



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:56 PM GMT

PDB ID : 1MQN
Title : BHA/LSTc
Authors : ha, y.; stevens, d.j.; shekel, j.j.; wiley, d.c.
Deposited on : 2002-09-16
Resolution : 3.20 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
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:

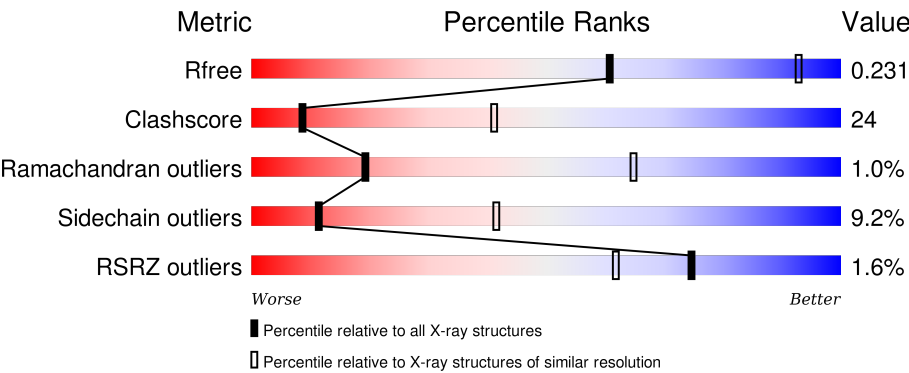
MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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	1124 (3.24-3.16)
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)

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	329	<div><div>2%</div><div>56%</div><div>36%</div><div>5%</div><div>.</div></div>
1	D	329	<div><div>%</div><div>53%</div><div>39%</div><div>5%</div><div>..</div></div>
1	G	329	<div><div>2%</div><div>53%</div><div>36%</div><div>7%</div><div>.</div></div>
2	B	221	<div><div>%</div><div>54%</div><div>21%</div><div>.</div><div>22%</div></div>
2	E	221	<div><div>2%</div><div>47%</div><div>29%</div><div>.</div><div>22%</div></div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	H	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
3	NAG	B	400	-	-	-	X
3	NAG	D	401	-	-	-	X
3	NAG	E	400	-	-	-	X
3	NAG	G	400	-	-	-	X
3	NAG	G	401	-	-	-	X
3	NAG	G	406	-	-	-	X
3	NAG	H	400	-	-	-	X
4	NAG	A	401	-	-	-	X
4	NAG	A	407	-	-	-	X
5	NAG	D	402	-	-	-	X

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 11982 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Hemagglutinin HA1 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	318	Total	C	N	O	S	0	0	0
			2425	1522	424	466	13			
1	D	318	Total	C	N	O	S	0	0	0
			2432	1526	425	468	13			
1	G	318	Total	C	N	O	S	0	0	0
			2426	1523	424	466	13			

- Molecule 2 is a protein called Hemagglutinin HA2 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	172	Total	C	N	O	S	0	0	0
			1398	867	247	278	6			
2	E	172	Total	C	N	O	S	0	0	0
			1401	869	248	278	6			
2	H	172	Total	C	N	O	S	0	0	0
			1404	871	249	278	6			

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		
3	E	1	Total	C	N	O	0	0
			14	8	1	5		
3	G	1	Total	C	N	O	0	0
			14	8	1	5		
3	G	1	Total	C	N	O	0	0
			14	8	1	5		
3	G	1	Total	C	N	O	0	0
			14	8	1	5		
3	H	1	Total	C	N	O	0	0
			14	8	1	5		

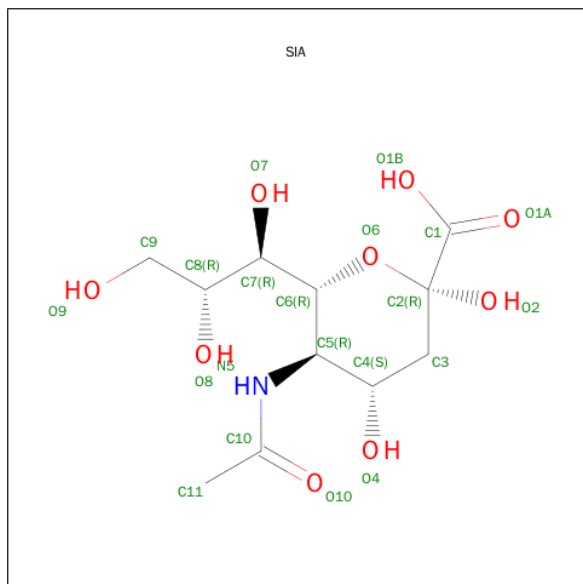
- Molecule 4 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	2	Total	C	N	O	0	0
			28	16	2	10		
4	A	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 5 is a polymer of unknown type called SUGAR (4-MER).

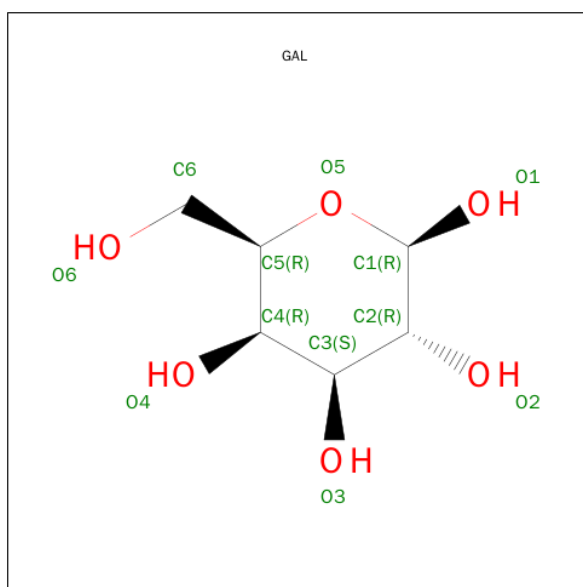
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	4	Total	C	N	O	0	0
			50	28	2	20		
5	D	4	Total	C	N	O	0	0
			50	28	2	20		
5	G	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 6 is SUGAR (2-MER) (three-letter code: SIA) (formula: $C_{11}H_{19}NO_9$).



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

- Molecule 7 is water (three-letter code: GAL) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			12	6	6		

- Molecule 8 is a polymer of unknown type called SUGAR (2-MER).

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

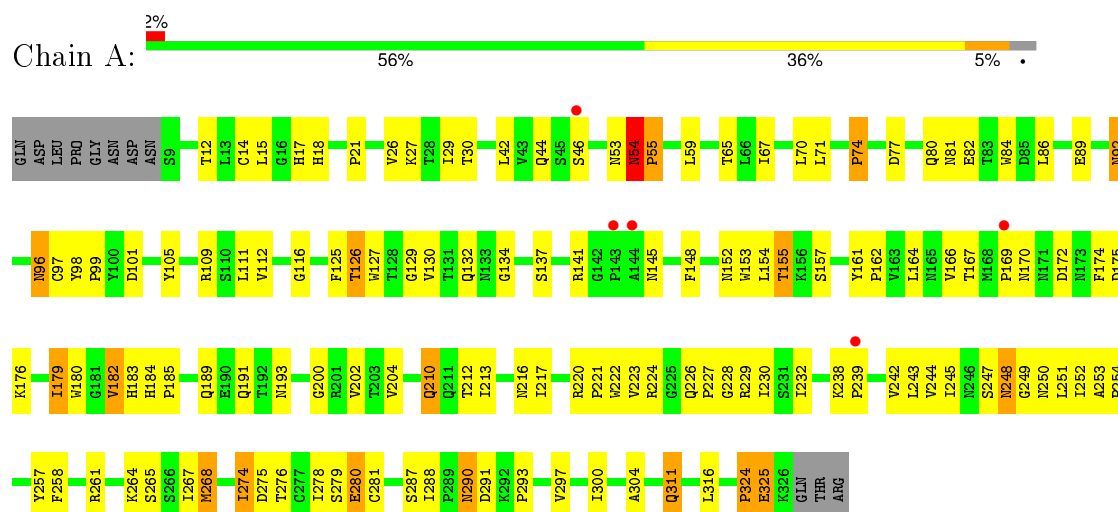
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	20	Total	O	0	0
			20	20		
9	B	14	Total	O	0	0
			14	14		
9	D	22	Total	O	0	0
			22	22		
9	E	12	Total	O	0	0
			12	12		
9	G	22	Total	O	0	0
			22	22		
9	H	10	Total	O	0	0
			10	10		

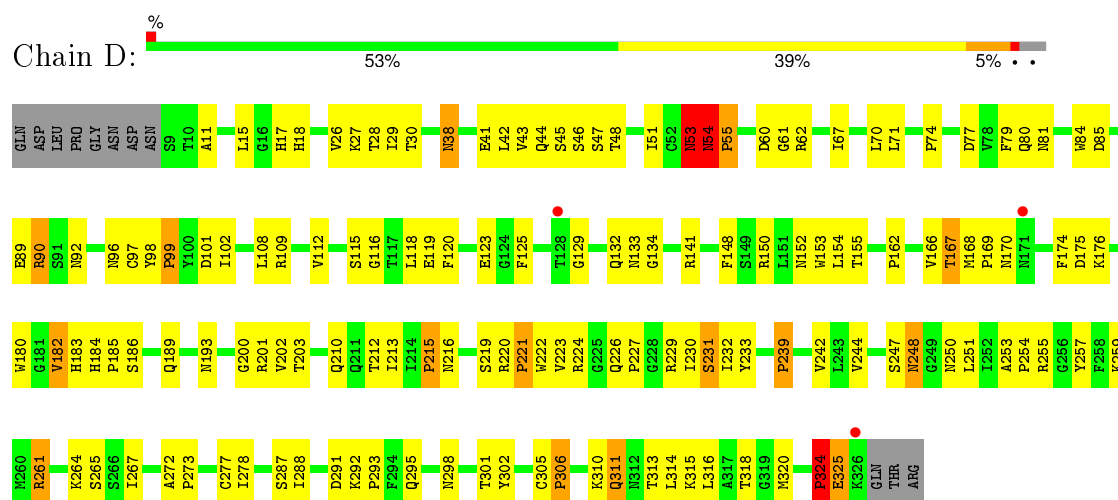
3 Residue-property plots

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.

