147:SER:N	6:B:215:HOH:O	2.30	0.57
2:D:76:ARG:NH2	6:F:205:HOH:O	2.32	0.57
1:C:97:PRO:HA	1:C:223:TYR:CZ	2.40	0.57
1:E:48:SER:HB2	1:E:279:ASN:HD22	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:91:ILE:CB	6:B:211:HOH:O	2.47	0.56
2:B:59:MET:HG3	2:F:94:TYR:CE1	2.40	0.56
1:C:173:GLY:N	6:C:406:HOH:O	2.11	0.56
2:D:70:PHE:HB3	2:D:74:GLU:HG3	1.86	0.56
1:E:7:ARG:NH2	2:F:133:GLU:OE2	2.38	0.56
1:A:97:PRO:HA	1:A:223:TYR:CE1	2.41	0.55
1:E:24:LEU:HD22	2:F:102:LEU:HD23	1.88	0.55
1:A:248:ASN:H	1:A:248:ASN:HD22	1.54	0.54
1:C:326:ALA:HB2	2:D:15:PRO:HD3	1.89	0.54
2:B:85:ASP:OD2	6:B:205:HOH:O	2.19	0.54
1:E:185:PRO:HG2	1:E:191:THR:HB	1.90	0.54
1:E:248:ASN:H	1:E:248:ASN:HD22	1.55	0.54
1:C:115:SER:HB2	1:C:261:GLU:HB3	1.91	0.53
1:A:115:SER:HB2	1:A:261:GLU:HB3	1.90	0.53
1:E:277:ARG:HD2	6:E:716:HOH:O	2.06	0.53
1:E:115:SER:HB2	1:E:261:GLU:HB3	1.90	0.53
1:A:199:ASP:N	1:A:200:PRO:HD3	2.24	0.53
1:E:161:TYR:OH	6:E:720:HOH:O	2.18	0.53
1:C:248:ASN:H	1:C:248:ASN:HD22	1.56	0.53
2:B:145:ASN:HB3	6:B:215:HOH:O	2.09	0.52
2:D:94:TYR:CE1	2:F:59:MET:HG3	2.44	0.52
1:C:327:ILE:H	1:C:327:ILE:CD1	2.23	0.52
1:C:24:LEU:HD22	2:D:102:LEU:HD23	1.91	0.52
1:C:188:VAL:HA	1:C:191:THR:HG23	1.92	0.52
1:A:220:ARG:O	1:A:227:ARG:HG3	2.09	0.52
1:C:220:ARG:O	1:C:227:ARG:HG3	2.10	0.52
1:A:326:ALA:HB2	2:B:15:PRO:CD	2.38	0.52
1:A:79:ARG:N	6:A:910:HOH:O	1.98	0.52
2:F:2:LEU:C	6:F:202:HOH:O	2.48	0.52
2:F:2:LEU:O	6:F:202:HOH:O	2.19	0.51
1:E:188:VAL:HA	1:E:191:THR:HG23	1.92	0.51
2:B:145:ASN:HB2	6:B:215:HOH:O	2.09	0.51
1:C:185:PRO:HG2	1:C:191:THR:HB	1.91	0.51
1:A:9:CYS:O	2:B:24:PHE:HA	2.11	0.51
1:A:185:PRO:HG2	1:A:191:THR:HB	1.92	0.51
1:A:223:TYR:C	1:A:224:ASN:O	2.47	0.51
2:F:74:GLU:CD	6:F:205:HOH:O	2.49	0.51
1:A:195:TYR:O	1:A:197:ASN:N	2.43	0.51
2:B:94:TYR:CE1	2:D:59:MET:HG3	2.45	0.51
1:C:25:LEU:HD21	2:F:51:LYS:HE3	1.92	0.51
1:E:199:ASP:N	1:E:200:PRO:HD3	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:VAL:HA	1:A:191:THR:HG23	1.92	0.50
1:C:199:ASP:N	1:C:200:PRO:HD3	2.25	0.50
2:D:75:LYS:HB3	2:D:79:MET:HE2	1.93	0.50
1:C:7:ARG:NH2	2:D:133:GLU:OE2	2.45	0.50
1:A:223:TYR:O	1:A:224:ASN:O	2.30	0.50
1:E:59:ASP:O	1:E:91:PRO:HD2	2.12	0.50
1:A:50:ASN:HD21	1:A:281:LYS:HB3	1.77	0.50
1:E:202:THR:HG23	1:E:247:SER:HB2	1.93	0.50
