Full wwPDB X-ray Structure Validation Report ⓘ

Apr 27, 2016 – 10:49 AM EDT

PDB ID	:	5I9Q
Title	:	Crystal structure of 3BNC55 Fab in complex with 426c.TM4deltaV1-3 gp120
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Deposited on	:	2016-02-20
Resolution	:	3.00 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:

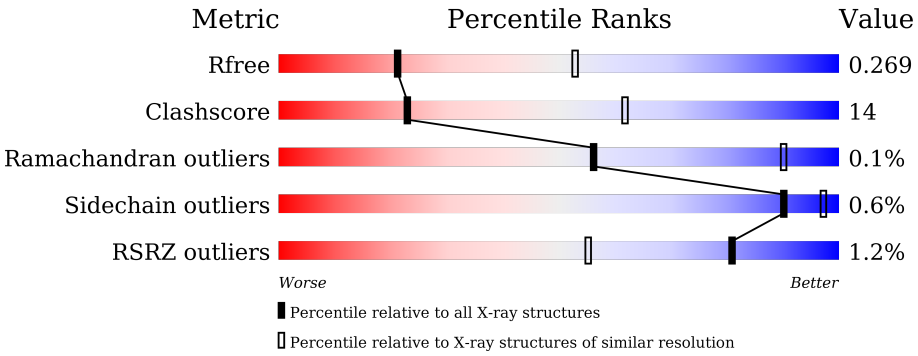
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20027457
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027457

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 3.00 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	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

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 <=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	353	2% 77% 18%
1	G	353	80% 16%
2	B	225	64% 25% 10%
2	H	225	78% 16% 5%
3	C	207	63% 36%
3	L	207	78% 21%

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
4	NAG	A	602	-	-	-	X
4	NAG	A	608	-	-	-	X
4	NAG	G	602	-	-	-	X
4	NAG	G	607	-	-	-	X
5	EDO	A	606	-	-	-	X
5	EDO	G	605	-	-	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 11445 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 426c.TM4dV1-3 p120.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	340	Total	C	N	O	S	0	0	0
			2497	1564	429	482	22			
1	G	339	Total	C	N	O	S	0	0	0
			2535	1594	435	484	22			

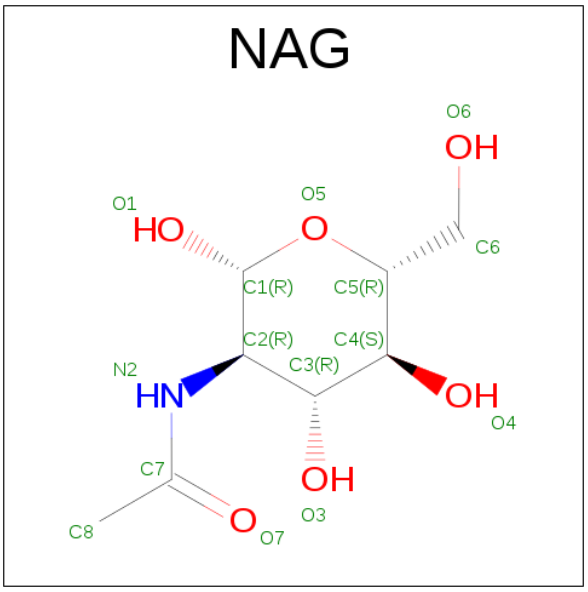
- Molecule 2 is a protein called 3BNC55 Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	202	Total	C	N	O	S	0	0	0
			1497	954	251	285	7			
2	H	213	Total	C	N	O	S	0	0	0
			1630	1037	272	314	7			

- Molecule 3 is a protein called 3BNC55 light chain.

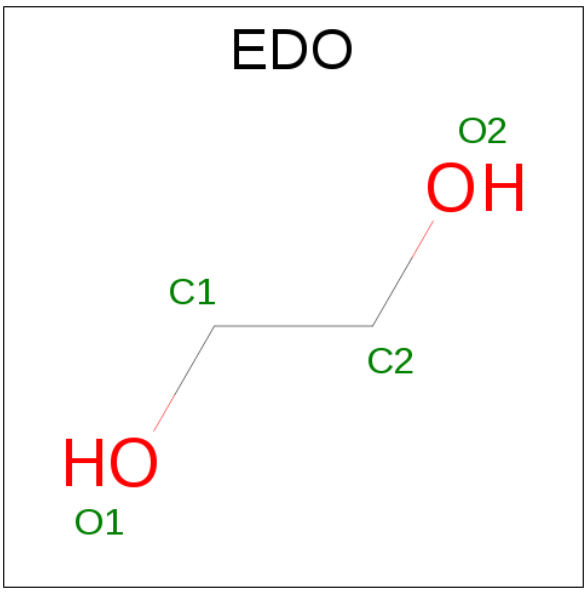
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	206	Total	C	N	O	S	0	0	0
			1442	908	233	295	6			
3	L	206	Total	C	N	O	S	0	0	0
			1560	975	264	315	6			

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



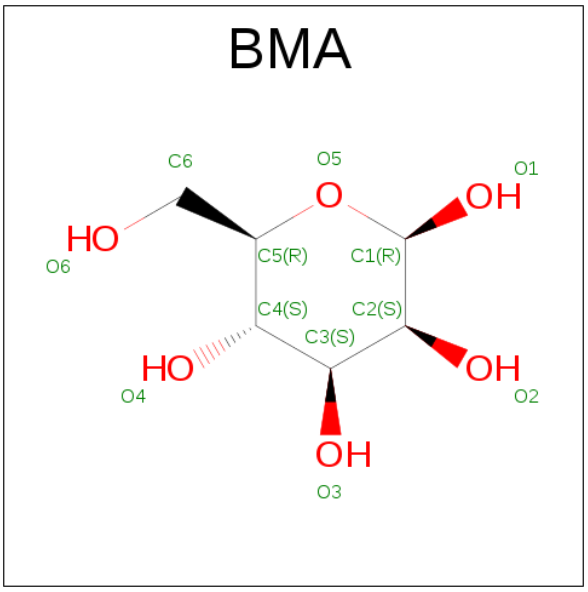
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N O 14 8 1 5	0	0
4	A	1	Total C N O 14 8 1 5	0	0
4	A	1	Total C N O 14 8 1 5	0	0
4	A	1	Total C N O 14 8 1 5	0	0
4	A	1	Total C N O 14 8 1 5	0	0
4	A	1	Total C N O 14 8 1 5	0	0
4	A	1	Total C N O 14 8 1 5	0	0
4	G	1	Total C N O 14 8 1 5	0	0
4	G	1	Total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

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



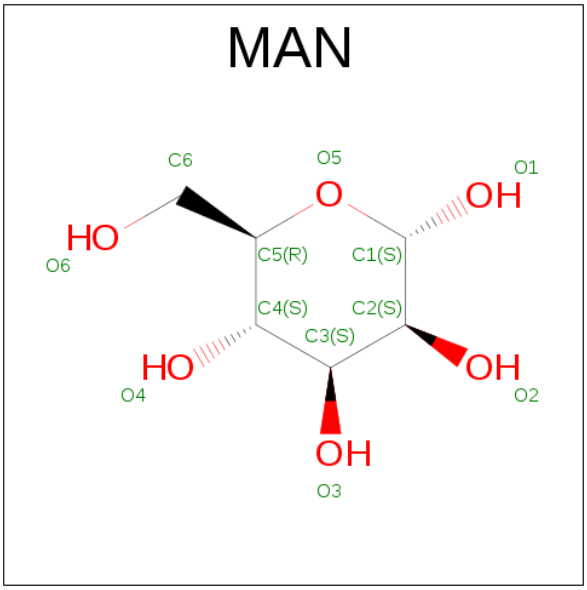
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	G	1	Total C O 4 2 2	0	0

- Molecule 6 is BETA-D-MANNOSE (three-letter code: BMA) (formula: $C_6H_{12}O_6$).