• Molecule 1: Hemagglutinin HA1 chain

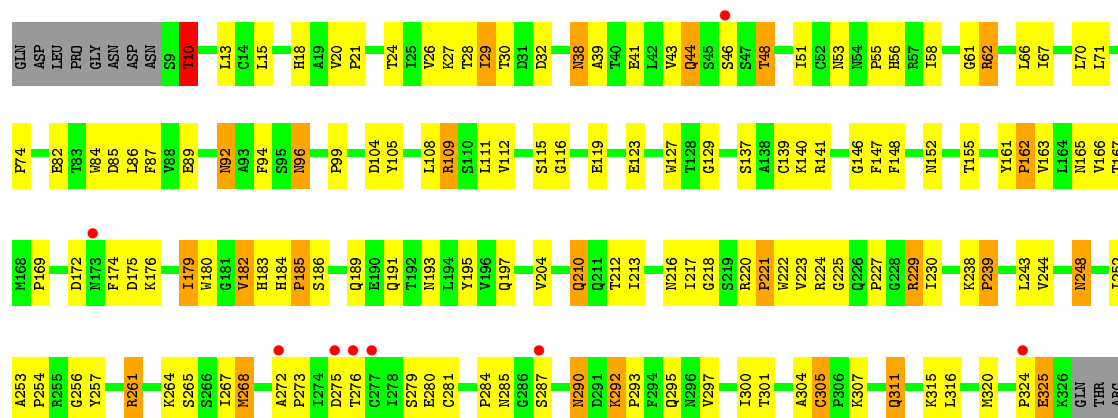


• Molecule 1: Hemagglutinin HA1 chain

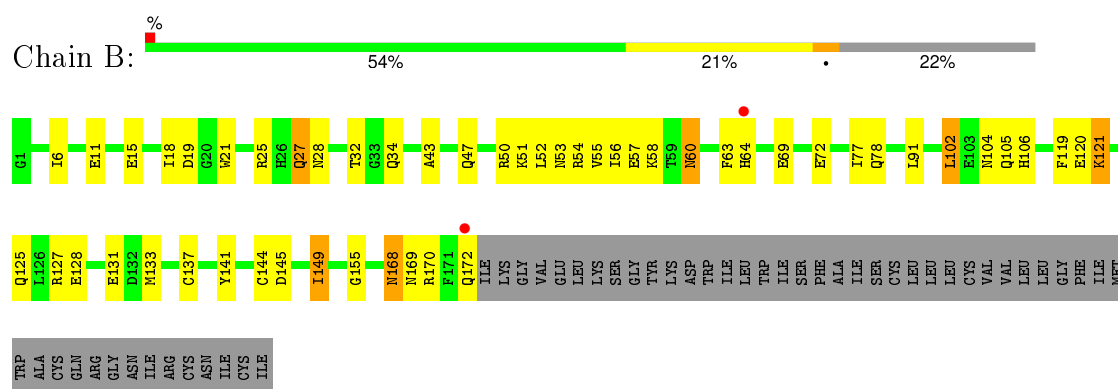


• Molecule 1: Hemagglutinin HA1 chain

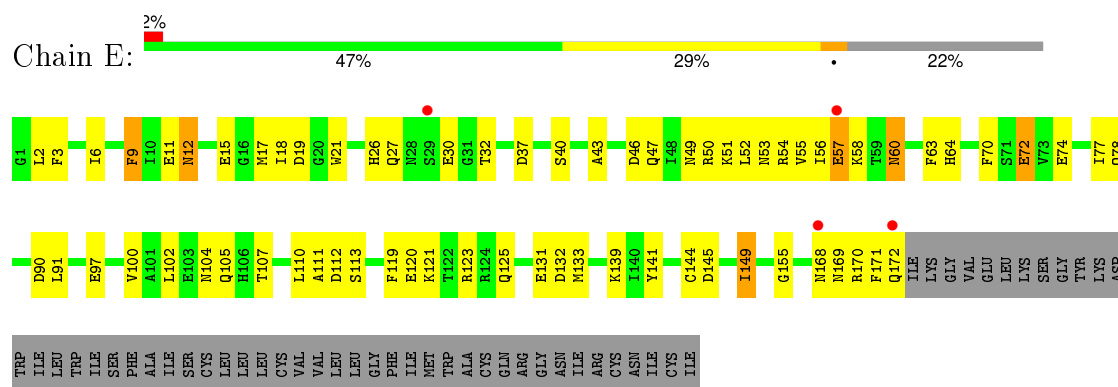




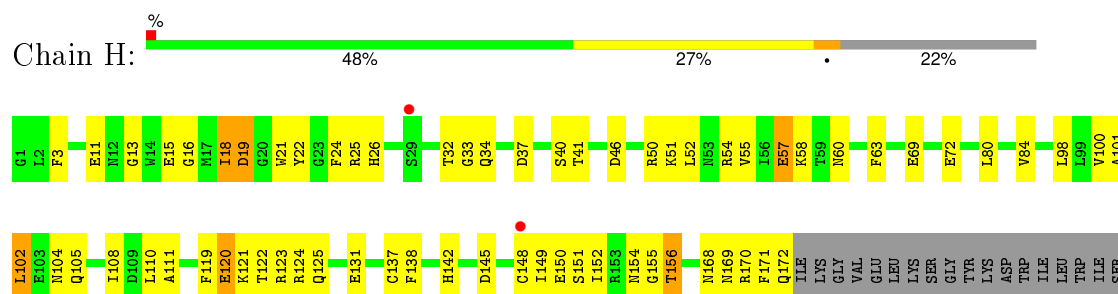
• Molecule 2: Hemagglutinin HA2 chain



• Molecule 2: Hemagglutinin HA2 chain



• Molecule 2: Hemagglutinin HA2 chain



PHE	ALA	ILE	SER	CYS	LEU	LEU	LEU	CYS	VAL	VAL	LEU	LEU	GLY	PHE	ILE	MET	TRP	ALA	CYS	GLN	ARG	GLY	ASN	ILE	ARG	CYS	ASN	ILE	CYS	ILE
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	147.32Å 148.43Å 250.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 3.20 38.74 – 3.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.00-3.20) 93.1 (38.74-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.98 (at 3.18Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.239 , 0.243 0.231 , 0.231	Depositor DCC
R_{free} test set	2252 reflections (5.60%)	DCC
Wilson B-factor (Å ²)	43.7	Xtriage
Anisotropy	1.076	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 60.2	EDS
Estimated twinning fraction	0.028 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 44845 reflections	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	11982	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.50% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GAL, SIA, BMA, 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	0.48	0/2482	0.81	4/3390 (0.1%)
1	D	0.56	0/2489	0.86	5/3398 (0.1%)
1	G	0.57	1/2483 (0.0%)	0.81	5/3391 (0.1%)
2	B	0.45	0/1422	0.62	0/1912
2	E	0.42	0/1425	0.65	0/1915
2	H	0.47	0/1428	0.73	1/1918 (0.1%)
All	All	0.51	1/11729 (0.0%)	0.77	15/15924 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	119	GLU	CB-CG	-5.32	1.42	1.52

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	54	ASN	C-N-CD	-20.24	76.08	120.60
1	A	54	ASN	C-N-CA	13.61	179.18	122.00
1	D	54	ASN	N-CA-C	11.37	141.70	111.00
1	D	54	ASN	C-N-CD	9.49	148.32	128.40
1	D	54	ASN	C-N-CA	-7.01	92.57	122.00
1	A	54	ASN	N-CA-C	6.93	129.71	111.00
1	G	305	CYS	CA-CB-SG	5.95	124.71	114.00
1	A	55	PRO	CA-N-CD	-5.85	103.31	111.50
2	H	137	CYS	CA-CB-SG	5.81	124.46	114.00
1	G	163	VAL	N-CA-C	-5.79	95.38	111.00
1	G	48	THR	N-CA-C	-5.72	95.56	111.00
1	D	53	ASN	C-N-CA	-5.59	107.72	121.70
1	D	55	PRO	N-CA-C	-5.55	97.67	112.10
1	G	10	THR	N-CA-C	5.17	124.95	111.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	141	ARG	N-CA-C	-5.17	97.06	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	2425	0	2334	133	0
1	D	2432	0	2347	149	0
1	G	2426	0	2338	160	0
2	B	1398	0	1308	49	0
2	E	1401	0	1317	79	0
2	H	1404	0	1326	83	0
3	A	14	0	13	0	0
3	B	14	0	13	0	0
3	D	28	0	26	0	0
3	E	14	0	13	0	0
3	G	42	0	39	11	0
3	H	14	0	13	2	0
4	A	56	0	50	2	0
5	A	50	0	43	2	0
5	D	50	0	43	1	0
5	G	50	0	43	3	0
6	A	20	0	17	1	0
7	A	12	0	10	0	0
8	D	32	0	27	2	0
9	A	20	0	0	2	0
9	B	14	0	0	0	0
9	D	22	0	0	2	0
9	E	12	0	0	0	0
9	G	22	0	0	4	0
9	H	10	0	0	1	0
All	All	11982	0	11320	549	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 24.