1:E:299:ASP:HA	6:E:704:HOH:O	2.12	0.50
1:A:26:GLU:N	6:A:903:HOH:O	2.27	0.49
2:B:34:ILE:O	2:B:34:ILE:HD12	2.12	0.49
2:B:3:PHE:CE2	6:F:202:HOH:O	2.64	0.49
2:F:105:ASP:HB3	6:F:204:HOH:O	2.11	0.49
1:C:202:THR:HG23	1:C:247:SER:HB2	1.94	0.49
2:D:102:LEU:HD22	2:F:106:LYS:NZ	2.28	0.49
1:A:59:ASP:O	1:A:91:PRO:HD2	2.12	0.49
1:C:50:ASN:HD21	1:C:281:LYS:HB3	1.78	0.49
1:A:75:ASN:N	6:A:914:HOH:O	2.06	0.49
2:B:102:LEU:HD22	2:D:106:LYS:NZ	2.27	0.48
1:E:50:ASN:HD21	1:E:281:LYS:HB3	1.77	0.48
2:B:111:HIS:O	2:B:115:VAL:HG13	2.13	0.48
1:C:59:ASP:O	1:C:91:PRO:HD2	2.12	0.48
2:D:34:ILE:HD12	2:D:34:ILE:O	2.12	0.48
1:E:5:GLN:OE1	2:F:140:LEU:O	2.31	0.48
2:F:105:ASP:CG	6:F:204:HOH:O	2.52	0.48
2:F:34:ILE:O	2:F:34:ILE:HD12	2.13	0.48
1:A:202:THR:HG23	1:A:247:SER:HB2	1.95	0.48
2:D:111:HIS:O	2:D:115:VAL:HG13	2.14	0.48
1:C:294:THR:HG23	2:D:56:ILE:HG23	1.95	0.48
1:A:197:ASN:H	1:A:197:ASN:ND2	2.11	0.48
2:F:75:LYS:HB3	2:F:79:MET:HE2	1.95	0.48
2:F:111:HIS:O	2:F:115:VAL:HG13	2.14	0.47
1:E:294:THR:HG23	2:F:56:ILE:HG23	1.96	0.47
1:A:321:LEU:HD23	1:A:321:LEU:H	1.78	0.47
1:A:24:LEU:HD22	2:B:102:LEU:CD2	2.43	0.47
1:C:223:TYR:O	1:C:224:ASN:HB2	2.14	0.47
2:D:20:GLY:HA2	2:D:41:THR:HG21	1.97	0.47
2:D:76:ARG:HA	2:D:79:MET:HE3	1.96	0.47
2:D:84:ILE:HD13	2:F:84:ILE:HD13	1.97	0.47
1:C:197:ASN:ND2	1:C:197:ASN:H	2.12	0.46
1:C:123:PRO:HA	1:C:124:PRO:HD3	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:76:ARG:HA	2:F:79:MET:HE3	1.96	0.46
1:C:296:GLN:HG2	1:C:298:ILE:H	1.80	0.46
2:B:9:PHE:HB3	2:D:124:ARG:CZ	2.45	0.46
1:E:220:ARG:O	1:E:227:ARG:HG2	2.15	0.46
2:D:53:ASN:ND2	6:D:210:HOH:O	2.09	0.46
2:F:20:GLY:HA2	2:F:41:THR:HG21	1.98	0.46
1:E:296:GLN:HG2	1:E:298:ILE:H	1.81	0.46
2:B:145:ASN:HB3	2:B:147:SER:H	1.81	0.46
1:A:248:ASN:N	1:A:248:ASN:HD22	2.13	0.46
1:A:327:ILE:H	1:A:327:ILE:CD1	2.23	0.46
1:E:197:ASN:H	1:E:197:ASN:ND2	2.13	0.46
1:C:197:ASN:H	1:C:197:ASN:HD22	1.63	0.46
1:A:272:ARG:CD	1:A:272:ARG:H	2.23	0.46
1:A:48:SER:CB	1:A:279:ASN:HD22	2.29	0.45
1:E:261:GLU:OE1	6:E:706:HOH:O	2.21	0.45
1:A:291:THR:N	6:A:906:HOH:O	2.37	0.45
1:A:294:THR:HG23	2:B:56:ILE:HG23	1.98	0.45
1:E:110:PHE:CE2	1:E:177:LEU:HD22	2.51	0.45
2:F:145:ASN:HB3	2:F:147:SER:H	1.82	0.45
1:A:296:GLN:HG2	1:A:298:ILE:H	1.81	0.45