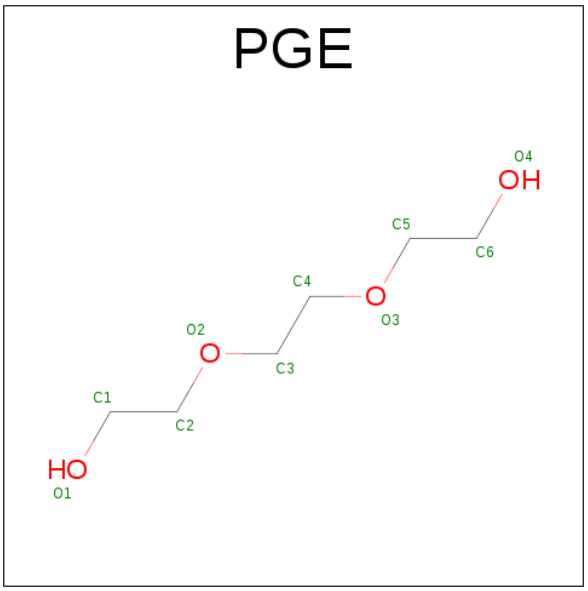
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 11 6 5	0	0
6	G	1	Total C O 11 6 5	0	0

- Molecule 7 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula: $C_6H_{12}O_6$).



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

- Molecule 8 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



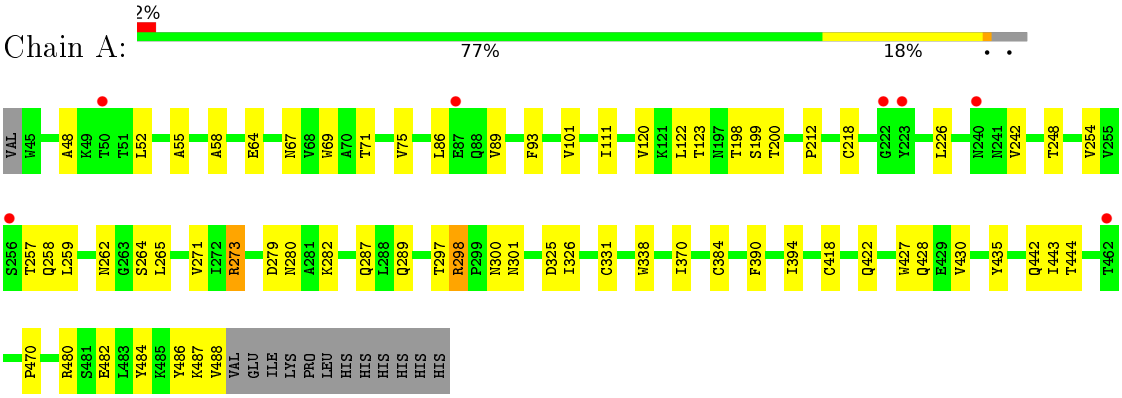
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	G	1	Total C O 10 6 4	0	0

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 (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.

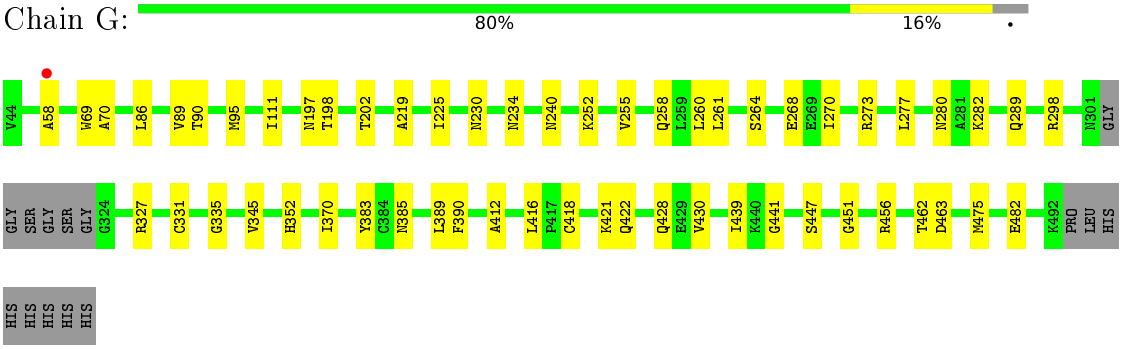
- Molecule 1: 426c.TM4dV1-3 p120

Chain A:



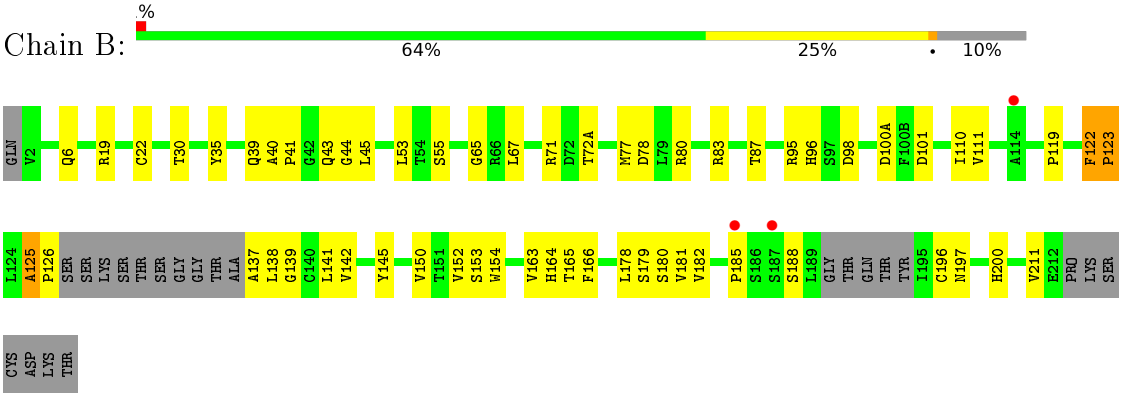
- Molecule 1: 426c.TM4dV1-3 p120

Chain G:



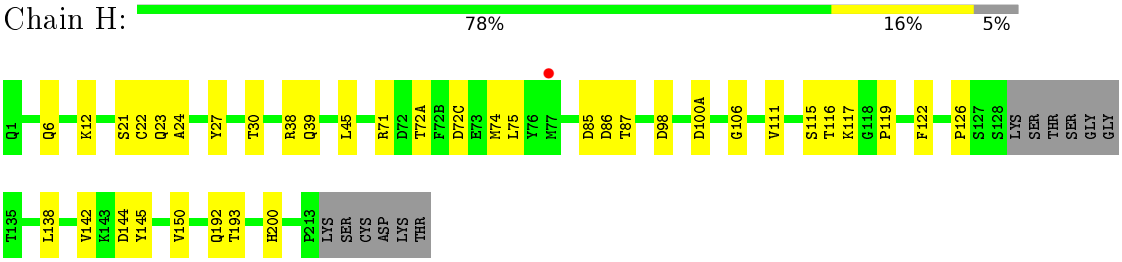
- Molecule 2: 3BNC55 Fab heavy chain

Chain B:



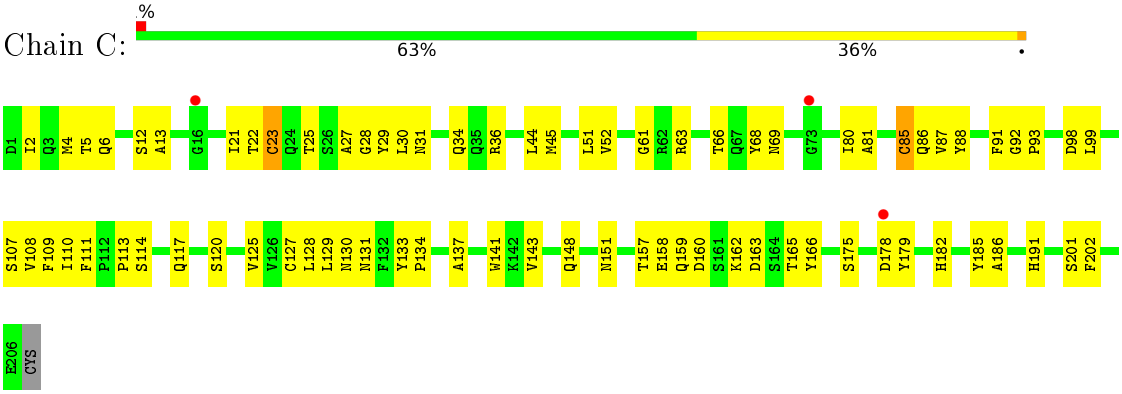
• Molecule 2: 3BNC55 Fab heavy chain

Chain H:



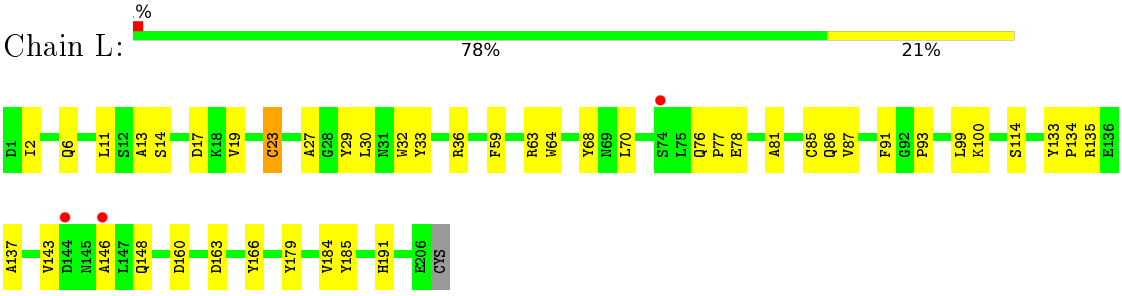
• Molecule 3: 3BNC55 light chain

Chain C:



• Molecule 3: 3BNC55 light chain

Chain L:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	122.85Å 122.85Å 264.96Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	37.54 – 3.00 39.76 – 2.80	Depositor EDS
% Data completeness (in resolution range)	80.4 (37.54-3.00) 70.1 (39.76-2.80)	Depositor EDS
R_{merge}	0.56	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.17 (at 2.81Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.251 , 0.270 0.248 , 0.269	Depositor DCC
R_{free} test set	1898 reflections (5.01%)	DCC
Wilson B-factor (Å^2)	77.5	Xtriage
Anisotropy	0.132	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 48.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.025 for -h,-k,l	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	11445	wwPDB-VP
Average B, all atoms (Å^2)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.78% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: PGE, EDO, NAG, BMA, 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	0.30	0/2550	0.48	1/3486 (0.0%)
1	G	0.29	0/2587	0.48	1/3532 (0.0%)
2	B	0.34	0/1539	0.59	2/2110 (0.1%)
2	H	0.28	0/1676	0.49	0/2292
3	C	0.44	0/1474	0.61	0/2024
3	L	0.31	0/1595	0.51	0/2178
All	All	0.32	0/11421	0.52	4/15622 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	298	ARG	N-CA-C	-5.65	95.74	111.00
2	B	122	PHE	C-N-CD	5.42	139.77	128.40
2	B	125	ALA	C-N-CD	5.21	139.35	128.40
1	G	252	LYS	C-N-CD	5.15	139.22	128.40

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	2497	0	2286	58	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	2535	0	2375	37	0
2	B	1497	0	1366	58	0
2	H	1630	0	1556	32	0
3	C	1442	0	1263	94	0
3	L	1560	0	1452	34	0
4	A	98	0	89	6	0
4	C	14	0	13	0	0
4	G	70	0	63	6	0
4	L	14	0	13	0	0
5	A	8	0	12	1	0
5	G	4	0	6	0	0
6	A	11	0	8	0	0
6	G	11	0	9	0	0
7	A	33	0	29	0	0
7	G	11	0	10	0	0
8	G	10	0	14	0	0
All	All	11445	0	10564	298	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 14.