All (549) 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)
2:H:154:ASN:OD1	2:H:156:THR:HG22	1.43	1.15
1:D:81:ASN:OD1	1:D:119:GLU:HA	1.67	0.94
1:D:27:LYS:HB3	2:H:54:ARG:HH12	1.34	0.91
1:G:24:THR:OG1	3:G:400:NAG:H62	1.68	0.91
1:D:216:ASN:CB	1:G:212:THR:HG21	2.01	0.91
1:D:293:PRO:HG3	2:E:55:VAL:O	1.70	0.90
2:H:154:ASN:OD1	2:H:156:THR:CG2	2.20	0.89
1:D:216:ASN:CG	1:G:212:THR:HG21	1.92	0.89
1:G:293:PRO:HG3	2:H:55:VAL:O	1.73	0.88
2:H:57:GLU:HG3	2:H:57:GLU:O	1.71	0.88
1:A:29:ILE:HD11	2:B:102:LEU:HD12	1.53	0.87
1:D:29:ILE:HD11	2:E:102:LEU:HD12	1.57	0.87
2:H:151:SER:HA	2:H:156:THR:HG23	1.57	0.86
1:D:129:GLY:HA3	1:D:162:PRO:HG2	1.56	0.85
1:A:167:THR:OG1	5:A:403:NAG:H62	1.77	0.85
1:D:97:CYS:O	1:D:224:ARG:NH1	2.12	0.83
2:E:123:ARG:HH22	2:H:123:ARG:NH2	1.77	0.83
1:G:71:LEU:HD23	1:G:179:ILE:HD11	1.61	0.82
1:G:86:LEU:HD21	1:G:268:MET:HE3	1.62	0.80
2:E:11:GLU:C	2:E:12:ASN:HD22	1.84	0.80
2:E:12:ASN:HD22	2:E:12:ASN:N	1.78	0.80
1:A:29:ILE:H	2:B:105:GLN:HE21	1.29	0.80
1:G:29:ILE:H	2:H:105:GLN:HE21	1.28	0.80
1:A:170:ASN:OD1	1:A:176:LYS:HE3	1.82	0.79
1:D:216:ASN:HB3	1:G:212:THR:HG21	1.61	0.79
1:G:71:LEU:CD2	1:G:179:ILE:HD11	2.12	0.79
1:D:221:PRO:O	1:D:229:ARG:NH2	2.14	0.79
1:G:220:ARG:CB	1:G:229:ARG:HH11	1.97	0.78
2:H:25:ARG:NE	2:H:34:GLN:OE1	2.12	0.77
2:E:6:ILE:HD12	2:E:112:ASP:HA	1.68	0.76
1:D:167:THR:HG22	1:D:242:VAL:CG2	2.16	0.76
1:A:274:ILE:HG12	1:A:274:ILE:O	1.87	0.75
1:A:248:ASN:H	1:A:248:ASN:HD22	1.32	0.74
1:G:189:GLN:O	1:G:193:ASN:HB2	1.86	0.74
2:H:21:TRP:HB2	2:H:41:THR:HG23	1.69	0.73
1:G:38:ASN:ND2	1:G:39:ALA:H	1.86	0.73
2:E:57:GLU:HG3	2:E:57:GLU:O	1.88	0.72
2:E:123:ARG:NH2	2:H:123:ARG:NH2	2.37	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:169:ASN:HA	2:E:172:GLN:HE21	1.53	0.72
1:D:302:TYR:CE2	2:E:63:PHE:HD2	2.08	0.72
1:D:325:GLU:OE1	2:E:15:GLU:HB2	1.90	0.71
1:D:27:LYS:HB3	2:H:54:ARG:NH1	2.04	0.71
2:B:57:GLU:HG3	2:B:57:GLU:O	1.90	0.71
2:H:169:ASN:HA	2:H:172:GLN:HE21	1.54	0.71
1:D:77:ASP:O	1:D:80:GLN:HG3	1.90	0.71
1:A:71:LEU:CD2	1:A:179:ILE:HD11	2.21	0.71
1:A:96:ASN:HA	1:A:224:ARG:HE	1.55	0.71
1:G:220:ARG:HB2	1:G:229:ARG:HH11	1.55	0.70
1:G:28:THR:HB	2:H:105:GLN:NE2	2.07	0.70
2:B:144:CYS:SG	2:B:149:ILE:HD12	2.31	0.70
1:D:29:ILE:H	2:E:105:GLN:HE21	1.40	0.69
2:H:120:GLU:HG3	2:H:123:ARG:NH1	2.07	0.69
1:D:170:ASN:OD1	1:D:176:LYS:HE3	1.92	0.69
1:G:29:ILE:HG22	1:G:30:THR:HG23	1.73	0.69
1:A:86:LEU:HD21	1:A:268:MET:HE3	1.74	0.69
1:D:220:ARG:HH11	1:G:210:GLN:HG3	1.57	0.69
2:E:123:ARG:NH2	2:H:123:ARG:HH21	1.91	0.68
1:G:248:ASN:HD22	1:G:248:ASN:H	1.41	0.68
1:A:15:LEU:HD22	2:B:119:PHE:HA	1.75	0.68
1:G:67:ILE:HG13	1:G:105:TYR:CZ	2.29	0.67
1:G:38:ASN:ND2	1:G:39:ALA:N	2.41	0.67
2:H:131:GLU:OE2	2:H:170:ARG:HD2	1.94	0.67
1:G:180:TRP:HB3	1:G:254:PRO:HG3	1.76	0.67
2:H:151:SER:CA	2:H:156:THR:HG23	2.25	0.67
1:D:248:ASN:HD22	1:D:248:ASN:H	1.41	0.67
1:G:222:TRP:CD1	1:G:227:PRO:HG3	2.30	0.67
1:G:44:GLN:N	1:G:292:LYS:HZ2	1.91	0.66
2:H:142:HIS:HE1	2:H:148:CYS:SG	2.18	0.66
1:G:183:HIS:HB2	1:G:252:ILE:HD11	1.76	0.66
1:D:167:THR:HG22	1:D:242:VAL:HG21	1.76	0.66
1:D:44:GLN:HG2	1:D:292:LYS:HD2	1.78	0.66
1:A:129:GLY:HA3	1:A:162:PRO:HG2	1.78	0.65
1:D:53:ASN:H	1:D:53:ASN:HD22	1.42	0.65
2:E:11:GLU:HB3	2:E:12:ASN:ND2	2.10	0.65
1:G:223:VAL:HG12	1:G:224:ARG:NH1	2.11	0.65
2:H:120:GLU:HG3	2:H:123:ARG:HH12	1.61	0.65
1:G:29:ILE:H	2:H:105:GLN:NE2	1.94	0.65
2:H:80:LEU:O	2:H:84:VAL:HG23	1.97	0.65
1:D:152:ASN:HB3	1:D:253:ALA:HB3	1.77	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:310:LYS:NZ	2:E:90:ASP:OD1	2.30	0.65
1:A:125:PHE:O	1:A:126:THR:HG23	1.96	0.65
1:D:84:TRP:CE2	1:D:116:GLY:HA2	2.31	0.65
1:G:43:VAL:C	1:G:292:LYS:NZ	2.51	0.64
2:H:21:TRP:CB	2:H:41:THR:HG23	2.27	0.64
1:G:316:LEU:HD23	2:H:52:LEU:HD13	1.78	0.64
1:G:109:ARG:NH1	1:G:267:ILE:HD13	2.12	0.64
2:B:15:GLU:O	2:B:18:ILE:HD11	1.98	0.64
1:A:84:TRP:CE2	1:A:116:GLY:HA2	2.32	0.64
1:D:43:VAL:HG23	1:D:314:LEU:HB2	1.79	0.64
2:H:169:ASN:HA	2:H:172:GLN:NE2	2.12	0.64
2:B:169:ASN:HA	2:B:172:GLN:HE21	1.63	0.64
1:A:183:HIS:HB2	1:A:252:ILE:HD11	1.78	0.64
1:G:13:LEU:HD11	2:H:24:PHE:HB3	1.80	0.63
2:B:102:LEU:HD21	2:E:102:LEU:HD23	1.79	0.63
1:D:53:ASN:HD22	1:D:53:ASN:N	1.96	0.63
1:D:55:PRO:HD3	9:D:409:HOH:O	1.97	0.63
1:A:30:THR:O	2:E:50:ARG:HD2	1.98	0.63
1:G:84:TRP:CE2	1:G:116:GLY:HA2	2.33	0.63
2:H:19:ASP:OD1	2:H:19:ASP:N	2.32	0.63
2:E:123:ARG:HH22	2:H:123:ARG:HH22	1.46	0.62
2:B:54:ARG:HA	2:B:58:LYS:NZ	2.15	0.62
1:G:220:ARG:HB3	1:G:229:ARG:HH11	1.64	0.61
1:D:180:TRP:HB3	1:D:254:PRO:HG3	1.81	0.61
1:A:189:GLN:O	1:A:193:ASN:HB2	2.00	0.61
1:G:223:VAL:CG1	1:G:224:ARG:NH1	2.63	0.61
1:D:291:ASP:O	2:E:56:ILE:HG13	1.99	0.61
1:G:316:LEU:HD23	2:H:52:LEU:CD1	2.30	0.61
2:H:11:GLU:HA	2:H:11:GLU:OE2	2.00	0.61
1:G:127:TRP:CH2	1:G:166:VAL:HG21	2.35	0.61
1:D:42:LEU:HD12	2:E:100:VAL:CG1	2.30	0.61
1:A:293:PRO:HG3	2:B:55:VAL:O	2.00	0.61
1:D:182:VAL:HG11	1:D:213:ILE:CG2	2.31	0.61
1:A:221:PRO:HG3	1:D:244:VAL:HG23	1.83	0.61
1:A:71:LEU:HD23	1:A:179:ILE:HD11	1.82	0.61
1:D:134:GLY:HA3	1:D:153:TRP:HB3	1.81	0.61
1:A:180:TRP:HB3	1:A:254:PRO:HG3	1.82	0.60
1:D:222:TRP:CD1	1:D:227:PRO:HG3	2.36	0.60
1:D:325:GLU:HG2	1:D:325:GLU:O	2.01	0.60
1:G:275:ASP:CG	1:G:276:THR:H	2.03	0.60
1:G:220:ARG:O	1:G:227:PRO:HA	2.02	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:53:ASN:O	1:D:54:ASN:HB3	2.00	0.60
1:A:291:ASP:O	2:B:56:ILE:HG13	2.01	0.60
1:G:115:SER:HA	1:G:261:ARG:O	2.01	0.59
1:D:38:ASN:OD1	1:D:318:THR:OG1	2.13	0.59
1:D:26:VAL:CG1	1:D:27:LYS:N	2.65	0.59
1:G:220:ARG:CB	1:G:229:ARG:NH1	2.64	0.59
2:H:22:TYR:O	2:H:37:ASP:N	2.35	0.59
1:G:56:HIS:O	1:G:58:ILE:HG13	2.02	0.59
2:H:26:HIS:O	2:H:32:THR:HA	2.02	0.59
1:A:216:ASN:HB3	1:D:212:THR:OG1	2.02	0.59
1:G:216:ASN:O	1:G:220:ARG:NH2	2.35	0.59
2:E:51:LYS:HE3	2:E:107:THR:OG1	2.03	0.59
1:D:201:ARG:HH11	1:D:201:ARG:HG2	1.67	0.59
2:E:37:ASP:OD2	2:E:40:SER:HB2	2.02	0.59
1:D:231:SER:HB3	1:D:233:TYR:HE1	1.66	0.59
1:D:278:ILE:HA	9:D:409:HOH:O	2.03	0.58
2:B:125:GLN:NE2	2:B:155:GLY:HA2	2.19	0.58
1:A:200:GLY:HA3	1:A:250:ASN:OD1	2.03	0.58
2:B:125:GLN:HE22	2:B:155:GLY:HA2	1.69	0.58
1:A:125:PHE:HB2	1:A:127:TRP:CD1	2.39	0.58
1:G:53:ASN:HB3	1:G:275:ASP:O	2.04	0.58
2:E:54:ARG:HA	2:E:58:LYS:NZ	2.18	0.58
1:A:170:ASN:HD22	1:A:238:LYS:C	2.07	0.58
5:D:402:NAG:H61	5:D:403:NAG:H82	1.86	0.58
2:B:25:ARG:NE	2:B:34:GLN:OE1	2.35	0.58
2:H:21:TRP:H	2:H:41:THR:CG2	2.16	0.57
1:A:129:GLY:O	1:A:157:SER:HB3	2.05	0.57
1:D:53:ASN:ND2	1:D:277:CYS:O	2.37	0.57
1:A:96:ASN:HA	1:A:224:ARG:NE	2.19	0.57
2:E:72:GLU:HG2	1:G:238:LYS:NZ	2.19	0.57
1:A:77:ASP:O	1:A:80:GLN:HG3	2.05	0.57
1:G:27:LYS:HG2	1:G:32:ASP:O	2.04	0.57
1:A:74:PRO:HA	1:A:141:ARG:HH21	1.69	0.57
2:E:17:MET:C	2:E:18:ILE:HD13	2.25	0.57
1:D:216:ASN:CG	1:G:212:THR:CG2	2.69	0.57
2:B:43:ALA:O	2:B:47:GLN:HG3	2.05	0.57
1:D:17:HIS:CD2	2:E:6:ILE:HG12	2.40	0.57
1:D:175:ASP:OD1	1:D:239:PRO:HD3	2.04	0.57
1:A:53:ASN:O	1:A:54:ASN:HB3	2.03	0.57
2:H:37:ASP:OD2	2:H:40:SER:HB3	2.05	0.56
1:A:175:ASP:OD1	1:A:239:PRO:HD3	2.04	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:97:CYS:SG	1:D:98:TYR:N	2.76	0.56
1:D:167:THR:HG23	1:D:244:VAL:HG22	1.86	0.56
1:D:222:TRP:NE1	1:D:227:PRO:HG3	2.19	0.56
1:A:137:SER:HA	1:A:145:ASN:OD1	2.06	0.56
1:A:217:ILE:HD12	1:A:217:ILE:N	2.20	0.56
2:E:12:ASN:ND2	2:E:12:ASN:N	2.51	0.56
1:D:324:PRO:O	1:D:325:GLU:CB	2.54	0.56
1:D:182:VAL:HG11	1:D:213:ILE:HG21	1.87	0.56
1:G:191:GLN:OE1	1:G:217:ILE:HD11	2.05	0.56
1:D:155:THR:HG21	8:D:406:SIA:H111	1.88	0.56
1:G:89:GLU:HG3	1:G:267:ILE:HD11	1.88	0.56
1:D:125:PHE:HD2	1:D:166:VAL:HG11	1.69	0.56
1:G:264:LYS:HB2	2:H:63:PHE:CG	2.41	0.56
1:D:220:ARG:NH1	1:G:210:GLN:HG3	2.21	0.56
1:G:39:ALA:O	3:G:400:NAG:H2	2.06	0.55
1:D:325:GLU:HB3	2:E:15:GLU:OE2	2.06	0.55
1:D:77:ASP:OD2	1:D:141:ARG:NH1	2.39	0.55
1:G:71:LEU:HD23	1:G:179:ILE:CD1	2.34	0.55
1:A:17:HIS:HA	2:B:21:TRP:O	2.06	0.55
2:B:27:GLN:HA	2:B:32:THR:HG22	1.87	0.55
2:B:131:GLU:OE2	2:B:170:ARG:HD2	2.07	0.55
2:H:123:ARG:HB2	2:H:138:PHE:CZ	2.42	0.55
1:G:220:ARG:HB3	1:G:229:ARG:NH1	2.22	0.55