1:C:88:PRO:HG3	1:C:270:GLN:HB3	1.99	0.45
1:C:48:SER:CB	1:C:279:ASN:HD22	2.30	0.45
1:C:272:ARG:H	1:C:272:ARG:CD	2.21	0.45
2:D:145:ASN:HB3	2:D:147:SER:H	1.81	0.45
1:C:195:TYR:CZ	1:C:250:GLY:HA2	2.51	0.45
1:C:110:PHE:CE2	1:C:177:LEU:HD22	2.52	0.45
2:F:71:ASN:OD1	2:F:73:VAL:HG23	2.17	0.45
1:A:321:LEU:HD23	1:A:321:LEU:N	2.32	0.45
1:A:110:PHE:CE2	1:A:177:LEU:HD22	2.51	0.45
2:B:20:GLY:HA2	2:B:41:THR:HG21	1.98	0.45
1:E:324:VAL:HG12	6:E:713:HOH:O	2.17	0.44
1:E:201:TYR:N	1:E:248:ASN:HD21	2.12	0.44
1:E:326:ALA:HB2	2:F:15:PRO:CD	2.46	0.44
1:A:197:ASN:HD22	1:A:197:ASN:H	1.64	0.44
1:A:277:ARG:H	1:A:277:ARG:HD2	1.82	0.44
1:A:153:TRP:CE3	3:A:801:SIA:H112	2.52	0.44
2:B:71:ASN:OD1	2:B:73:VAL:HG23	2.17	0.44
2:D:71:ASN:OD1	2:D:73:VAL:HG23	2.17	0.44
1:C:277:ARG:HD2	1:C:277:ARG:H	1.82	0.44
2:B:124:ARG:CZ	2:F:9:PHE:HB3	2.48	0.44
1:E:277:ARG:H	1:E:277:ARG:HD2	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:122:ILE:HB	6:C:403:HOH:O	2.18	0.44
1:E:195:TYR:CZ	1:E:250:GLY:HA2	2.53	0.44
1:E:197:ASN:H	1:E:197:ASN:HD22	1.64	0.44
1:E:224:ASN:ND2	1:E:224:ASN:N	2.64	0.44
2:B:106:LYS:NZ	2:F:102:LEU:HD22	2.33	0.43
1:E:321:LEU:HD23	1:E:321:LEU:H	1.82	0.43
1:A:88:PRO:HG3	1:A:270:GLN:HB3	1.99	0.43
2:D:125:GLU:OE2	2:D:155:GLY:HA2	2.17	0.43
2:B:75:LYS:HB3	2:B:79:MET:HE2	2.01	0.43
1:E:327:ILE:CD1	1:E:327:ILE:H	2.22	0.43
1:E:48:SER:CB	1:E:279:ASN:HD22	2.30	0.43
1:C:201:TYR:N	1:C:248:ASN:HD21	2.11	0.43
1:C:188:VAL:HA	1:C:191:THR:CG2	2.49	0.43
2:B:25:GLN:HA	2:B:33:GLY:O	2.19	0.43
2:F:26:HIS:CD2	2:F:26:HIS:C	2.92	0.43
1:A:315:LEU:HA	6:A:905:HOH:O	2.18	0.43
2:B:125:GLU:OE2	2:B:155:GLY:HA2	2.18	0.43
2:D:22:TYR:CD1	2:D:115:VAL:HG12	2.54	0.43
1:E:161:TYR:HB3	1:E:197:ASN:ND2	2.33	0.43
1:C:24:LEU:HD22	2:D:102:LEU:CD2	2.49	0.43
2:F:125:GLU:OE2	2:F:155:GLY:HA2	2.18	0.43
1:E:88:PRO:HG3	1:E:270:GLN:HB3	2.00	0.43
1:E:295:PHE:N	6:E:715:HOH:O	2.51	0.42
2:D:26:HIS:CD2	2:D:26:HIS:C	2.92	0.42
1:E:90:ALA:HA	1:E:91:PRO:HD3	1.93	0.42
1:E:321:LEU:HD23	1:E:321:LEU:N	2.34	0.42
1:C:321:LEU:H	1:C:321:LEU:HD23	1.83	0.42
1:C:161:TYR:HB3	1:C:197:ASN:ND2	2.34	0.42
1:C:152:VAL:CG2	1:C:253:ALA:HB3	2.49	0.42
1:C:321:LEU:N	1:C:321:LEU:HD23	2.35	0.42
1:A:161:TYR:HB3	1:A:197:ASN:ND2	2.34	0.42
1:C:10:VAL:HG21	2:D:119:HIS:HA	2.02	0.42