All (298) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:ARG:NH1	1:A:484:TYR:CE1	1.99	1.27
1:A:273:ARG:NH1	1:A:484:TYR:CD1	2.02	1.26
2:B:138:LEU:O	2:B:181:VAL:HB	1.50	1.10
1:A:212:PRO:HG2	4:A:608:NAG:O7	1.51	1.09
1:A:297:THR:HG23	1:A:444:THR:HG22	1.39	1.04
1:A:248:THR:HG22	1:A:486:TYR:CE2	1.94	1.02
1:A:248:THR:HG22	1:A:486:TYR:CD2	1.97	0.99
3:C:23:CYS:SG	3:C:30:LEU:HD11	2.05	0.96
1:A:248:THR:CG2	1:A:486:TYR:CD2	2.48	0.95
2:B:126:PRO:HB3	2:B:137:ALA:O	1.68	0.92
1:A:212:PRO:CG	4:A:608:NAG:O7	2.18	0.91
3:C:179:TYR:CE1	3:C:185:TYR:CE1	2.59	0.89
3:C:179:TYR:HE1	3:C:185:TYR:CE1	1.90	0.88
1:A:297:THR:HG23	1:A:444:THR:CG2	2.06	0.85
2:B:19:ARG:NE	2:B:78:ASP:OD1	2.11	0.84
1:A:248:THR:CG2	1:A:486:TYR:CE2	2.60	0.83
1:A:297:THR:CG2	1:A:444:THR:HG22	2.09	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:175:SER:OG	3:C:178:ASP:OD2	1.98	0.81
1:G:430:VAL:CG1	2:H:72(A):THR:HG21	2.12	0.79
1:A:273:ARG:NH2	1:A:287:GLN:OE1	2.16	0.79
3:C:98:ASP:CB	3:C:159:GLN:NE2	2.46	0.77
1:A:248:THR:HG21	1:A:486:TYR:CD2	2.19	0.77
3:L:14:SER:OG	3:L:17:ASP:OD2	2.04	0.76
1:G:280:ASN:ND2	1:G:456:ARG:O	2.18	0.76
1:A:273:ARG:NH1	1:A:484:TYR:CG	2.54	0.75
1:A:212:PRO:CD	4:A:608:NAG:O7	2.37	0.73
3:C:2:ILE:HG13	3:C:27:ALA:CB	2.17	0.73
1:A:212:PRO:HD2	4:A:608:NAG:O7	1.91	0.71
3:C:148:GLN:HB3	3:C:151:ASN:HD21	1.56	0.70
1:G:95:MET:HE1	1:G:234:ASN:O	1.91	0.70
3:C:131:ASN:HA	3:C:165:THR:HB	1.72	0.70
2:B:40:ALA:HB1	2:B:41:PRO:HD2	1.73	0.69
3:C:2:ILE:HG13	3:C:27:ALA:HB3	1.74	0.69
1:G:298:ARG:NH1	1:G:441:GLY:O	2.26	0.68
2:B:153:SER:O	2:B:197:ASN:N	2.19	0.68
3:C:128:LEU:C	3:C:129:LEU:HD12	2.15	0.67
1:G:298:ARG:NH2	1:G:439:ILE:O	2.28	0.66
3:C:6:GLN:HG2	3:C:23:CYS:HB3	1.77	0.65
3:C:179:TYR:CD1	3:C:185:TYR:CZ	2.85	0.65
2:B:145:TYR:CE2	2:B:150:VAL:CG2	2.80	0.65
2:B:145:TYR:CE2	2:B:150:VAL:HG23	2.32	0.65
3:C:6:GLN:HG3	3:C:23:CYS:HB2	1.79	0.64
2:H:192:GLN:OE1	2:H:193:THR:N	2.31	0.64
3:C:98:ASP:CB	3:C:159:GLN:HE22	2.10	0.63
1:G:234:ASN:O	1:G:273:ARG:HG2	1.98	0.63
1:G:447:SER:HB3	4:G:606:NAG:HN2	1.63	0.63
3:C:29:TYR:HD2	3:C:88:TYR:HH	1.46	0.63
3:L:143:VAL:CG2	3:L:148:GLN:HE21	2.12	0.62
1:G:430:VAL:HG11	2:H:72(A):THR:HG21	1.82	0.62
3:L:27:ALA:HB1	3:L:87:VAL:HG21	1.79	0.62
3:C:179:TYR:HD1	3:C:185:TYR:OH	1.83	0.62
3:C:66:THR:O	3:C:66:THR:HG22	2.00	0.62
3:C:22:THR:OG1	3:C:69:ASN:OD1	2.12	0.61
3:C:131:ASN:CA	3:C:165:THR:HB	2.31	0.61
2:H:145:TYR:CE1	2:H:150:VAL:HG23	2.34	0.61
3:C:179:TYR:HD1	3:C:185:TYR:CZ	2.19	0.61
3:C:4:MET:HE2	3:C:92:GLY:HA2	1.81	0.61
1:A:264:SER:OG	1:A:482:GLU:OE1	2.18	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:93:PHE:HE2	1:A:487:LYS:CB	2.16	0.59
2:H:126:PRO:HG3	2:H:138:LEU:HB3	1.83	0.59
3:C:159:GLN:CG	3:C:166:TYR:CZ	2.86	0.59
1:G:86:LEU:HB3	1:G:89:VAL:HG11	1.83	0.59
1:A:101:VAL:HG21	1:A:480:ARG:HG2	1.85	0.59
1:A:282:LYS:NZ	2:B:98:ASP:OD1	2.28	0.59
2:H:39:GLN:HB3	2:H:45:LEU:HD23	1.84	0.58
1:A:273:ARG:NH1	1:A:484:TYR:CZ	2.49	0.58
1:A:93:PHE:CE2	1:A:487:LYS:CB	2.85	0.58
2:B:39:GLN:HB3	2:B:45:LEU:HD23	1.85	0.58
2:B:163:VAL:HG22	2:B:182:VAL:CB	2.34	0.58
3:C:131:ASN:HA	3:C:165:THR:HG1	1.69	0.58
3:C:131:ASN:HA	3:C:165:THR:CB	2.33	0.57
2:B:87:THR:HG23	2:B:110:ILE:HA	1.86	0.57
2:B:122:PHE:O	2:B:141:LEU:HB3	2.04	0.56
2:B:138:LEU:C	2:B:181:VAL:HB	2.22	0.56
3:C:2:ILE:HG13	3:C:27:ALA:HB2	1.88	0.56
3:C:109:PHE:CD2	3:C:109:PHE:N	2.74	0.55
3:C:179:TYR:HD1	3:C:185:TYR:HH	1.51	0.55
2:B:138:LEU:O	2:B:181:VAL:CB	2.40	0.55
1:A:430:VAL:HG11	2:B:72(A):THR:HG21	1.88	0.55
3:C:131:ASN:C	3:C:165:THR:HB	2.27	0.55
2:B:163:VAL:HA	2:B:182:VAL:CB	2.37	0.54
2:H:142:VAL:HG11	2:H:150:VAL:HG11	1.88	0.54
3:C:107:SER:HB2	3:C:109:PHE:HE2	1.72	0.54
2:B:43:GLN:HG3	2:B:44:GLY:N	2.23	0.53
3:C:159:GLN:NE2	3:C:166:TYR:OH	2.36	0.53
1:A:427:TRP:HD1	5:A:606:EDO:HO2	1.55	0.53
1:A:55:ALA:HA	1:A:75:VAL:O	2.09	0.53
3:C:159:GLN:HG2	3:C:166:TYR:CE2	2.43	0.53
3:L:27:ALA:CB	3:L:87:VAL:HG21	2.39	0.53
2:B:185:PRO:HD2	2:B:188:SER:CB	2.39	0.53
2:B:65:GLY:O	2:B:80:ARG:CZ	2.57	0.53
3:C:2:ILE:CG1	3:C:27:ALA:HB3	2.39	0.53
3:C:159:GLN:HG3	3:C:166:TYR:CZ	2.44	0.53
2:H:23:GLN:HG3	2:H:74:MET:HG2	1.90	0.53
2:B:185:PRO:HD2	2:B:188:SER:HB3	1.90	0.52
3:C:159:GLN:HG2	3:C:166:TYR:CZ	2.44	0.52
3:L:63:ARG:HD3	3:L:68:TYR:CE1	2.45	0.52
3:C:129:LEU:N	3:C:129:LEU:CD1	2.72	0.52
2:B:145:TYR:CE2	2:B:150:VAL:HG21	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:148:GLN:OE1	3:C:151:ASN:ND2	2.42	0.52