2:E:132:ASP:OD2	2:H:124:ARG:NE	2.35	0.55
1:G:175:ASP:OD1	1:G:239:PRO:HD3	2.07	0.54
2:H:21:TRP:CG	2:H:41:THR:HG23	2.43	0.54
2:E:37:ASP:OD2	2:E:40:SER:CB	2.56	0.54
1:D:60:ASP:OD2	1:D:90:ARG:NH1	2.40	0.54
1:A:169:PRO:HA	1:A:242:VAL:HG23	1.90	0.54
2:E:60:ASN:HD22	2:E:60:ASN:C	2.09	0.54
1:A:152:ASN:HB3	1:A:253:ALA:HB3	1.89	0.54
2:E:144:CYS:SG	2:E:149:ILE:HD12	2.47	0.54
1:G:53:ASN:OD1	1:G:276:THR:HA	2.08	0.53
1:G:26:VAL:HG13	2:H:104:ASN:ND2	2.22	0.53
1:G:275:ASP:CG	1:G:276:THR:N	2.62	0.53
1:A:176:LYS:HD3	1:A:257:TYR:CD2	2.43	0.53
1:A:92:ASN:C	1:A:92:ASN:HD22	2.10	0.53
4:A:402:NAG:O3	4:A:402:NAG:H83	2.09	0.53
2:E:43:ALA:O	2:E:47:GLN:HG3	2.09	0.53
2:H:26:HIS:CE1	2:H:33:GLY:HA3	2.44	0.53
2:H:37:ASP:OD2	2:H:40:SER:CB	2.57	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:17:MET:O	2:E:18:ILE:HD13	2.08	0.53
1:G:167:THR:HG22	1:G:169:PRO:HD3	1.90	0.53
1:G:27:LYS:CG	1:G:32:ASP:O	2.57	0.52
1:A:281:CYS:HB2	1:A:304:ALA:O	2.10	0.52
1:G:220:ARG:HB2	1:G:227:PRO:O	2.08	0.52
1:D:184:HIS:HE2	1:D:231:SER:HB2	1.74	0.52
1:D:295:GLN:NE2	1:D:298:ASN:O	2.40	0.52
1:G:186:SER:HA	1:G:218:GLY:O	2.09	0.52
1:D:248:ASN:N	1:D:248:ASN:HD22	2.04	0.52
2:B:28:ASN:HD22	2:B:145:ASP:HA	1.75	0.52
1:D:302:TYR:HE2	2:E:63:PHE:HB3	1.75	0.52
1:A:96:ASN:ND2	1:A:96:ASN:C	2.63	0.52
1:G:108:LEU:O	1:G:112:VAL:HG23	2.10	0.52
1:A:29:ILE:H	2:B:105:GLN:NE2	2.04	0.52
1:G:43:VAL:N	9:G:419:HOH:O	2.34	0.52
1:A:81:ASN:ND2	4:A:401:NAG:C7	2.73	0.52
1:A:275:ASP:CG	1:A:276:THR:N	2.63	0.52
1:G:212:THR:O	1:G:212:THR:HG23	2.10	0.52
1:D:99:PRO:HB3	1:D:229:ARG:HE	1.75	0.52
1:G:26:VAL:CG1	2:H:104:ASN:ND2	2.73	0.52
1:A:77:ASP:HB3	1:A:80:GLN:HE21	1.75	0.52
1:A:244:VAL:HB	1:G:221:PRO:HD3	1.91	0.52
1:G:297:VAL:HA	3:G:406:NAG:C8	2.40	0.52
1:D:200:GLY:HA3	1:D:250:ASN:OD1	2.10	0.51
2:B:19:ASP:N	2:B:19:ASP:OD1	2.43	0.51
1:G:137:SER:O	1:G:140:LYS:HE3	2.10	0.51
1:G:301:THR:HB	1:G:305:CYS:SG	2.50	0.51
1:D:30:THR:O	2:H:50:ARG:HD2	2.10	0.51
2:B:27:GLN:CB	2:B:32:THR:HG22	2.40	0.51
1:A:26:VAL:HG13	2:B:104:ASN:ND2	2.26	0.51
2:B:50:ARG:HD2	1:G:30:THR:O	2.11	0.51
1:A:223:VAL:HG12	1:A:224:ARG:NH1	2.26	0.51
1:G:281:CYS:HB2	1:G:304:ALA:O	2.10	0.51
1:G:139:CYS:HB3	1:G:146:GLY:O	2.10	0.51
1:D:102:ILE:HG12	1:D:232:ILE:HB	1.93	0.51
1:A:248:ASN:N	1:A:248:ASN:HD22	1.99	0.51
1:D:84:TRP:HZ3	1:D:118:LEU:HG	1.75	0.51
1:A:65:THR:HG21	1:A:105:TYR:OH	2.11	0.51
1:G:220:ARG:HB2	1:G:229:ARG:NH1	2.24	0.51
1:G:279:SER:OG	1:G:287:SER:HB3	2.10	0.51
1:D:47:SER:HA	1:D:288:ILE:HG22	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:220:ARG:HD2	1:G:229:ARG:HD3	1.91	0.51
2:H:58:LYS:HG3	9:H:410:HOH:O	2.10	0.50
2:B:77:ILE:HG23	2:B:78:GLN:N	2.26	0.50
1:G:28:THR:HB	2:H:105:GLN:HE21	1.75	0.50
1:G:325:GLU:HG2	2:H:13:GLY:O	2.12	0.50
1:G:172:ASP:HB3	1:G:174:PHE:CE2	2.45	0.50
1:D:316:LEU:HD23	2:E:52:LEU:HD13	1.93	0.50
1:D:302:TYR:CE2	2:E:63:PHE:CD2	2.94	0.50
1:G:297:VAL:HG13	3:G:406:NAG:H81	1.92	0.50
1:D:15:LEU:CD2	2:E:119:PHE:HA	2.42	0.50
2:H:54:ARG:O	2:H:58:LYS:HE3	2.12	0.50
1:G:182:VAL:HG11	1:G:213:ILE:HG21	1.93	0.50
1:A:221:PRO:HG3	1:D:244:VAL:CG2	2.41	0.50
2:H:168:ASN:O	2:H:172:GLN:HB3	2.12	0.50
1:A:26:VAL:CG1	1:A:27:LYS:N	2.74	0.50
1:D:85:ASP:O	1:D:265:SER:HA	2.11	0.50
1:D:189:GLN:O	1:D:193:ASN:HB2	2.12	0.50
1:A:212:THR:HG21	1:G:216:ASN:HB2	1.93	0.50
1:D:29:ILE:H	2:E:105:GLN:NE2	2.08	0.50
1:A:183:HIS:O	1:A:185:PRO:HD3	2.11	0.50
2:H:46:ASP:O	2:H:50:ARG:HG3	2.11	0.50
1:A:222:TRP:CD1	1:A:227:PRO:HG3	2.47	0.50
2:E:11:GLU:HB3	2:E:12:ASN:HD22	1.75	0.49
2:B:27:GLN:HB2	2:B:32:THR:HG22	1.92	0.49
1:D:295:GLN:HB3	1:D:306:PRO:HB2	1.94	0.49
1:D:301:THR:HB	1:D:305:CYS:SG	2.52	0.49
2:E:125:GLN:NE2	2:E:155:GLY:HA2	2.26	0.49
1:D:186:SER:HB3	1:D:227:PRO:HB2	1.94	0.49
1:A:279:SER:OG	1:A:287:SER:HB3	2.12	0.49
1:A:71:LEU:HD21	1:A:179:ILE:HD11	1.92	0.49
1:G:195:TYR:O	1:G:197:GLN:N	2.45	0.49
1:A:204:VAL:CG1	1:A:243:LEU:HD11	2.42	0.49
1:D:174:PHE:HZ	1:D:257:TYR:HH	1.59	0.49
1:G:325:GLU:OE2	2:H:15:GLU:N	2.24	0.49
1:G:222:TRP:CE3	1:G:225:GLY:HA2	2.48	0.49
2:E:30:GLU:OE1	2:E:145:ASP:HB2	2.12	0.49
2:E:54:ARG:O	2:E:58:LYS:HD2	2.13	0.49
2:E:54:ARG:HA	2:E:58:LYS:HZ1	1.78	0.49
1:D:27:LYS:HE2	2:H:54:ARG:NH2	2.28	0.48
2:H:142:HIS:CE1	2:H:148:CYS:SG	3.05	0.48
1:G:13:LEU:HD13	2:H:26:HIS:HB3	1.94	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:71:LEU:HB3	1:G:148:PHE:CD2	2.48	0.48
1:G:26:VAL:CG1	1:G:27:LYS:N	2.75	0.48
1:D:109:ARG:NH1	1:D:267:ILE:HD13	2.27	0.48
1:D:221:PRO:HD3	1:G:244:VAL:HB	1.96	0.48
1:A:155:THR:HG21	6:A:409:SIA:H111	1.96	0.48
1:G:24:THR:OG1	3:G:400:NAG:C6	2.54	0.48
1:A:99:PRO:HG3	1:A:223:VAL:CG1	2.43	0.48
1:G:127:TRP:CZ3	1:G:166:VAL:HG21	2.47	0.48
2:B:11:GLU:HA	2:B:11:GLU:OE1	2.13	0.48
1:A:70:LEU:HD12	1:A:258:PHE:CE2	2.48	0.48
1:D:26:VAL:HG13	1:D:27:LYS:N	2.29	0.48
2:H:25:ARG:HG2	2:H:34:GLN:HB2	1.96	0.48
1:D:320:MET:CE	2:E:21:TRP:HB3	2.44	0.48
1:D:219:SER:HB2	1:G:165:ASN:OD1	2.14	0.48
1:A:316:LEU:HD23	2:B:52:LEU:CD1	2.44	0.48
1:A:210:GLN:HG3	1:G:220:ARG:NH1	2.28	0.48
1:A:125:PHE:HD1	1:A:127:TRP:H	1.57	0.48
1:G:26:VAL:HG12	1:G:27:LYS:N	2.28	0.48
2:H:150:GLU:HG2	3:H:400:NAG:O6	2.13	0.48
2:H:151:SER:HA	2:H:156:THR:CG2	2.35	0.48
1:D:293:PRO:HG2	2:E:55:VAL:HG12	1.96	0.48
1:D:320:MET:HB3	2:E:111:ALA:HB1	1.96	0.48
1:G:180:TRP:CE2	1:G:204:VAL:HG21	2.49	0.48
1:G:176:LYS:HE2	1:G:257:TYR:CE2	2.49	0.48
2:H:100:VAL:HG23	2:H:101:ALA:N	2.29	0.48
1:G:152:ASN:HB3	1:G:253:ALA:HB3	1.95	0.48
2:E:141:TYR:CG	2:E:170:ARG:HG2	2.49	0.48
3:G:400:NAG:H83	3:G:400:NAG:O3	2.14	0.47
1:A:71:LEU:HD21	1:A:232:ILE:HD13	1.96	0.47
1:D:220:ARG:HB2	1:D:227:PRO:O	2.14	0.47
2:B:102:LEU:HD21	2:E:102:LEU:CD2	2.43	0.47
1:D:320:MET:HE3	2:E:21:TRP:HB3	1.96	0.47
1:D:231:SER:HB3	1:D:233:TYR:CE1	2.48	0.47
1:D:67:ILE:O	1:D:70:LEU:HB3	2.14	0.47
1:A:210:GLN:HE21	1:A:210:GLN:HB3	1.53	0.47
2:B:54:ARG:O	2:B:58:LYS:HD2	2.14	0.47
2:E:131:GLU:OE2	2:E:170:ARG:HD2	2.13	0.47
2:E:3:PHE:CE1	2:E:113:SER:HB2	2.49	0.47
1:A:125:PHE:O	1:A:126:THR:CG2	2.62	0.47
1:D:183:HIS:O	1:D:185:PRO:HD3	2.15	0.47
1:A:274:ILE:CG1	1:A:274:ILE:O	2.61	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:176:LYS:HD3	1:D:257:TYR:CD2	2.50	0.47
1:D:226:GLN:NE2	8:D:406:SIA:O1B	2.48	0.47
1:G:44:GLN:N	1:G:292:LYS:NZ	2.63	0.47
2:B:168:ASN:O	2:B:172:GLN:HB3	2.14	0.47
1:D:233:TYR:CD1	1:D:233:TYR:N	2.83	0.47
2:B:141:TYR:CG	2:B:170:ARG:HG2	2.49	0.47
1:A:169:PRO:CA	1:A:242:VAL:HG23	2.45	0.47
1:D:324:PRO:O	1:D:325:GLU:HB3	2.15	0.47
1:A:249:GLY:O	1:A:250:ASN:HB2	2.14	0.47
1:A:164:LEU:N	1:A:247:SER:O	2.48	0.47
1:A:12:THR:HG23	2:B:133:MET:CE	2.44	0.47
1:G:55:PRO:HG2	1:G:280:GLU:OE1	2.15	0.47
2:H:125:GLN:NE2	2:H:155:GLY:HA2	2.30	0.47
5:A:403:NAG:O3	5:A:403:NAG:H83	2.15	0.47
1:G:221:PRO:O	1:G:229:ARG:NH2	2.48	0.47
1:G:176:LYS:HD3	1:G:257:TYR:CD2	2.50	0.47
1:A:166:VAL:HG22	1:A:245:ILE:HB	1.97	0.47
2:E:2:LEU:HB3	2:H:3:PHE:CZ	2.49	0.47
1:D:28:THR:HB	2:E:105:GLN:NE2	2.30	0.46
1:G:223:VAL:HG23	1:G:229:ARG:NH2	2.30	0.46
1:A:12:THR:HG23	2:B:133:MET:HE3	1.97	0.46
1:D:53:ASN:O	1:D:54:ASN:CB	2.55	0.46
2:H:150:GLU:HG3	3:H:400:NAG:O5	2.15	0.46
1:D:99:PRO:HG3	1:D:223:VAL:CG1	2.45	0.46
1:G:109:ARG:NH1	1:G:267:ILE:CD1	2.77	0.46
2:E:74:GLU:HG3	2:E:78:GLN:NE2	2.30	0.46
2:E:77:ILE:HG22	9:G:424:HOH:O	2.15	0.46
1:G:139:CYS:SG	1:G:147:PHE:HA	2.56	0.46
1:G:41:GLU:OE1	1:G:41:GLU:HA	2.15	0.46
1:A:222:TRP:NE1	1:A:227:PRO:HG3	2.31	0.46
1:D:133:ASN:OD1	1:D:255:ARG:NH2	2.48	0.46
1:A:74:PRO:HG3	1:A:141:ARG:NH2	2.31	0.46
2:E:125:GLN:HE22	2:E:155:GLY:HA2	1.80	0.46
2:E:26:HIS:O	2:E:32:THR:HG22	2.16	0.46
1:A:14:CYS:HA	2:B:137:CYS:HA	1.98	0.46
2:E:55:VAL:O	2:E:55:VAL:HG12	2.15	0.46
1:G:220:ARG:HD2	1:G:229:ARG:CD	2.46	0.46
1:G:15:LEU:HD22	2:H:119:PHE:HA	1.98	0.46
1:D:125:PHE:CD2	1:D:166:VAL:HG11	2.51	0.46
1:D:61:GLY:O	1:D:79:PHE:CZ	2.69	0.46
1:A:210:GLN:HG3	1:G:220:ARG:HH11	1.80	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:167:THR:HG22	1:D:242:VAL:HG22	1.96	0.46
1:A:182:VAL:HG11	1:A:213:ILE:HG21	1.97	0.46
1:A:42:LEU:O	1:A:293:PRO:HD2	2.16	0.46
5:G:402:NAG:H61	5:G:403:NAG:C7	2.46	0.46