2:B:26:HIS:C	2:B:26:HIS:CD2	2.93	0.42
2:F:25:GLN:HA	2:F:33:GLY:O	2.19	0.42
1:A:224:ASN:O	1:A:225:GLY:C	2.56	0.42
2:D:25:GLN:HA	2:D:33:GLY:O	2.19	0.42
1:E:251:PHE:CZ	1:E:253:ALA:HA	2.55	0.42
2:B:29:GLU:C	6:B:207:HOH:O	2.36	0.42
1:C:296:GLN:O	1:C:309:TYR:HA	2.20	0.42
1:A:251:PHE:CZ	1:A:253:ALA:HA	2.55	0.42
1:A:152:VAL:CG2	1:A:253:ALA:HB3	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:166:SER:N	6:B:208:HOH:O	2.52	0.42
2:B:71:ASN:OD1	2:B:74:GLU:HG2	2.20	0.42
2:D:71:ASN:OD1	2:D:74:GLU:HG2	2.20	0.42
1:A:267:ARG:NH1	2:B:67:ARG:HD3	2.34	0.42
2:B:48:ILE:O	2:B:52:ILE:HD13	2.20	0.42
1:E:188:VAL:HA	1:E:191:THR:CG2	2.49	0.41
2:B:32:THR:HA	2:B:33:GLY:HA3	1.82	0.41
2:F:25:GLN:HG3	2:F:33:GLY:O	2.20	0.41
2:D:9:PHE:HB3	2:F:124:ARG:CZ	2.50	0.41
1:E:79:ARG:HA	1:E:116:PHE:O	2.21	0.41
1:A:188:VAL:HA	1:A:191:THR:CG2	2.49	0.41
1:E:272:ARG:CD	1:E:272:ARG:H	2.21	0.41
2:B:25:GLN:HG3	2:B:33:GLY:O	2.20	0.41
1:E:227:ARG:HH11	1:E:227:ARG:CG	2.27	0.41
2:B:5:ALA:HB3	2:B:112:ASP:OD2	2.19	0.41
2:D:5:ALA:HB3	2:D:112:ASP:OD2	2.20	0.41
1:A:296:GLN:O	1:A:309:TYR:HA	2.20	0.41
2:D:25:GLN:HG3	2:D:33:GLY:O	2.20	0.41
1:A:179:LEU:HD23	1:A:234:TRP:HB3	2.03	0.41
1:E:152:VAL:CG2	1:E:253:ALA:HB3	2.50	0.41
1:E:324:VAL:HA	1:E:325:PRO:HD3	1.90	0.41
1:E:24:LEU:HD22	2:F:102:LEU:CD2	2.49	0.41
1:E:296:GLN:O	1:E:309:TYR:HA	2.21	0.41
2:F:30:GLN:HB2	2:F:30:GLN:HE21	1.65	0.41
1:E:292:ASN:HA	1:E:292:ASN:HD22	1.70	0.41
1:A:324:VAL:HA	1:A:325:PRO:HD3	1.90	0.41
2:F:48:ILE:O	2:F:52:ILE:HD13	2.21	0.41
2:B:22:TYR:CD1	2:B:115:VAL:HG12	2.56	0.41
1:A:123:PRO:HA	1:A:124:PRO:HD3	1.80	0.41
1:C:251:PHE:CZ	1:C:253:ALA:HA	2.56	0.40
1:A:284:THR:C	1:A:286:VAL:H	2.25	0.40
1:A:184:HIS:O	1:A:228:SER:HB2	2.21	0.40
1:C:316:LYS:CG	6:C:412:HOH:O	2.30	0.40
2:F:44:ALA:HA	6:F:201:HOH:O	2.19	0.40
2:F:22:TYR:CD1	2:F:115:VAL:HG12	2.56	0.40
1:E:69:ASN:HA	1:E:70:PRO:HD3	1.96	0.40
2:F:71:ASN:OD1	2:F:74:GLU:HG2	2.22	0.40
1:C:202:THR:HG21	1:C:251:PHE:CD1	2.57	0.40
1:A:292:ASN:HD22	1:A:292:ASN:HA	1.70	0.40
1:E:179:LEU:HD23	1:E:234:TRP:HB3	2.03	0.40
2:B:164:GLU:C	6:B:208:HOH:O	2.44	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:25:GLN:HG3	2:D:34:ILE:HG23	2.04	0.40
1:C:179:LEU:HD23	1:C:234:TRP:HB3	2.03	0.40
1:E:111:SER:HB2	1:E:267:ARG:N	2.36	0.40