3:C:157:THR:HG22	3:C:158:GLU:O	2.10	0.52
3:C:30:LEU:HD23	3:C:31:ASN:N	2.24	0.52
1:A:298:ARG:NH1	1:A:326:ILE:O	2.40	0.52
1:G:430:VAL:HG13	2:H:72(A):THR:HG21	1.91	0.52
3:L:2:ILE:CG1	3:L:27:ALA:HB2	2.39	0.51
3:C:45:MET:HE1	3:C:61:GLY:HA3	1.91	0.51
2:H:12:LYS:O	2:H:111:VAL:HA	2.10	0.51
2:H:38:ARG:NH2	2:H:85:ASP:O	2.42	0.51
2:B:65:GLY:O	2:B:80:ARG:NH1	2.43	0.51
3:C:6:GLN:HG2	3:C:23:CYS:CB	2.40	0.51
3:C:4:MET:SD	3:C:87:VAL:HG12	2.51	0.51
1:A:390:PHE:CG	1:A:470:PRO:HG3	2.46	0.51
3:C:98:ASP:CB	3:C:159:GLN:HE21	2.24	0.51
3:C:111:PHE:CD2	3:C:111:PHE:N	2.79	0.51
1:G:430:VAL:HG21	2:H:30:THR:HG21	1.93	0.51
3:C:160:ASP:OD1	3:C:162:LYS:N	2.41	0.51
3:C:6:GLN:CG	3:C:23:CYS:CB	2.89	0.51
3:L:76:GLN:HG2	3:L:77:PRO:HD2	1.92	0.51
3:C:129:LEU:N	3:C:129:LEU:HD12	2.23	0.51
2:H:150:VAL:HG22	2:H:200:HIS:HD2	1.74	0.51
3:C:34:GLN:HB2	3:C:44:LEU:HD11	1.92	0.50
3:C:111:PHE:CE2	3:C:128:LEU:HD12	2.45	0.50
1:A:226:LEU:HD22	1:A:242:VAL:CG1	2.42	0.50
1:G:430:VAL:HG11	2:H:72(A):THR:CG2	2.41	0.50
1:A:428:GLN:N	1:A:428:GLN:OE1	2.37	0.50
3:C:4:MET:HE2	3:C:92:GLY:CA	2.41	0.50
3:L:143:VAL:HG13	3:L:184:VAL:O	2.12	0.50
2:B:100(A):ASP:OD1	2:B:100(A):ASP:N	2.45	0.49
3:C:179:TYR:CD1	3:C:185:TYR:CE1	2.99	0.49
1:G:258:GLN:NE2	1:G:370:ILE:O	2.46	0.49
2:H:85:ASP:OD1	2:H:85:ASP:N	2.45	0.49
3:L:29:TYR:O	3:L:87:VAL:HG23	2.13	0.49
3:L:6:GLN:HB3	3:L:93:PRO:HG2	1.95	0.49
1:A:212:PRO:HG2	4:A:608:NAG:C7	2.36	0.49
3:C:31:ASN:HB2	3:C:86:GLN:HG2	1.95	0.49
2:H:87:THR:HG22	2:H:111:VAL:H	1.77	0.49
2:B:6:GLN:HG2	2:B:22:CYS:SG	2.53	0.49
3:C:107:SER:CB	3:C:109:PHE:HE2	2.24	0.49
3:L:143:VAL:CG2	3:L:148:GLN:NE2	2.74	0.49
1:G:240:ASN:HD21	4:G:602:NAG:C7	2.24	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:145:TYR:CE1	2:H:150:VAL:CG2	2.96	0.49
2:B:180:SER:O	2:B:181:VAL:HG13	2.13	0.49
3:L:143:VAL:HG23	3:L:148:GLN:HG3	1.94	0.49
3:L:160:ASP:HB3	3:L:163:ASP:OD1	2.13	0.48
3:C:6:GLN:CG	3:C:23:CYS:HB2	2.43	0.48
1:A:297:THR:HG22	1:A:298:ARG:N	2.28	0.48
3:C:108:VAL:C	3:C:109:PHE:CD2	2.87	0.48
3:C:179:TYR:HE1	3:C:185:TYR:CD1	2.27	0.48
3:C:107:SER:CB	3:C:109:PHE:CE2	2.97	0.48
3:C:133:TYR:CD1	3:C:134:PRO:HA	2.49	0.48
3:C:80:ILE:HG13	3:C:80:ILE:O	2.13	0.47
3:L:143:VAL:O	3:L:146:ALA:HB3	2.13	0.47
1:A:279:ASP:OD2	2:B:95:ARG:NH2	2.45	0.47
3:C:110:ILE:HD13	3:C:202:PHE:HD2	1.80	0.47
3:C:80:ILE:CG1	3:C:80:ILE:O	2.61	0.47
2:H:6:GLN:OE1	2:H:106:GLY:N	2.40	0.47
3:L:143:VAL:HG23	3:L:148:GLN:HE21	1.78	0.47
1:A:86:LEU:HD23	1:A:89:VAL:HG11	1.96	0.47
3:L:13:ALA:O	3:L:100:LYS:N	2.47	0.47
2:B:178:LEU:HD12	2:B:179:SER:H	1.78	0.47
1:G:219:ALA:HB2	1:G:225:ILE:HG13	1.97	0.47
1:G:282:LYS:NZ	2:H:98:ASP:OD1	2.46	0.47
3:C:36:ARG:HA	3:C:81:ALA:HB1	1.95	0.47
1:G:197:ASN:OD1	1:G:198:THR:N	2.47	0.47
1:G:230:ASN:ND2	4:G:602:NAG:O7	2.47	0.47
1:A:123:THR:HG23	1:A:198:THR:H	1.80	0.47
3:C:117:GLN:O	3:C:120:SER:HB2	2.15	0.47
3:C:137:ALA:HB2	3:C:191:HIS:HD2	1.79	0.47
3:C:12:SER:HA	3:C:98:ASP:O	2.15	0.46
3:L:23:CYS:SG	3:L:30:LEU:HD11	2.55	0.46
3:L:135:ARG:HB2	3:L:166:TYR:CE1	2.50	0.46
2:H:45:LEU:HD12	3:L:91:PHE:CE2	2.51	0.46
3:C:163:ASP:OD1	3:C:165:THR:HG23	2.16	0.46
2:H:100(A):ASP:N	2:H:100(A):ASP:OD1	2.49	0.46
1:A:248:THR:HG21	1:A:486:TYR:HD2	1.79	0.46
2:B:142:VAL:O	2:B:142:VAL:HG23	2.16	0.46
2:B:35:TYR:OH	2:B:95:ARG:NH1	2.49	0.46
3:L:33:TYR:HE1	3:L:86:GLN:HG2	1.81	0.46
1:A:258:GLN:NE2	1:A:370:ILE:O	2.49	0.46
1:A:422:GLN:NE2	1:A:435:TYR:O	2.47	0.46
2:B:71:ARG:HH21	2:B:72(A):THR:HG23	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:200:THR:HG21	1:G:202:THR:OG1	2.16	0.46
1:G:383:TYR:CE2	1:G:421:LYS:HB2	2.51	0.46
2:B:154:TRP:CZ2	2:B:181:VAL:HA	2.51	0.46
2:B:165:THR:HG23	2:B:180:SER:HB2	1.98	0.46
1:A:442:GLN:HG2	1:A:444:THR:HG23	1.97	0.45
3:C:5:THR:O	3:C:23:CYS:HA	2.16	0.45
2:H:115:SER:O	2:H:116:THR:OG1	2.26	0.45
1:A:58:ALA:HB1	1:A:71:THR:HG23	1.97	0.45
4:G:606:NAG:H62	4:G:607:NAG:C7	2.46	0.45
2:B:119:PRO:HB3	2:B:145:TYR:HB3	1.99	0.45
2:B:185:PRO:HB2	2:B:188:SER:CB	2.47	0.45
3:C:6:GLN:CG	3:C:23:CYS:HB3	2.45	0.45
1:A:297:THR:HA	1:A:443:ILE:O	2.17	0.45
1:A:69:TRP:CD2	1:A:111:ILE:HG12	2.52	0.45
2:B:96:HIS:ND1	2:B:101:ASP:OD1	2.41	0.45
3:C:113:PRO:HD3	3:C:125:VAL:HG22	1.99	0.45
1:A:48:ALA:O	1:A:488:VAL:O	2.35	0.45
1:A:271:VAL:CG1	1:A:273:ARG:HE	2.29	0.45
1:A:271:VAL:HG11	1:A:273:ARG:NE	2.32	0.45
1:A:331:CYS:SG	1:A:384:CYS:SG	3.15	0.45
1:G:58:ALA:HB2	1:G:70:ALA:HB3	1.99	0.44
3:L:59:PHE:HD2	3:L:70:LEU:HD11	1.82	0.44