1:A:71:LEU:HB3	1:A:148:PHE:CD2	2.51	0.45
1:D:180:TRP:HH2	1:D:213:ILE:CD1	2.28	0.45
5:G:402:NAG:H61	5:G:403:NAG:N2	2.31	0.45
1:G:285:ASN:ND2	3:G:406:NAG:C7	2.79	0.45
2:H:98:LEU:HG	2:H:102:LEU:HD22	1.97	0.45
1:G:44:GLN:O	1:G:295:GLN:HA	2.16	0.45
1:G:204:VAL:CG1	1:G:243:LEU:HD11	2.46	0.45
1:G:84:TRP:CZ2	1:G:116:GLY:HA2	2.51	0.45
2:E:77:ILE:HG23	2:E:78:GLN:N	2.31	0.45
1:G:67:ILE:O	1:G:70:LEU:N	2.50	0.45
1:G:167:THR:OG1	5:G:402:NAG:H62	2.15	0.45
1:G:129:GLY:HA3	1:G:162:PRO:HG2	1.99	0.45
1:D:54:ASN:O	1:D:55:PRO:C	2.43	0.45
1:D:123:GLU:HB3	1:D:168:MET:CE	2.47	0.45
1:A:26:VAL:CG1	2:B:104:ASN:ND2	2.79	0.45
2:E:133:MET:SD	2:E:139:LYS:HB2	2.57	0.45
1:G:99:PRO:HG3	1:G:223:VAL:CG1	2.46	0.45
1:A:80:GLN:O	1:A:81:ASN:HB2	2.17	0.45
1:A:96:ASN:HD22	1:A:96:ASN:C	2.20	0.45
1:D:30:THR:HG22	2:H:51:LYS:HB2	1.99	0.45
1:G:139:CYS:O	1:G:146:GLY:N	2.50	0.45
1:D:27:LYS:HE2	2:H:54:ARG:NH1	2.32	0.45
2:B:102:LEU:HD23	2:H:102:LEU:HD21	1.99	0.45
1:G:183:HIS:ND1	1:G:195:TYR:OH	2.36	0.45
1:D:180:TRP:CZ3	1:D:202:VAL:HG11	2.52	0.45
1:D:202:VAL:HG22	1:D:251:LEU:HB2	1.98	0.45
1:A:220:ARG:NH1	1:D:203:THR:HG21	2.32	0.45
1:A:67:ILE:HG13	1:A:105:TYR:CZ	2.52	0.45
1:A:97:CYS:SG	1:A:98:TYR:N	2.86	0.45
1:A:99:PRO:HB2	1:A:229:ARG:HD3	1.98	0.45
2:E:46:ASP:HB3	2:E:50:ARG:NH2	2.33	0.44
1:A:26:VAL:HG12	1:A:27:LYS:N	2.31	0.44
2:H:110:LEU:HD23	2:H:110:LEU:C	2.37	0.44
1:D:108:LEU:O	1:D:112:VAL:HG23	2.18	0.44
1:G:94:PHE:HE1	1:G:96:ASN:HB2	1.82	0.44
1:D:302:TYR:CD2	2:E:63:PHE:HA	2.52	0.44
1:G:82:GLU:HA	1:G:82:GLU:OE2	2.17	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:54:ARG:HD3	1:G:32:ASP:HB3	1.99	0.44
1:A:184:HIS:HB3	1:A:220:ARG:NH2	2.32	0.44
1:A:17:HIS:CE1	2:B:6:ILE:HG23	2.52	0.44
1:G:48:THR:HG23	9:G:415:HOH:O	2.18	0.44
1:D:29:ILE:O	1:D:29:ILE:HG22	2.17	0.44
1:D:90:ARG:NH2	1:D:272:ALA:O	2.50	0.44
1:G:212:THR:CG2	1:G:212:THR:O	2.64	0.44
1:A:89:GLU:OE2	1:A:109:ARG:NH1	2.50	0.44
1:G:123:GLU:HB2	1:G:256:GLY:HA2	2.00	0.44
2:H:123:ARG:HB2	2:H:138:PHE:CE2	2.53	0.44
1:G:311:GLN:HG2	1:G:311:GLN:H	1.37	0.44
1:G:184:HIS:HB3	1:G:220:ARG:NH2	2.33	0.44
9:A:417:HOH:O	1:D:212:THR:HG21	2.18	0.44
1:A:53:ASN:O	1:A:54:ASN:CB	2.63	0.44
1:G:66:LEU:HD22	1:G:267:ILE:HD12	1.99	0.43
1:A:264:LYS:HB2	2:B:63:PHE:CG	2.53	0.43
1:A:300:ILE:HD11	2:B:69:GLU:HG3	2.00	0.43
1:A:280:GLU:HA	1:A:280:GLU:OE1	2.18	0.43
1:D:53:ASN:ND2	1:D:277:CYS:H	2.16	0.43
1:A:116:GLY:HA3	1:A:265:SER:OG	2.19	0.43
1:D:11:ALA:CB	2:E:144:CYS:HB3	2.48	0.43
1:D:26:VAL:HG13	2:E:104:ASN:ND2	2.33	0.43
1:A:228:GLY:O	1:A:229:ARG:HG2	2.19	0.43
1:G:183:HIS:O	1:G:185:PRO:HD3	2.17	0.43
1:G:297:VAL:HG13	3:G:406:NAG:C8	2.48	0.43
1:A:111:LEU:HD12	1:A:111:LEU:C	2.39	0.43
1:A:89:GLU:HG3	1:A:267:ILE:HD11	2.01	0.43
1:G:300:ILE:HD11	2:H:69:GLU:HG3	2.00	0.43
1:D:17:HIS:HA	2:E:21:TRP:O	2.19	0.43
1:D:134:GLY:CA	1:D:153:TRP:HB3	2.47	0.43
2:E:72:GLU:HG2	1:G:238:LYS:HZ3	1.83	0.43
1:A:74:PRO:HG3	1:A:141:ARG:HH21	1.84	0.43
1:G:85:ASP:O	1:G:265:SER:HA	2.19	0.43
1:A:161:TYR:CE2	1:A:249:GLY:N	2.87	0.43
1:G:174:PHE:O	1:G:239:PRO:HG3	2.19	0.43
1:A:98:TYR:CD2	1:A:230:ILE:HG12	2.53	0.43
2:E:171:PHE:CE1	2:H:171:PHE:HE2	2.36	0.43
1:D:51:ILE:HA	1:D:287:SER:OG	2.18	0.43
1:A:161:TYR:CZ	1:A:249:GLY:HA2	2.54	0.43
1:G:15:LEU:HD11	2:H:122:THR:HG21	2.00	0.43
1:G:61:GLY:O	1:G:62:ARG:HB2	2.19	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:60:ASN:HD22	2:B:60:ASN:C	2.22	0.43
1:G:24:THR:HG21	1:G:39:ALA:HB3	2.01	0.43
1:D:325:GLU:CG	1:D:325:GLU:O	2.65	0.43
1:G:41:GLU:HG3	1:G:292:LYS:HZ3	1.84	0.43
1:A:130:VAL:HG13	1:A:162:PRO:HD2	2.01	0.43
1:A:311:GLN:HG2	1:A:311:GLN:H	1.37	0.43
1:A:134:GLY:HA3	1:A:153:TRP:HB3	2.00	0.43
1:D:119:GLU:HB2	1:D:259:LYS:CG	2.48	0.42
1:A:221:PRO:HD3	1:D:244:VAL:HB	2.01	0.42
1:G:84:TRP:CD1	1:G:87:PHE:HB2	2.54	0.42
1:D:28:THR:HB	2:E:105:GLN:HE21	1.85	0.42
1:D:221:PRO:HG3	1:G:244:VAL:HG23	2.00	0.42
2:H:21:TRP:H	2:H:41:THR:HG23	1.84	0.42
1:G:67:ILE:HG13	1:G:105:TYR:CE1	2.54	0.42
1:D:182:VAL:HG23	1:D:215:PRO:HG3	2.02	0.42
1:D:264:LYS:HB2	2:E:63:PHE:CG	2.54	0.42
2:B:54:ARG:HA	2:B:58:LYS:HZ1	1.82	0.42
1:D:182:VAL:CG2	1:D:215:PRO:HG3	2.49	0.42
1:G:92:ASN:HD22	1:G:92:ASN:HA	1.55	0.42
1:D:221:PRO:HG3	1:G:244:VAL:CG2	2.49	0.42
1:A:74:PRO:HA	1:A:77:ASP:OD2	2.19	0.42
1:A:275:ASP:CG	1:A:276:THR:H	2.21	0.42
1:D:27:LYS:HE2	2:H:54:ARG:CZ	2.49	0.42
1:D:26:VAL:HG22	1:D:315:LYS:HB2	2.01	0.42
1:A:42:LEU:HD22	1:A:293:PRO:HG2	2.01	0.42
1:G:297:VAL:CG1	3:G:406:NAG:H82	2.48	0.42
1:G:320:MET:HB3	2:H:111:ALA:HB1	2.01	0.42
1:D:26:VAL:HG13	1:D:27:LYS:H	1.84	0.42
1:G:223:VAL:CG1	1:G:224:ARG:HH12	2.30	0.42
1:A:74:PRO:CA	1:A:141:ARG:HH21	2.33	0.42
1:D:89:GLU:OE2	1:D:109:ARG:NH1	2.52	0.42
1:D:132:GLN:HG2	1:D:154:LEU:CD2	2.50	0.42
1:A:71:LEU:O	1:A:148:PHE:HB3	2.20	0.42
2:H:11:GLU:OE2	2:H:11:GLU:CA	2.68	0.42
2:E:2:LEU:HB3	2:H:3:PHE:HZ	1.85	0.42
2:H:16:GLY:O	2:H:18:ILE:HG13	2.19	0.42
1:A:288:ILE:HG21	1:A:297:VAL:HG21	2.01	0.42
1:A:92:ASN:C	1:A:92:ASN:ND2	2.73	0.42
1:D:316:LEU:HD23	2:E:52:LEU:CD1	2.49	0.42
1:A:67:ILE:HG13	1:A:105:TYR:CE1	2.55	0.42
1:D:120:PHE:CD2	1:D:150:ARG:HD2	2.54	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:324:PRO:O	1:A:325:GLU:CB	2.67	0.42
2:B:18:ILE:O	2:B:18:ILE:HG22	2.19	0.42
1:A:290:ASN:HD22	1:A:290:ASN:C	2.23	0.42
1:A:134:GLY:CA	1:A:153:TRP:HB3	2.51	0.41
1:G:221:PRO:O	1:G:229:ARG:NH1	2.54	0.41
1:G:99:PRO:HG3	1:G:223:VAL:HB	2.02	0.41
1:A:216:ASN:CB	1:D:212:THR:OG1	2.67	0.41
1:A:172:ASP:HB3	1:A:174:PHE:CE2	2.54	0.41
1:A:202:VAL:HG22	1:A:251:LEU:HB2	2.02	0.41
2:E:18:ILE:O	2:E:18:ILE:HG22	2.19	0.41
1:G:297:VAL:HG12	3:G:406:NAG:H82	2.02	0.41
2:H:125:GLN:HE22	2:H:155:GLY:HA2	1.84	0.41
1:A:132:GLN:HG2	1:A:154:LEU:CD2	2.50	0.41
2:E:53:ASN:HA	2:E:56:ILE:CG2	2.51	0.41
1:G:279:SER:CB	1:G:287:SER:HB3	2.50	0.41
1:D:71:LEU:HB3	1:D:148:PHE:CD2	2.56	0.41
2:E:70:PHE:CD1	2:E:70:PHE:N	2.89	0.41
1:G:43:VAL:C	1:G:292:LYS:HZ2	2.19	0.41
1:D:42:LEU:CD1	2:E:100:VAL:CG1	2.99	0.41
2:B:27:GLN:CA	2:B:32:THR:HG22	2.49	0.41
1:D:115:SER:HA	1:D:261:ARG:O	2.20	0.41
1:G:182:VAL:HG11	1:G:213:ILE:CG2	2.50	0.41
1:D:311:GLN:HE22	2:E:97:GLU:HB2	1.86	0.41
1:G:222:TRP:NE1	1:G:227:PRO:HG3	2.36	0.41
2:E:9:PHE:C	2:E:9:PHE:CD1	2.94	0.41
1:G:290:ASN:C	1:G:290:ASN:HD22	2.23	0.41
1:A:111:LEU:HD12	1:A:112:VAL:N	2.36	0.41
1:G:51:ILE:CD1	1:G:272:ALA:HB3	2.51	0.41
2:E:110:LEU:HD23	2:E:110:LEU:C	2.41	0.41
1:G:24:THR:HG21	3:G:400:NAG:O6	2.20	0.41
1:D:216:ASN:OD1	1:G:212:THR:CG2	2.69	0.41
1:G:325:GLU:H	1:G:325:GLU:HG3	1.64	0.41
2:B:121:LYS:HB3	2:B:121:LYS:HE3	1.84	0.41
1:G:44:GLN:HG2	9:G:411:HOH:O	2.21	0.41
2:B:53:ASN:HA	2:B:56:ILE:CG2	2.51	0.41
1:G:284:PRO:HG2	1:G:300:ILE:HB	2.03	0.41
1:A:167:THR:CG2	1:A:242:VAL:HG21	2.51	0.40
1:G:28:THR:HG21	2:H:108:ILE:HD12	2.03	0.40
1:G:99:PRO:HB3	1:G:229:ARG:HE	1.85	0.40
2:H:131:GLU:OE2	2:H:170:ARG:CD	2.67	0.40
1:A:54:ASN:O	1:A:278:ILE:HA	2.22	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:226:GLN:HA	1:A:227:PRO:HD3	1.77	0.40
1:D:109:ARG:NH1	1:D:267:ILE:CD1	2.85	0.40
2:B:127:ARG:HB3	2:B:128:GLU:H	1.67	0.40
1:D:226:GLN:HA	1:D:227:PRO:HD3	1.86	0.40
2:H:145:ASP:O	2:H:148:CYS:N	2.55	0.40
1:A:125:PHE:HD1	1:A:127:TRP:CD1	2.38	0.40
1:A:185:PRO:HG2	1:A:191:GLN:OE1	2.20	0.40
1:A:184:HIS:HB3	1:A:220:ARG:HH21	1.86	0.40
1:A:54:ASN:HA	9:A:422:HOH:O	2.21	0.40
1:D:248:ASN:ND2	1:D:248:ASN:H	2.15	0.40
2:B:51:LYS:NZ	2:B:106:HIS:ND1	2.59	0.40
1:A:59:LEU:CD1	1:A:82:GLU:HG2	2.51	0.40
1:G:30:THR:H	2:H:105:GLN:HE22	1.68	0.40
2:H:148:CYS:O	2:H:152:ILE:HG13	2.21	0.40
1:D:84:TRP:CZ2	1:D:116:GLY:HA2	2.57	0.40
1:D:202:VAL:HA	1:D:247:SER:HB2	2.02	0.40
1:G:264:LYS:HB2	2:H:63:PHE:CD1	2.57	0.40
1:A:65:THR:HG23	1:A:89:GLU:OE1	2.20	0.40
1:A:216:ASN:O	1:A:220:ARG:NH2	2.55	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	316/329 (96%)	282 (89%)	29 (9%)	5 (2%)	12	54
1	D	316/329 (96%)	289 (92%)	23 (7%)	4 (1%)	15	59
1	G	316/329 (96%)	292 (92%)	20 (6%)	4 (1%)	15	59
2	B	170/221 (77%)	155 (91%)	15 (9%)	0	100	100
2	E	170/221 (77%)	155 (91%)	14 (8%)	1 (1%)	30	75

