



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 11:42 AM BST

PDB ID : 1MQL
Title : BHA of Ukr/63
Authors : ha, y.; stevens, d.j.; shehel, j.j.; wiley, d.c.
Deposited on : 2002-09-16
Resolution : 2.90 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

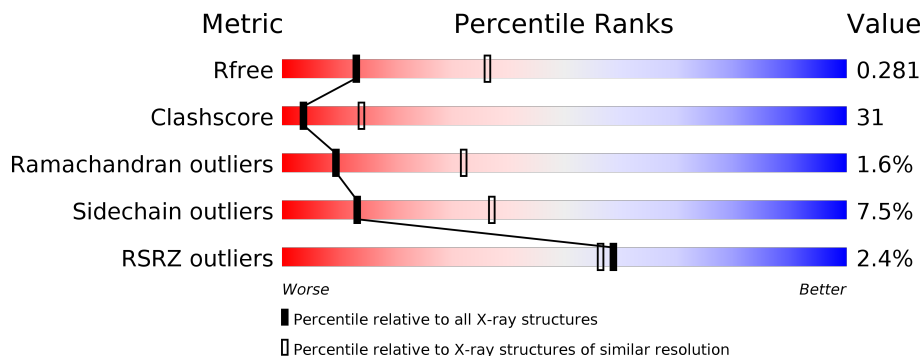
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 respectively. 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	
1	D	329	
1	G	329	
2	B	221	
2	E	221	
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	A	330	-	-	-	X
3	NAG	A	332	-	-	-	X
3	NAG	A	335	-	-	X	-
3	NAG	H	341	-	-	-	X
4	NDG	D	332	-	-	X	-
4	NDG	E	241	-	-	-	X
4	NDG	G	330	-	-	X	-
4	NDG	G	333	-	-	-	X
4	NDG	G	336	-	-	-	X
5	MAN	A	336	-	-	X	-
5	MAN	D	334	X	-	X	-
5	MAN	D	335	X	-	-	-
5	MAN	G	331	X	-	X	-
5	MAN	G	332	X	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 11890 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
			Total	C	N	O	S			
1	A	318	Total 2425	C 1522	N 424	O 466	S 13	0	0	0
1	D	318	Total 2432	C 1526	N 425	O 468	S 13	0	0	0
1	G	318	Total 2426	C 1523	N 424	O 466	S 13	0	0	0

- Molecule 2 is a protein called Hemagglutinin HA2 chain.

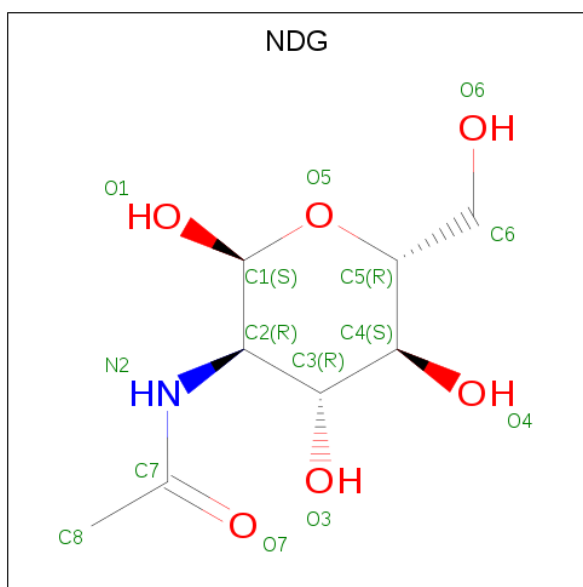
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	172	Total 1398	C 867	N 247	O 278	S 6	0	0	0
2	E	172	Total 1401	C 869	N 248	O 278	S 6	0	0	0
2	H	172	Total 1404	C 871	N 249	O 278	S 6	0	0	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