2:B:43:GLN:HG3	2:B:44:GLY:H	1.82	0.44
1:G:335:GLY:HA3	1:G:412:ALA:O	2.17	0.44
1:G:428:GLN:N	1:G:428:GLN:OE1	2.43	0.44
2:H:21:SER:HA	2:H:75:LEU:O	2.18	0.44
3:C:6:GLN:HB2	3:C:93:PRO:HD2	2.00	0.44
2:B:67:LEU:HD11	2:B:77:MET:SD	2.58	0.44
3:C:179:TYR:CE1	3:C:185:TYR:CZ	3.01	0.44
3:C:6:GLN:HB2	3:C:93:PRO:CG	2.48	0.44
3:L:133:TYR:CD1	3:L:134:PRO:HA	2.53	0.44
2:B:30:THR:HG23	2:B:53:LEU:HA	1.99	0.44
3:C:28:GLY:O	3:C:87:VAL:HG21	2.18	0.44
3:L:36:ARG:NH1	3:L:78:GLU:O	2.51	0.44
3:C:148:GLN:HB3	3:C:151:ASN:ND2	2.27	0.43
1:G:90:THR:HG22	1:G:240:ASN:HA	2.00	0.43
3:L:27:ALA:HB3	3:L:87:VAL:HG11	2.00	0.43
1:G:69:TRP:CD2	1:G:111:ILE:HG12	2.53	0.43
1:A:254:VAL:HG21	1:A:262:ASN:HB2	2.01	0.43
2:H:38:ARG:NH2	2:H:86:ASP:HA	2.33	0.43
2:H:72(C):ASP:HB3	2:H:74:MET:HG3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:110:ILE:HD13	3:C:202:PHE:CD2	2.54	0.43
3:C:30:LEU:HA	3:C:86:GLN:O	2.18	0.43
1:G:255:VAL:HG13	1:G:475:MET:SD	2.58	0.43
3:L:32:TRP:CZ3	3:L:85:CYS:HB3	2.53	0.43
1:G:389:LEU:HD12	1:G:390:PHE:CD1	2.53	0.43
1:G:327:ARG:NH1	1:G:422:GLN:OE1	2.46	0.43
2:B:154:TRP:CH2	2:B:196:CYS:SG	3.12	0.43
2:H:122:PHE:HB3	3:L:114:SER:OG	2.19	0.43
3:C:25:THR:O	3:C:25:THR:HG23	2.19	0.43
1:G:268:GLU:O	1:G:289:GLN:NE2	2.52	0.43
1:G:462:THR:HG23	1:G:463:ASP:N	2.34	0.43
3:C:186:ALA:HA	3:C:201:SER:HB3	2.01	0.43
1:A:257:THR:O	1:A:259:LEU:N	2.48	0.42
2:B:65:GLY:O	2:B:80:ARG:NH2	2.51	0.42
1:G:389:LEU:CD2	1:G:416:LEU:HD21	2.49	0.42
3:C:131:ASN:OD1	3:C:165:THR:OG1	2.35	0.42
3:C:157:THR:HG22	3:C:158:GLU:N	2.35	0.42
3:L:11:LEU:HD21	3:L:19:VAL:HG13	2.00	0.42
3:C:28:GLY:O	3:C:87:VAL:CG2	2.67	0.42
1:G:331:CYS:SG	1:G:418:CYS:SG	3.17	0.42
3:L:179:TYR:O	3:L:185:TYR:OH	2.38	0.42
3:C:143:VAL:CG1	3:C:182:HIS:CB	2.97	0.42
1:A:123:THR:HG22	1:A:199:SER:OG	2.18	0.42
1:A:325:ASP:N	4:G:601:NAG:O4	2.53	0.42
2:B:145:TYR:CD2	2:B:150:VAL:CG2	3.03	0.42
3:L:2:ILE:HG13	3:L:27:ALA:HB2	2.01	0.42
2:B:83:ARG:O	2:B:111:VAL:HG11	2.20	0.42
3:L:30:LEU:HA	3:L:86:GLN:O	2.19	0.42
1:A:331:CYS:SG	1:A:418:CYS:SG	3.18	0.42
2:B:139:GLY:HA2	2:B:154:TRP:CH2	2.54	0.42
2:H:87:THR:CG2	2:H:111:VAL:H	2.33	0.42
3:L:36:ARG:HG2	3:L:81:ALA:HB2	2.01	0.42
3:C:63:ARG:CB	3:C:68:TYR:CD2	3.03	0.42
2:H:6:GLN:HG2	2:H:22:CYS:SG	2.59	0.42
3:L:137:ALA:HB2	3:L:191:HIS:HD2	1.84	0.42
1:G:277:LEU:HD13	1:G:352:HIS:HB3	2.01	0.42
2:H:119:PRO:HB2	2:H:142:VAL:HG13	2.02	0.42
3:L:99:LEU:HD23	3:L:99:LEU:HA	1.95	0.42
3:C:13:ALA:O	3:C:99:LEU:HA	2.20	0.41
1:G:270:ILE:HD13	1:G:345:VAL:HG22	2.02	0.41
1:G:264:SER:OG	1:G:482:GLU:OE1	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:152:VAL:HA	2:B:197:ASN:O	2.20	0.41
2:B:55:SER:CB	2:B:71:ARG:HE	2.33	0.41
1:A:120:VAL:HG12	1:A:122:LEU:HD22	2.02	0.41
2:B:166:PHE:O	2:B:178:LEU:HD11	2.20	0.41
2:B:150:VAL:HG22	2:B:200:HIS:HD2	1.85	0.41
1:A:52:LEU:HB3	1:A:218:CYS:O	2.20	0.41
2:B:164:HIS:CE1	3:C:130:ASN:OD1	2.74	0.41
2:B:142:VAL:HG23	2:B:178:LEU:HB3	2.03	0.41
2:H:24:ALA:HB1	2:H:27:TYR:CE1	2.56	0.41
1:A:265:LEU:HD21	1:A:289:GLN:HA	2.02	0.41
1:A:390:PHE:CD1	1:A:470:PRO:HG3	2.55	0.41
3:C:127:CYS:HB2	3:C:141:TRP:CH2	2.55	0.41
3:C:51:LEU:HD23	3:C:52:VAL:O	2.21	0.41
1:G:261:LEU:HD13	4:G:606:NAG:H82	2.02	0.41
2:B:123:PRO:HD2	3:C:114:SER:HB3	2.03	0.41
3:C:21:ILE:HG22	3:C:22:THR:N	2.35	0.41
3:C:6:GLN:OE1	3:C:85:CYS:SG	2.79	0.41
3:C:166:TYR:N	3:C:166:TYR:CD2	2.89	0.41
1:A:64:GLU:OE1	1:A:67:ASN:ND2	2.49	0.41
2:B:180:SER:O	2:B:181:VAL:CG1	2.68	0.41
2:B:45:LEU:HD12	3:C:91:PHE:CE2	2.56	0.41
1:A:300:ASN:OD1	1:A:301:ASN:N	2.54	0.41
1:A:338:TRP:CD1	1:A:394:ILE:HD13	2.56	0.41
2:B:125:ALA:O	3:C:111:PHE:HD1	2.04	0.41
3:C:2:ILE:CG1	3:C:27:ALA:CB	2.94	0.41
4:A:608:NAG:H61	4:A:609:NAG:N2	2.36	0.40
2:B:185:PRO:O	2:B:188:SER:HB3	2.21	0.40
1:G:260:LEU:HD12	1:G:451:GLY:HA3	2.03	0.40
2:H:145:TYR:CD1	2:H:150:VAL:CG2	3.04	0.40
2:B:145:TYR:CD2	2:B:150:VAL:HG21	2.56	0.40
2:B:45:LEU:HD12	3:C:91:PHE:CD2	2.56	0.40
2:B:55:SER:HB3	2:B:71:ARG:HE	1.87	0.40
2:H:117:LYS:HG2	2:H:144:ASP:O	2.22	0.40
2:B:138:LEU:HB2	2:B:211:VAL:HG11	2.03	0.40
3:L:63:ARG:HG3	3:L:64:TRP: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	338/353 (96%)	329 (97%)	9 (3%)	0	100 100
1	G	335/353 (95%)	328 (98%)	7 (2%)	0	100 100
2	B	196/225 (87%)	190 (97%)	5 (3%)	1 (0%)	34 76
2	H	209/225 (93%)	203 (97%)	6 (3%)	0	100 100
3	C	204/207 (99%)	201 (98%)	3 (2%)	0	100 100
3	L	204/207 (99%)	200 (98%)	4 (2%)	0	100 100
All	All	1486/1570 (95%)	1451 (98%)	34 (2%)	1 (0%)	56 90