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	322/324 (99%)	304 (94%)	16 (5%)	2 (1%)	30	54
1	C	322/324 (99%)	307 (95%)	15 (5%)	0	100	100
1	E	322/324 (99%)	306 (95%)	15 (5%)	1 (0%)	46	70
2	B	163/165 (99%)	153 (94%)	8 (5%)	2 (1%)	16	33
2	D	163/165 (99%)	152 (93%)	9 (6%)	2 (1%)	16	33
2	F	163/165 (99%)	153 (94%)	8 (5%)	2 (1%)	16	33
All	All	1455/1467 (99%)	1375 (94%)	71 (5%)	9 (1%)	30	54

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	224	ASN
2	B	145	ASN
2	D	145	ASN
2	F	145	ASN
2	B	33	GLY
2	D	33	GLY
2	F	33	GLY
1	A	225	GLY
1	E	222	GLY

### 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	285/285 (100%)	258 (90%)	27 (10%)	11	19
1	C	285/285 (100%)	260 (91%)	25 (9%)	12	23
1	E	285/285 (100%)	257 (90%)	28 (10%)	10	18
2	B	140/140 (100%)	128 (91%)	12 (9%)	13	24
2	D	140/140 (100%)	129 (92%)	11 (8%)	15	29
2	F	140/140 (100%)	129 (92%)	11 (8%)	15	29
All	All	1275/1275 (100%)	1161 (91%)	114 (9%)	12	22