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	H	170/221 (77%)	153 (90%)	17 (10%)	0	100	100
All	All	1458/1650 (88%)	1326 (91%)	118 (8%)	14 (1%)	19	65

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	55	PRO
1	A	324	PRO
1	A	325	GLU
1	D	324	PRO
1	D	325	GLU
1	G	10	THR
1	A	126	THR
1	D	62	ARG
1	G	21	PRO
1	G	62	ARG
1	G	104	ASP
1	D	54	ASN
2	E	57	GLU
1	A	21	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	268/288 (93%)	249 (93%)	19 (7%)	18	57
1	D	270/288 (94%)	241 (89%)	29 (11%)	8	34
1	G	268/288 (93%)	234 (87%)	34 (13%)	5	25
2	B	145/190 (76%)	135 (93%)	10 (7%)	19	59
2	E	146/190 (77%)	133 (91%)	13 (9%)	12	44
2	H	147/190 (77%)	137 (93%)	10 (7%)	20	59
All	All	1244/1434 (87%)	1129 (91%)	115 (9%)	11	41

All (115) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	HIS
1	A	44	GLN
1	A	46	SER
1	A	54	ASN
1	A	74	PRO
1	A	92	ASN
1	A	96	ASN
1	A	101	ASP
1	A	155	THR
1	A	179	ILE
1	A	182	VAL
1	A	210	GLN
1	A	248	ASN
1	A	261	ARG
1	A	268	MET
1	A	274	ILE
1	A	280	GLU
1	A	290	ASN
1	A	311	GLN
2	B	27	GLN
2	B	60	ASN
2	B	64	HIS
2	B	72	GLU
2	B	91	LEU
2	B	102	LEU
2	B	120	GLU
2	B	121	LYS
2	B	149	ILE
2	B	168	ASN
1	D	18	HIS
1	D	38	ASN
1	D	41	GLU
1	D	45	SER
1	D	46	SER
1	D	48	THR
1	D	53	ASN
1	D	74	PRO
1	D	90	ARG
1	D	92	ASN
1	D	96	ASN
1	D	99	PRO
1	D	101	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	167	THR
1	D	169	PRO
1	D	182	VAL
1	D	210	GLN
1	D	215	PRO
1	D	221	PRO
1	D	230	ILE
1	D	231	SER
1	D	239	PRO
1	D	248	ASN
1	D	261	ARG
1	D	273	PRO
1	D	306	PRO
1	D	311	GLN
1	D	313	THR
1	D	324	PRO
2	E	9	PHE
2	E	12	ASN
2	E	19	ASP
2	E	27	GLN
2	E	49	ASN
2	E	60	ASN
2	E	64	HIS
2	E	72	GLU
2	E	91	LEU
2	E	120	GLU
2	E	121	LYS
2	E	149	ILE
2	E	168	ASN
1	G	10	THR
1	G	18	HIS
1	G	20	VAL
1	G	29	ILE
1	G	38	ASN
1	G	44	GLN
1	G	46	SER
1	G	74	PRO
1	G	92	ASN
1	G	96	ASN
1	G	109	ARG
1	G	111	LEU
1	G	155	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	G	161	TYR
1	G	162	PRO
1	G	179	ILE
1	G	182	VAL
1	G	185	PRO
1	G	210	GLN
1	G	221	PRO
1	G	229	ARG
1	G	230	ILE
1	G	239	PRO
1	G	248	ASN
1	G	261	ARG
1	G	268	MET
1	G	273	PRO
1	G	290	ASN
1	G	292	LYS
1	G	307	LYS
1	G	311	GLN
1	G	315	LYS
1	G	324	PRO
1	G	325	GLU
2	H	18	ILE
2	H	19	ASP
2	H	57	GLU
2	H	60	ASN
2	H	72	GLU
2	H	102	LEU
2	H	120	GLU
2	H	121	LYS
2	H	149	ILE
2	H	156	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (50) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	HIS
1	A	92	ASN
1	A	96	ASN
1	A	171	ASN
1	A	210	GLN
1	A	211	GLN
1	A	216	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	248	ASN
1	A	290	ASN
1	A	296	ASN
2	B	27	GLN
2	B	60	ASN
2	B	105	GLN
2	B	168	ASN
2	B	172	GLN
1	D	18	HIS
1	D	53	ASN
1	D	54	ASN
1	D	92	ASN
1	D	96	ASN
1	D	171	ASN
1	D	210	GLN
1	D	226	GLN
1	D	248	ASN
1	D	296	ASN
1	D	311	GLN
2	E	12	ASN
2	E	26	HIS
2	E	27	GLN
2	E	53	ASN
2	E	60	ASN
2	E	105	GLN
2	E	125	GLN
2	E	168	ASN
2	E	172	GLN
1	G	92	ASN
1	G	96	ASN
1	G	171	ASN
1	G	211	GLN
1	G	248	ASN
1	G	290	ASN
1	G	296	ASN
2	H	12	ASN
2	H	26	HIS
2	H	27	GLN
2	H	60	ASN
2	H	105	GLN
2	H	142	HIS
2	H	168	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	H	172	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