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	123	PRO

5.3.2 Protein sidechains (i)

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	260/313 (83%)	258 (99%)	2 (1%)	86 96
1	G	271/313 (87%)	270 (100%)	1 (0%)	93 98
2	B	155/195 (80%)	155 (100%)	0	100 100
2	H	181/195 (93%)	180 (99%)	1 (1%)	90 97
3	C	142/182 (78%)	140 (99%)	2 (1%)	74 93
3	L	169/182 (93%)	168 (99%)	1 (1%)	90 97

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1178/1380 (85%)	1171 (99%)	7 (1%)	90 97

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	273	ARG
1	A	280	ASN
1	G	385	ASN
3	C	23	CYS
3	C	85	CYS
2	H	71	ARG
3	L	23	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	43	GLN
2	B	164	HIS
3	C	159	GLN
3	L	148	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

There are no carbohydrates in this entry.

5.6 Ligand geometry

24 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	$\#\|Z\| > 2$
4	NAG	A	601	1	14,14,15	0.34	0	15,19,21	0.44	0
4	NAG	A	602	1	14,14,15	0.23	0	15,19,21	0.59	1 (6%)
4	NAG	A	603	1	14,14,15	0.37	0	15,19,21	0.57	0
4	NAG	A	604	1	14,14,15	0.24	0	15,19,21	0.53	0
4	NAG	A	605	1	14,14,15	0.29	0	15,19,21	0.45	0
5	EDO	A	606	-	3,3,3	0.46	0	2,2,2	0.33	0
5	EDO	A	607	-	3,3,3	0.47	0	2,2,2	0.01	0
4	NAG	A	608	1,4	14,14,15	1.40	3 (21%)	15,19,21	0.86	1 (6%)
4	NAG	A	609	4,6	14,14,15	1.28	1 (7%)	15,19,21	0.94	0
6	BMA	A	610	4,7	11,11,12	1.48	2 (18%)	15,15,17	1.26	1 (6%)
7	MAN	A	611	7,6	11,11,12	1.58	2 (18%)	15,15,17	1.00	1 (6%)
7	MAN	A	612	7	11,11,12	1.39	2 (18%)	15,15,17	1.54	1 (6%)
7	MAN	A	613	6	11,11,12	1.49	2 (18%)	15,15,17	1.03	2 (13%)
4	NAG	C	301	3	14,14,15	0.36	0	15,19,21	0.41	0
4	NAG	G	601	1	14,14,15	0.49	0	15,19,21	0.27	0
4	NAG	G	602	1	14,14,15	0.67	1 (7%)	15,19,21	0.80	1 (6%)
4	NAG	G	603	1	14,14,15	0.26	0	15,19,21	0.39	0
8	PGE	G	604	-	9,9,9	0.33	0	8,8,8	0.30	0
5	EDO	G	605	-	3,3,3	0.52	0	2,2,2	0.26	0
4	NAG	G	606	1,4	14,14,15	0.65	0	15,19,21	0.47	0
4	NAG	G	607	4,6	14,14,15	0.34	0	15,19,21	0.33	0
6	BMA	G	608	4,7	11,11,12	0.66	0	15,15,17	0.96	1 (6%)
7	MAN	G	609	6	11,11,12	0.63	0	15,15,17	1.09	2 (13%)
4	NAG	L	301	3	14,14,15	0.17	0	15,19,21	0.42	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	A	601	1	-	0/6/23/26	0/1/1/1
4	NAG	A	602	1	-	0/6/23/26	0/1/1/1
4	NAG	A	603	1	-	0/6/23/26	0/1/1/1
4	NAG	A	604	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	A	605	1	-	0/6/23/26	0/1/1/1
5	EDO	A	606	-	-	0/1/1/1	0/0/0/0
5	EDO	A	607	-	-	0/1/1/1	0/0/0/0
4	NAG	A	608	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	609	4,6	-	0/6/23/26	0/1/1/1
6	BMA	A	610	4,7	-	0/2/19/22	0/1/1/1
7	MAN	A	611	7,6	-	0/2/19/22	0/1/1/1
7	MAN	A	612	7	-	0/2/19/22	0/1/1/1
7	MAN	A	613	6	-	0/2/19/22	0/1/1/1
4	NAG	C	301	3	-	0/6/23/26	0/1/1/1
4	NAG	G	601	1	-	0/6/23/26	0/1/1/1
4	NAG	G	602	1	-	0/6/23/26	0/1/1/1
4	NAG	G	603	1	-	0/6/23/26	0/1/1/1
8	PGE	G	604	-	-	0/7/7/7	0/0/0/0
5	EDO	G	605	-	-	0/1/1/1	0/0/0/0
4	NAG	G	606	1,4	-	0/6/23/26	0/1/1/1
4	NAG	G	607	4,6	-	0/6/23/26	0/1/1/1
6	BMA	G	608	4,7	-	0/2/19/22	0/1/1/1
7	MAN	G	609	6	-	0/2/19/22	0/1/1/1
4	NAG	L	301	3	-	0/6/23/26	0/1/1/1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	613	MAN	C2-C3	-3.54	1.47	1.52
7	A	611	MAN	C2-C3	-3.15	1.48	1.52
6	A	610	BMA	C2-C3	-3.12	1.48	1.52
7	A	612	MAN	C2-C3	-2.70	1.48	1.52
4	A	608	NAG	O5-C1	2.04	1.47	1.43
4	A	608	NAG	C7-N2	2.12	1.42	1.34
4	A	608	NAG	O7-C7	2.13	1.28	1.23
4	A	609	NAG	C7-N2	2.14	1.42	1.34
4	G	602	NAG	C1-C2	2.31	1.55	1.52
7	A	613	MAN	O5-C1	2.57	1.47	1.43
7	A	612	MAN	O5-C1	2.76	1.48	1.43
6	A	610	BMA	O5-C1	3.02	1.48	1.43
7	A	611	MAN	O5-C1	3.51	1.49	1.43