All (114) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	ARG
1	A	14	SER
1	A	18	SER
1	A	73	THR
1	A	79	ARG
1	A	119	THR
1	A	121	LEU
1	A	125	THR
1	A	141	ASN
1	A	167	THR
1	A	190	GLU
1	A	191	THR
1	A	192	LYS
1	A	214	LYS
1	A	224	ASN
1	A	227	ARG
1	A	248	ASN
1	A	271	SER
1	A	272	ARG
1	A	274	ARG
1	A	277	ARG
1	A	296	GLN

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Mol	Chain	Res	Type
1	A	300	LYS
1	A	317	LEU
1	A	321	LEU
1	A	324	VAL
1	A	327	ILE
2	B	11	GLU
2	B	17	LEU
2	B	22	TYR
2	B	30	GLN
2	B	72	GLN
2	B	73	VAL
2	B	98	LEU
2	B	115	VAL
2	B	116	LYS
2	B	123	ARG
2	B	144	CYS
2	B	146	ASP
1	C	7	ARG
1	C	14	SER
1	C	18	SER
1	C	73	THR
1	C	79	ARG
1	C	119	THR
1	C	121	LEU
1	C	125	THR
1	C	141	ASN
1	C	167	THR
1	C	190	GLU
1	C	191	THR
1	C	192	LYS
1	C	214	LYS
1	C	227	ARG
1	C	248	ASN
1	C	271	SER
1	C	272	ARG
1	C	274	ARG
1	C	277	ARG
1	C	296	GLN
1	C	317	LEU
1	C	321	LEU
1	C	324	VAL
1	C	327	ILE

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Mol	Chain	Res	Type
2	D	17	LEU
2	D	22	TYR
2	D	30	GLN
2	D	72	GLN
2	D	73	VAL
2	D	98	LEU
2	D	115	VAL
2	D	116	LYS
2	D	123	ARG
2	D	144	CYS
2	D	146	ASP
1	E	7	ARG
1	E	14	SER
1	E	17	SER
1	E	18	SER
1	E	73	THR
1	E	79	ARG
1	E	119	THR
1	E	121	LEU
1	E	125	THR
1	E	139	ARG
1	E	141	ASN
1	E	167	THR
1	E	190	GLU
1	E	191	THR
1	E	192	LYS
1	E	214	LYS
1	E	224	ASN
1	E	227	ARG
1	E	248	ASN
1	E	271	SER
1	E	272	ARG
1	E	274	ARG
1	E	277	ARG
1	E	296	GLN
1	E	317	LEU
1	E	321	LEU
1	E	324	VAL
1	E	327	ILE
2	F	17	LEU
2	F	22	TYR
2	F	30	GLN

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Mol	Chain	Res	Type
2	F	72	GLN
2	F	73	VAL
2	F	98	LEU
2	F	115	VAL
2	F	116	LYS
2	F	123	ARG
2	F	144	CYS
2	F	146	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (38) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	50	ASN
1	A	141	ASN
1	A	150	ASN
1	A	197	ASN
1	A	224	ASN
1	A	248	ASN
1	A	270	GLN
1	A	279	ASN
1	A	292	ASN
2	B	25	GLN
2	B	30	GLN
2	B	54	ASN
2	B	117	ASN
1	C	50	ASN
1	C	150	ASN
1	C	197	ASN
1	C	224	ASN
1	C	248	ASN
1	C	270	GLN
1	C	279	ASN
1	C	292	ASN
2	D	25	GLN
2	D	30	GLN
2	D	54	ASN
2	D	117	ASN
1	E	50	ASN
1	E	150	ASN
1	E	197	ASN
1	E	224	ASN
1	E	226	GLN

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Mol	Chain	Res	Type
1	E	248	ASN
1	E	270	GLN
1	E	279	ASN
1	E	292	ASN
2	F	25	GLN
2	F	30	GLN
2	F	54	ASN
2	F	117	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 ⓘ

5 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	A	801	3	16,20,21	2.13	6 (37%)	18,28,31	2.51	5 (27%)
3	GAL	A	802	3	12,12,12	0.48	0	17,17,17	1.48	3 (17%)
5	SIA	E	602	5	16,20,21	2.13	6 (37%)	18,28,31	2.66	3 (16%)
5	GAL	E	603	5	11,11,12	0.61	0	14,15,17	1.70	2 (14%)
5	NAG	E	604	5	15,15,15	0.45	0	17,21,21	0.91	1 (5%)