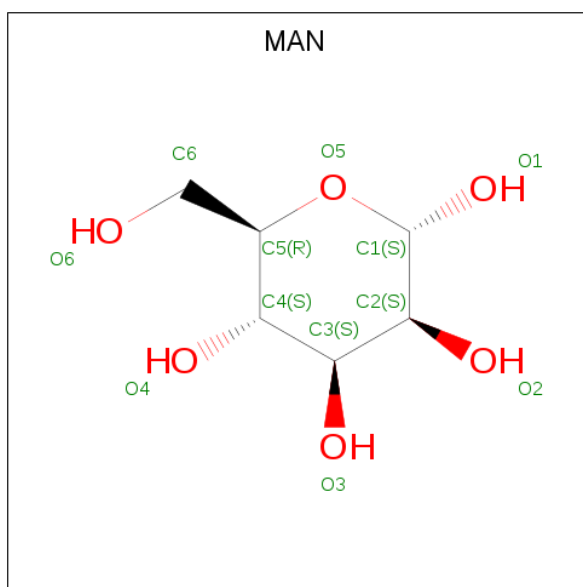
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	Total 15	8	1	6	0	0
3	A	1	Total 15	8	1	6	0	0
3	A	1	Total 15	8	1	6	0	0
3	A	1	Total 15	8	1	6	0	0
3	D	1	Total 15	8	1	6	0	0
3	G	1	Total 15	8	1	6	0	0
3	H	1	Total 15	8	1	6	0	0

- Molecule 4 is 2-acetamido-2-deoxy-alpha-D-glucopyranose (three-letter code: NDG) (formula: C₈H₁₅N₁O₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	A	1	15	8	1	6	0	0
4	A	1	15	8	1	6	0	0
4	B	1	15	8	1	6	0	0
4	B	1	15	8	1	6	0	0
4	D	1	15	8	1	6	0	0
4	D	1	15	8	1	6	0	0
4	D	1	15	8	1	6	0	0
4	E	1	15	8	1	6	0	0
4	G	1	15	8	1	6	0	0
4	G	1	15	8	1	6	0	0
4	G	1	15	8	1	6	0	0
4	G	1	15	8	1	6	0	0

- Molecule 5 is alpha-D-mannopyranose (three-letter code: MAN) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 12 6 6	0	0
5	A	1	Total C O 12 6 6	0	0
5	D	1	Total C O 12 6 6	0	0
5	D	1	Total C O 12 6 6	0	0
5	G	1	Total C O 12 6 6	0	0
5	G	1	Total C O 12 6 6	0	0

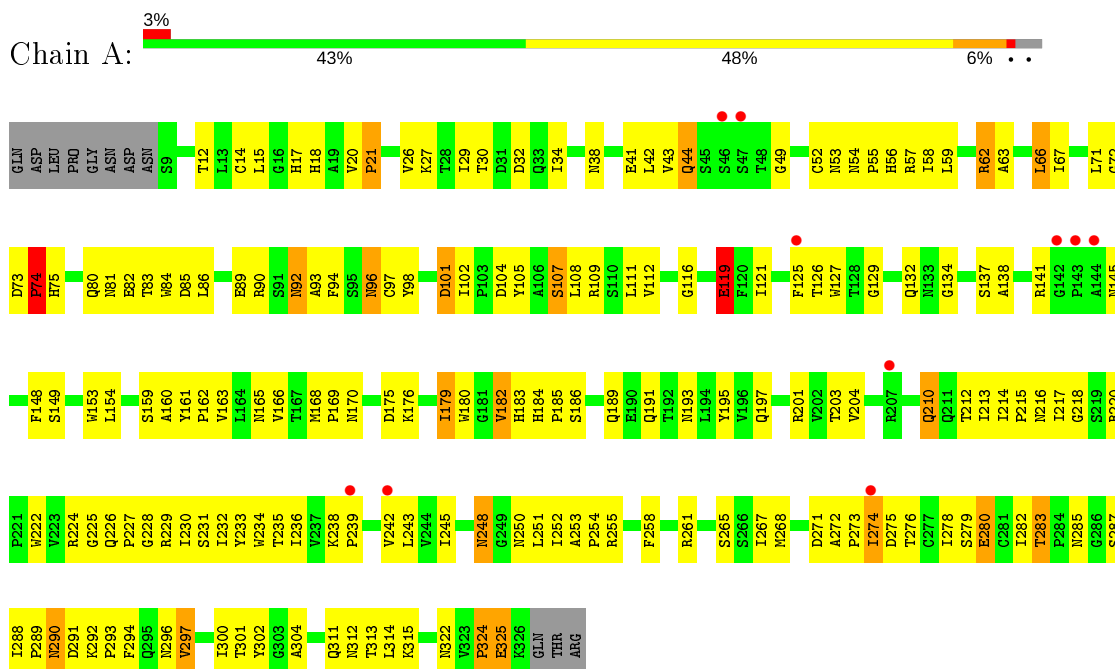
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	10	Total O 10 10	0	0
6	B	5	Total O 5 5	0	0
6	D	11	Total O 11 11	0	0
6	E	7	Total O 7 7	0	0
6	G	9	Total O 9 9	0	0
6	H	5	Total O 5 5	0	0