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	A	610	BMA	C1-O5-C5	-2.83	107.97	112.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	G	609	MAN	O2-C2-C3	-2.28	105.59	110.19
7	A	613	MAN	O3-C3-C2	-2.28	105.84	110.01
4	A	608	NAG	C2-N2-C7	-2.03	120.47	123.11
4	A	602	NAG	C1-O5-C5	2.08	115.20	112.14
7	A	611	MAN	C1-O5-C5	2.08	115.20	112.14
4	G	602	NAG	C1-O5-C5	2.21	115.39	112.14
6	G	608	BMA	C1-C2-C3	2.26	112.29	109.55
7	A	613	MAN	C1-C2-C3	2.34	112.39	109.55
7	G	609	MAN	C1-O5-C5	3.03	116.60	112.14
7	A	612	MAN	C1-C2-C3	4.88	115.47	109.55

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	606	EDO	1	0
4	A	608	NAG	6	0
4	A	609	NAG	1	0
4	G	601	NAG	1	0
4	G	602	NAG	2	0
4	G	606	NAG	3	0
4	G	607	NAG	1	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, 95^{th} 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	340/353 (96%)	-0.12	7 (2%)	67	36	45, 67, 112, 143	0
1	G	339/353 (96%)	-0.25	1 (0%)	94	84	41, 63, 90, 122	0
2	B	202/225 (89%)	-0.01	3 (1%)	76	49	54, 78, 120, 137	0
2	H	213/225 (94%)	-0.34	1 (0%)	91	76	37, 56, 76, 409	0
3	C	206/207 (99%)	0.14	3 (1%)	76	49	57, 85, 116, 128	0
3	L	206/207 (99%)	-0.15	3 (1%)	76	49	42, 67, 102, 116	0
All	All	1506/1570 (95%)	-0.13	18 (1%)	81	55	37, 68, 111, 409	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	77	MET	4.0
2	B	114	ALA	3.0
1	A	462	THR	2.6
2	B	185	PRO	2.6
1	G	58	ALA	2.4
3	L	74	SER	2.4
3	L	146	ALA	2.4
1	A	256	SER	2.3
3	C	178	ASP	2.3
1	A	240	ASN	2.3
2	B	187	SER	2.3
1	A	50	THR	2.2
1	A	87	GLU	2.2
1	A	222	GLY	2.2
3	C	73	GLY	2.1
1	A	223	TYR	2.0
3	L	144	ASP	2.0
3	C	16	GLY	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)

There are no carbohydrates in this entry.

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^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
5	EDO	G	605	4/4	0.76	0.76	26.67	67,69,77,120	0
4	NAG	A	608	14/15	0.68	0.58	8.68	44,56,59,65	14
4	NAG	G	602	14/15	0.80	0.40	4.78	76,90,104,105	14
5	EDO	A	606	4/4	0.90	0.46	3.01	46,54,57,59	0
4	NAG	G	607	14/15	0.71	0.26	2.07	87,93,110,120	0
4	NAG	C	301	14/15	0.82	0.34	1.95	90,104,107,111	0
4	NAG	G	601	14/15	0.82	0.27	1.91	74,81,97,103	0
4	NAG	A	602	14/15	0.64	0.47	1.43	131,147,153,153	0
4	NAG	G	606	14/15	0.85	0.25	1.01	67,74,84,91	0
4	NAG	A	601	14/15	0.78	0.31	0.82	104,114,126,134	0
4	NAG	L	301	14/15	0.82	0.22	0.43	60,82,162,177	0
5	EDO	A	607	4/4	0.92	0.20	-0.04	50,52,55,58	4
8	PGE	G	604	10/10	0.84	0.17	-0.05	66,74,77,78	0
4	NAG	A	604	14/15	0.88	0.20	-0.33	50,61,73,73	0
6	BMA	G	608	11/12	0.59	0.37	-	117,122,132,140	0
4	NAG	G	603	14/15	0.80	0.51	-	81,103,107,108	14
6	BMA	A	610	11/12	0.74	0.19	-	53,60,62,68	11
7	MAN	A	612	11/12	0.82	0.26	-	58,61,66,68	11
7	MAN	A	611	11/12	0.88	0.18	-	55,57,61,70	11
7	MAN	A	613	11/12	0.71	0.23	-	57,61,67,68	11
4	NAG	A	609	14/15	0.62	0.47	-	48,52,61,62	14
4	NAG	A	605	14/15	0.72	0.53	-	99,119,127,128	14
7	MAN	G	609	11/12	0.82	0.39	-	122,134,139,139	0
4	NAG	A	603	14/15	0.80	0.28	-	102,109,114,114	0

6.5 Other polymers (i)

There are no such residues in this entry.