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	A	801	3	-	0/14/34/38	0/1/1/1
3	GAL	A	802	3	-	0/2/22/22	0/1/1/1
5	SIA	E	602	5	-	0/14/34/38	0/1/1/1
5	GAL	E	603	5	-	0/2/19/22	0/1/1/1
5	NAG	E	604	5	-	0/6/26/26	0/1/1/1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	801	SIA	C7-C6	-4.49	1.47	1.52
5	E	602	SIA	C7-C6	-4.00	1.47	1.52
5	E	602	SIA	O8-C8	-3.35	1.35	1.43
3	A	801	SIA	O8-C8	-3.20	1.36	1.43
3	A	801	SIA	C6-C5	-2.62	1.48	1.53
5	E	602	SIA	C6-C5	-2.57	1.48	1.53
3	A	801	SIA	C10-N5	2.83	1.45	1.34
3	A	801	SIA	C5-N5	2.84	1.50	1.45
5	E	602	SIA	C5-N5	2.84	1.50	1.45
5	E	602	SIA	C10-N5	2.84	1.45	1.34
3	A	801	SIA	O6-C6	3.09	1.49	1.43
5	E	602	SIA	O6-C6	3.72	1.50	1.43

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	602	SIA	O6-C2-C3	-9.88	90.87	109.86
3	A	801	SIA	O6-C2-C3	-8.75	93.04	109.86
3	A	802	GAL	C4-C3-C2	-3.61	104.05	110.79
3	A	801	SIA	C7-C6-C5	-3.24	109.41	114.32
5	E	603	GAL	O3-C3-C2	-3.02	104.54	110.00
3	A	802	GAL	O4-C4-C3	-2.40	104.92	110.34
3	A	801	SIA	C8-C7-C6	-2.06	108.86	113.01
5	E	604	NAG	C4-C3-C2	2.02	113.23	110.43
3	A	801	SIA	C11-C10-N5	2.26	120.44	116.11
3	A	802	GAL	O2-C2-C3	2.26	115.44	110.34
5	E	602	SIA	C11-C10-N5	2.41	120.72	116.11
3	A	801	SIA	O9-C9-C8	2.56	116.67	111.10
5	E	602	SIA	O9-C9-C8	2.71	117.00	111.10
5	E	603	GAL	C1-C2-C3	5.16	115.64	109.54

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	801	SIA	1	0
5	E	602	SIA	2	0

## 5.6 Ligand geometry

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	$\# Z  > 2$
4	NAG	E	601	1	14,14,15	0.28	0	15,19,21	0.53	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
4	NAG	E	601	1	-	0/6/23/26	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.

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 ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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	324/324 (100%)	0.50	17 (5%)	31 26	38, 70, 111, 147	0
1	C	324/324 (100%)	0.69	29 (8%)	12 9	43, 80, 115, 156	0
1	E	324/324 (100%)	0.42	12 (3%)	45 40	41, 71, 107, 181	0
2	B	165/165 (100%)	0.81	12 (7%)	18 14	35, 61, 106, 280	0
2	D	165/165 (100%)	0.79	13 (7%)	15 12	38, 67, 119, 189	0
2	F	165/165 (100%)	1.16	28 (16%)	2 1	36, 72, 148, 211	0
All	All	1467/1467 (100%)	0.67	111 (7%)	17 13	35, 72, 118, 280	0

All (111) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	166	SER	15.6
2	D	163	ALA	12.6
1	E	4	ILE	11.5
2	B	164	GLU	11.4
2	D	166	SER	10.2
2	B	163	ALA	9.1
1	C	327	ILE	8.6
1	A	4	ILE	8.0
2	F	165	GLU	6.8
2	F	163	ALA	6.4
2	F	29	GLU	6.2
1	C	4	ILE	6.1
1	C	326	ALA	6.0
1	C	277	ARG	5.5
2	F	164	GLU	5.4
2	F	16	GLY	5.2
2	D	164	GLU	5.1
2	F	162	TYR	5.0
2	D	161	GLU	4.8