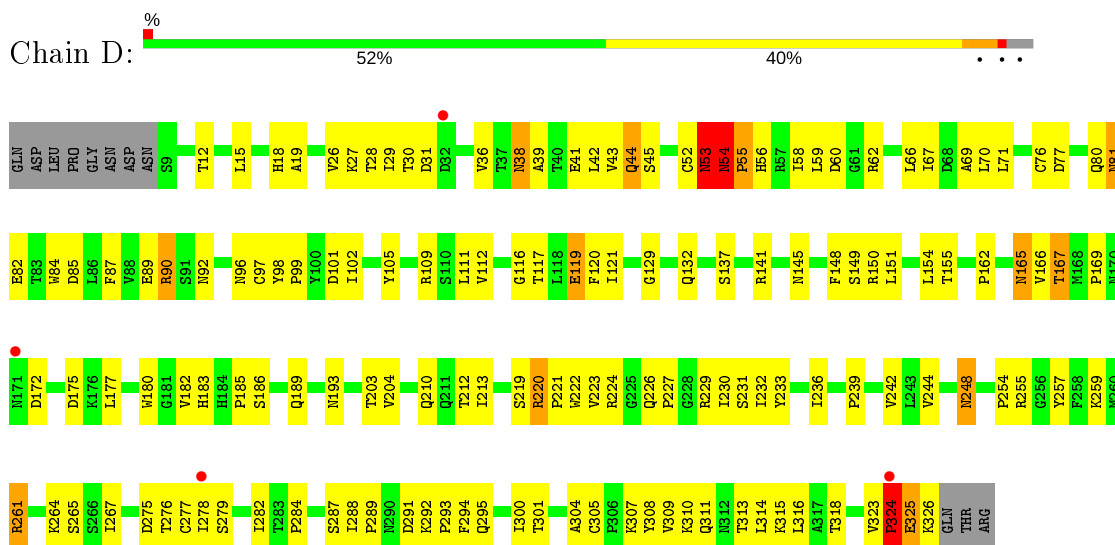
3 Residue-property plots [i](#)