18 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$
4	NAG	A	401	1,4	14,14,15	0.60	0	15,19,21	0.66	0
4	NAG	A	402	4	14,14,15	0.69	0	15,19,21	0.69	0
5	NAG	A	403	1,5	14,14,15	0.48	0	15,19,21	0.90	1 (6%)
5	NAG	A	404	5	14,14,15	0.58	0	15,19,21	0.72	1 (6%)
5	BMA	A	405	5	11,11,12	0.79	0	14,15,17	1.36	1 (7%)
5	MAN	A	406	5	11,11,12	0.57	0	14,15,17	0.66	1 (7%)
4	NAG	A	407	1,4	14,14,15	0.99	1 (7%)	15,19,21	1.38	3 (20%)
4	NAG	A	408	4	14,14,15	0.54	0	15,19,21	0.90	1 (6%)
5	NAG	D	402	1,5	14,14,15	0.64	0	15,19,21	0.72	0
5	NAG	D	403	5	14,14,15	0.73	0	15,19,21	0.78	0
5	BMA	D	404	5	11,11,12	0.51	0	14,15,17	1.58	3 (21%)
5	MAN	D	405	5	11,11,12	0.63	0	14,15,17	0.75	0
8	SIA	D	406	8	16,20,21	0.62	0	18,28,31	0.78	1 (5%)
8	GAL	D	407	8	12,12,12	0.73	1 (8%)	17,17,17	0.97	1 (5%)
5	NAG	G	402	1,5	14,14,15	0.45	0	15,19,21	0.74	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	G	403	5	14,14,15	0.51	0	15,19,21	1.18	1 (6%)
5	BMA	G	404	5	11,11,12	0.77	0	14,15,17	1.29	1 (7%)
5	MAN	G	405	5	11,11,12	1.14	1 (9%)	14,15,17	1.26	2 (14%)