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Mol	Chain	Res	Type	RSRZ
2	D	165	GLU	4.7
2	F	33	GLY	4.7
2	D	29	GLU	4.4
1	C	18	SER	4.2
2	F	2	LEU	4.2
2	F	160	THR	4.1
2	B	2	LEU	4.0
1	C	76	PHE	4.0
2	F	146	ASP	3.9
1	C	198	SER	3.8
1	A	274	ARG	3.7
1	C	188	VAL	3.7
1	E	160	ARG	3.7
1	E	141	ASN	3.5
2	B	166	SER	3.5
1	E	16	ASN	3.4
2	D	133	GLU	3.4
2	F	18	ILE	3.4
1	A	45	THR	3.4
2	F	19	ASN	3.3
2	B	19	ASN	3.2
1	A	272	ARG	3.2
1	C	242	MET	3.2
1	E	327	ILE	3.1
2	B	165	GLU	3.1
2	B	147	SER	3.1
1	A	160	ARG	3.1
2	B	161	GLU	3.1
2	D	2	LEU	3.0
1	C	79	ARG	3.0
1	C	19	GLU	2.9
2	D	162	TYR	2.9
2	F	139	GLU	2.8
2	D	31	GLY	2.8
2	D	141	LEU	2.8
2	F	3	PHE	2.8
1	C	59	ASP	2.8
1	E	78	ILE	2.7
1	C	143	GLY	2.7
1	A	47	CYS	2.7
1	C	78	ILE	2.6
1	A	139	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
2	F	131	ILE	2.6
1	E	14	SER	2.5
1	C	51	GLY	2.5
1	A	242	MET	2.5
2	B	113	ALA	2.5
2	F	34	ILE	2.5
2	F	144	CYS	2.5
1	C	141	ASN	2.5
1	E	72	CYS	2.4
1	A	59	ASP	2.4
1	A	79	ARG	2.4
1	A	5	GLN	2.4
1	C	13	LEU	2.4
2	F	149	MET	2.4
2	D	160	THR	2.4
1	E	272	ARG	2.4
2	D	143	LYS	2.4
1	C	16	ASN	2.4
1	C	275	MET	2.4
1	E	6	ASP	2.3
1	C	31	VAL	2.3
1	A	327	ILE	2.3
2	F	147	SER	2.3
1	C	117	SER	2.3
1	C	196	VAL	2.3
2	B	146	ASP	2.3
2	F	31	GLY	2.3
1	E	278	CYS	2.3
1	A	18	SER	2.3
2	F	30	GLN	2.3
2	F	157	TYR	2.3
1	A	273	ILE	2.2
1	C	127	TRP	2.2
1	E	242	MET	2.2
1	C	160	ARG	2.2
1	A	278	CYS	2.2
2	F	148	CYS	2.2
2	F	138	PHE	2.2
1	C	272	ARG	2.2
1	C	28	GLY	2.2
2	F	140	LEU	2.2
1	A	72	CYS	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	5	ALA	2.1
2	B	29	GLU	2.1
1	A	207	LYS	2.1
1	C	122	ILE	2.1
2	F	159	HIS	2.1
1	C	22	ASP	2.1
1	C	274	ARG	2.0
2	F	73	VAL	2.0

## 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
5	SIA	E	602	20/21	0.89	0.18	0.36	72,85,96,96	0
3	SIA	A	801	20/21	0.94	0.14	-1.18	90,102,109,111	0
5	GAL	E	603	11/12	0.85	0.18	-	121,134,150,152	0
5	NAG	E	604	15/15	0.66	0.41	-	163,175,183,185	0
3	GAL	A	802	12/12	0.79	0.30	-	132,146,159,163	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
4	NAG	E	601	14/15	0.77	0.32	-	137,145,151,152	0

## 6.5 Other polymers

There are no such residues in this entry.