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	A	401	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	402	4	-	1/6/23/26	0/1/1/1
5	NAG	A	403	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	404	5	-	0/6/23/26	0/1/1/1
5	BMA	A	405	5	-	0/2/19/22	0/1/1/1
5	MAN	A	406	5	-	0/2/19/22	0/1/1/1
4	NAG	A	407	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	408	4	-	0/6/23/26	0/1/1/1
5	NAG	D	402	1,5	-	0/6/23/26	0/1/1/1
5	NAG	D	403	5	-	0/6/23/26	0/1/1/1
5	BMA	D	404	5	-	0/2/19/22	0/1/1/1
5	MAN	D	405	5	-	0/2/19/22	0/1/1/1
8	SIA	D	406	8	-	0/14/34/38	0/1/1/1
8	GAL	D	407	8	-	0/2/22/22	0/1/1/1
5	NAG	G	402	1,5	-	0/6/23/26	0/1/1/1
5	NAG	G	403	5	-	0/6/23/26	0/1/1/1
5	BMA	G	404	5	-	0/2/19/22	0/1/1/1
5	MAN	G	405	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)
8	D	407	GAL	O1-C1	-2.33	1.31	1.39
5	G	405	MAN	O5-C5	2.50	1.48	1.43
4	A	407	NAG	C1-C2	2.76	1.56	1.52

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	G	403	NAG	C2-N2-C7	-3.30	118.80	123.04
4	A	407	NAG	C4-C3-C2	-3.18	106.29	111.23

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	404	BMA	C1-C2-C3	-2.96	106.04	109.54
5	A	403	NAG	C2-N2-C7	-2.90	119.31	123.04
5	G	404	BMA	C2-C3-C4	-2.72	106.43	111.04
4	A	408	NAG	C2-N2-C7	-2.37	119.99	123.04
4	A	407	NAG	C2-N2-C7	-2.31	120.07	123.04
5	A	404	NAG	C2-N2-C7	-2.08	120.37	123.04
8	D	406	SIA	C8-C7-C6	-2.03	108.92	113.01
5	A	406	MAN	C1-O5-C5	2.05	114.85	112.25
4	A	407	NAG	O4-C4-C3	2.05	114.96	110.34
5	D	404	BMA	C2-C3-C4	2.20	114.78	111.04
8	D	407	GAL	O1-C1-C2	2.27	115.29	109.21
5	G	405	MAN	O2-C2-C1	2.44	114.10	109.21
5	D	404	BMA	O3-C3-C2	2.50	114.51	110.00
5	G	405	MAN	C2-C3-C4	2.80	115.81	111.04
5	A	405	BMA	C3-C4-C5	3.97	117.11	110.20

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	402	NAG	O7-C7-N2-C2

There are no ring outliers.

8 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	401	NAG	1	0
4	A	402	NAG	1	0
5	A	403	NAG	2	0
5	D	402	NAG	1	0
5	D	403	NAG	1	0
8	D	406	SIA	2	0
5	G	402	NAG	3	0
5	G	403	NAG	2	0

5.6 Ligand geometry ⓘ

11 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	400	1	14,14,15	0.71	0	15,19,21	0.82	1 (6%)
6	SIA	A	409	7	16,20,21	0.62	0	18,28,31	0.78	1 (5%)
7	GAL	A	410	6	12,12,12	0.72	1 (8%)	17,17,17	0.96	1 (5%)
3	NAG	B	400	2	14,14,15	0.65	0	15,19,21	1.01	1 (6%)
3	NAG	D	400	1	14,14,15	1.10	1 (7%)	15,19,21	1.61	3 (20%)
3	NAG	D	401	1	14,14,15	0.87	0	15,19,21	1.29	2 (13%)
3	NAG	E	400	2	14,14,15	0.59	0	15,19,21	0.75	1 (6%)
3	NAG	G	400	1	14,14,15	1.21	1 (7%)	15,19,21	2.63	4 (26%)
3	NAG	G	401	1	14,14,15	0.74	0	15,19,21	1.44	2 (13%)
3	NAG	G	406	1	14,14,15	0.81	1 (7%)	15,19,21	1.19	1 (6%)
3	NAG	H	400	2	14,14,15	1.35	3 (21%)	15,19,21	1.27	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	400	1	-	0/6/23/26	0/1/1/1
6	SIA	A	409	7	-	0/14/34/38	0/1/1/1
7	GAL	A	410	6	-	0/2/22/22	0/1/1/1
3	NAG	B	400	2	-	0/6/23/26	0/1/1/1
3	NAG	D	400	1	-	0/6/23/26	0/1/1/1
3	NAG	D	401	1	-	0/6/23/26	0/1/1/1
3	NAG	E	400	2	-	0/6/23/26	0/1/1/1
3	NAG	G	400	1	-	0/6/23/26	0/1/1/1
3	NAG	G	401	1	-	0/6/23/26	0/1/1/1
3	NAG	G	406	1	-	0/6/23/26	0/1/1/1
3	NAG	H	400	2	-	0/6/23/26	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	410	GAL	O1-C1	-2.31	1.31	1.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	406	NAG	O5-C5	2.00	1.47	1.43
3	H	400	NAG	C4-C5	2.20	1.57	1.53
3	H	400	NAG	C8-C7	2.43	1.55	1.50
3	D	400	NAG	O5-C5	2.70	1.49	1.43
3	G	400	NAG	C1-C2	2.89	1.56	1.52
3	H	400	NAG	C1-C2	3.41	1.57	1.52

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	400	NAG	C6-C5-C4	-5.79	98.73	113.02
3	G	400	NAG	C2-N2-C7	-4.44	117.33	123.04
3	G	401	NAG	C2-N2-C7	-4.34	117.47	123.04
3	G	400	NAG	C4-C3-C2	-3.54	105.72	111.23
3	D	400	NAG	C1-O5-C5	-3.37	107.97	112.25
3	B	400	NAG	C2-N2-C7	-3.25	118.86	123.04
3	G	406	NAG	C3-C4-C5	-3.21	104.61	110.20
3	D	400	NAG	C2-N2-C7	-2.84	119.39	123.04
3	A	400	NAG	C2-N2-C7	-2.54	119.78	123.04
3	H	400	NAG	O7-C7-C8	-2.27	117.90	122.06
3	E	400	NAG	C2-N2-C7	-2.24	120.16	123.04
3	D	401	NAG	C3-C4-C5	-2.19	106.38	110.20
6	A	409	SIA	C8-C7-C6	-2.05	108.88	113.01
7	A	410	GAL	O1-C1-C2	2.26	115.26	109.21
3	G	401	NAG	C1-O5-C5	2.68	115.65	112.25
3	D	401	NAG	O7-C7-N2	2.69	127.34	121.86
3	H	400	NAG	C8-C7-N2	2.76	121.39	116.11
3	D	400	NAG	O5-C5-C6	3.10	114.07	107.35
3	G	400	NAG	C1-O5-C5	4.53	117.99	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	409	SIA	1	0
3	G	400	NAG	5	0
3	G	406	NAG	6	0
3	H	400	NAG	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 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	318/329 (96%)	-0.01	5 (1%) 74 62	23, 41, 61, 79	0
1	D	318/329 (96%)	-0.13	3 (0%) 85 78	13, 35, 54, 77	0
1	G	318/329 (96%)	0.00	8 (2%) 61 47	19, 38, 59, 93	0
2	B	172/221 (77%)	-0.25	2 (1%) 81 69	10, 37, 57, 85	0
2	E	172/221 (77%)	-0.02	4 (2%) 64 49	16, 40, 64, 82	0
2	H	172/221 (77%)	-0.02	2 (1%) 81 69	15, 39, 61, 84	0
All	All	1470/1650 (89%)	-0.06	24 (1%) 74 62	10, 38, 60, 93	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	143	PRO	3.5
2	E	57	GLU	3.1
2	H	29	SER	3.1
1	A	144	ALA	2.8
1	G	46	SER	2.8
1	G	277	CYS	2.8
1	G	275	ASP	2.7
1	G	272	ALA	2.6
1	D	326	LYS	2.6
2	H	148	CYS	2.5
1	G	276	THR	2.4
1	G	287	SER	2.4
1	D	171	ASN	2.4
2	E	168	ASN	2.3
1	D	128	THR	2.3
1	A	46	SER	2.3
1	G	324	PRO	2.2
1	A	169	PRO	2.2
1	A	239	PRO	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	E	29	SER	2.2
2	B	172	GLN	2.1
1	G	173	ASN	2.1
2	E	172	GLN	2.1
2	B	64	HIS	2.1

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](#)

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(\AA^2)	Q<0.9
4	NAG	A	407	14/15	0.90	0.46	3.30	76,81,90,93	0
4	NAG	A	401	14/15	0.79	0.33	2.18	87,92,98,99	0
5	NAG	D	402	14/15	0.92	0.32	2.12	49,53,57,59	0
8	SIA	D	406	20/21	0.92	0.28	1.80	40,45,53,55	0
5	NAG	G	402	14/15	0.93	0.27	1.07	28,31,36,38	0
5	NAG	A	404	14/15	0.93	0.36	0.75	61,63,68,74	0
5	NAG	A	403	14/15	0.87	0.29	0.44	52,55,58,61	0
5	NAG	D	403	14/15	0.92	0.26	0.40	60,62,64,71	0
5	MAN	A	406	11/12	0.69	0.51	-	93,95,97,97	0
5	BMA	G	404	11/12	0.83	0.31	-	62,66,70,77	0
5	BMA	D	404	11/12	0.87	0.32	-	78,81,83,88	0
4	NAG	A	408	14/15	0.58	0.49	-	100,104,106,107	0
8	GAL	D	407	12/12	0.84	0.47	-	59,78,81,82	0
4	NAG	A	402	14/15	0.55	0.58	-	103,105,107,107	0
5	BMA	A	405	11/12	0.82	0.36	-	77,80,83,89	0
5	MAN	G	405	11/12	0.81	0.38	-	84,87,88,88	0
5	NAG	G	403	14/15	0.95	0.19	-	38,42,45,53	0
5	MAN	D	405	11/12	0.65	0.39	-	92,96,99,99	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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	NAG	E	400	14/15	0.75	0.71	10.08	88,93,95,96	0
3	NAG	G	400	14/15	0.53	0.52	6.89	90,97,99,101	0
3	NAG	B	400	14/15	0.85	0.59	5.09	77,82,83,83	0
3	NAG	G	406	14/15	0.73	0.45	4.78	75,79,83,84	0
3	NAG	G	401	14/15	0.78	0.34	3.89	64,68,70,72	0
3	NAG	H	400	14/15	0.78	0.54	3.05	86,89,90,92	0
3	NAG	D	401	14/15	0.74	0.45	2.58	82,88,92,93	0
6	SIA	A	409	20/21	0.89	0.28	1.08	53,56,64,64	0
3	NAG	D	400	14/15	0.81	0.27	0.93	71,74,77,78	0
3	NAG	A	400	14/15	0.77	0.48	-	74,79,83,83	0
7	GAL	A	410	12/12	0.83	0.37	-	65,82,83,84	0

6.5 Other polymers [i](#)

There are no such residues in this entry.