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

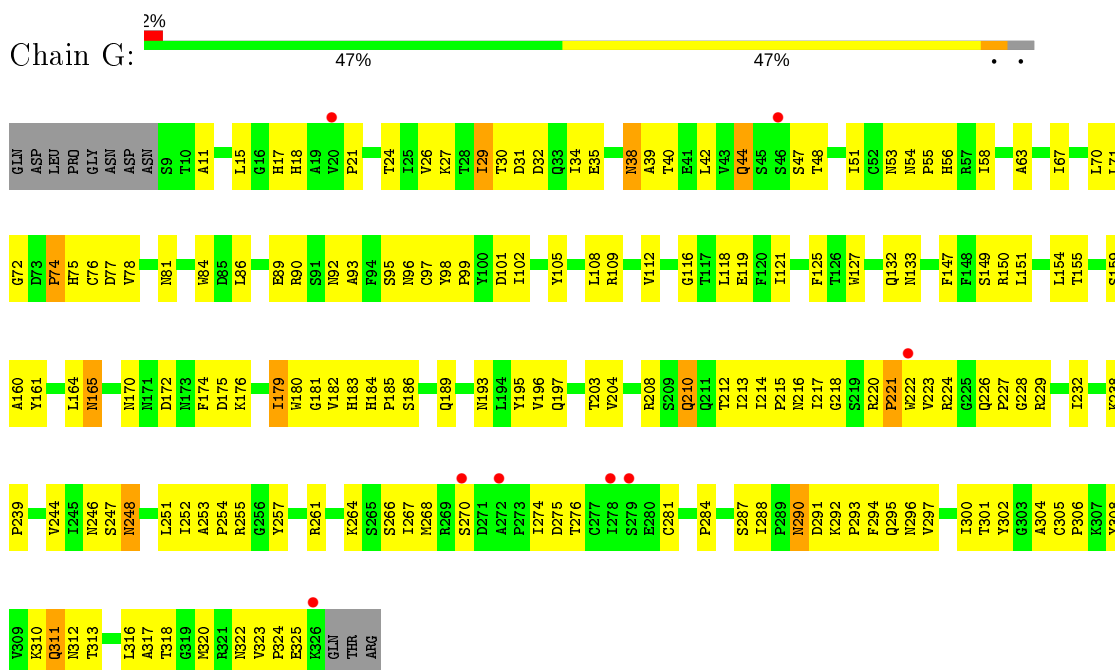
- Molecule 1: Hemagglutinin HA1 chain



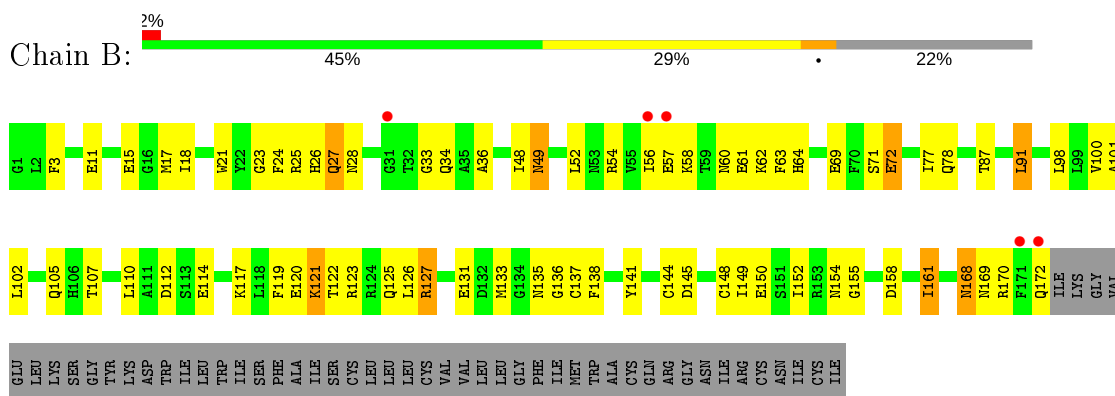
- Molecule 1: Hemagglutinin HA1 chain



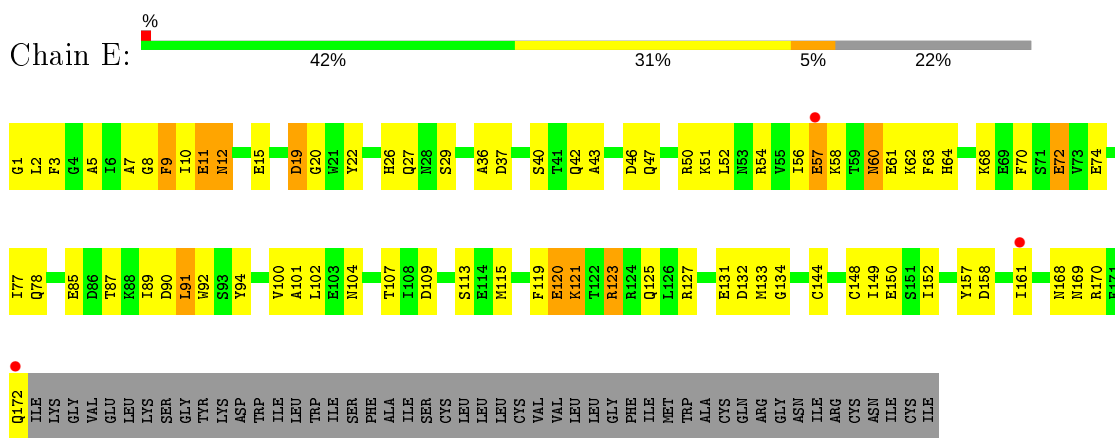
• Molecule 1: Hemagglutinin HA1 chain



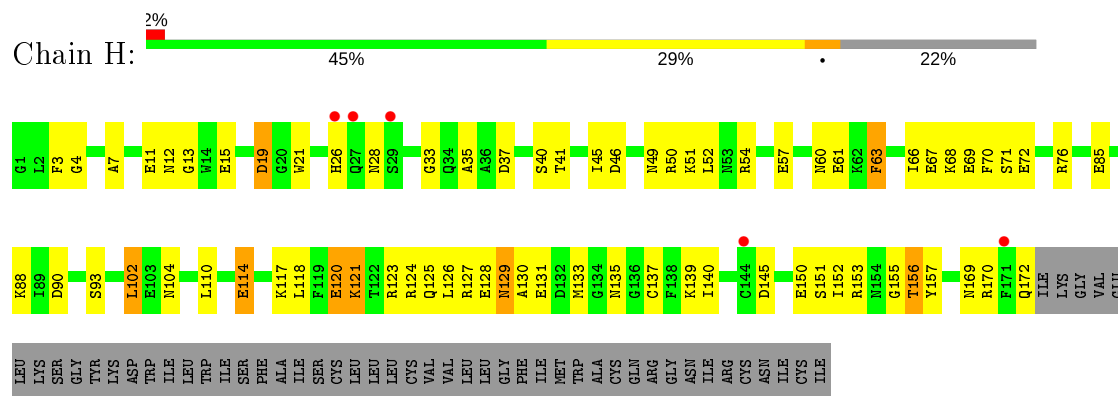
• Molecule 2: Hemagglutinin HA2 chain



• Molecule 2: Hemagglutinin HA2 chain



• Molecule 2: Hemagglutinin HA2 chain



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	147.68Å 147.10Å 251.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.90 40.15 – 2.91	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.00-2.90) 90.4 (40.15-2.91)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.49 (at 2.90Å)	Xtrriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.269 , 0.306 0.245 , 0.281	Depositor DCC
R_{free} test set	2979 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	64.4	Xtrriage
Anisotropy	0.632	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 43.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.019 for -k,-h,-l	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	11890	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.43% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: NAG, NDG, 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	0.45	1/2482 (0.0%)	0.68	0/3390
1	D	0.46	1/2489 (0.0%)	0.75	3/3398 (0.1%)
1	G	0.47	1/2483 (0.0%)	0.72	0/3391
2	B	0.45	0/1422	0.63	0/1912
2	E	0.42	0/1425	0.63	0/1915
2	H	0.40	0/1428	0.65	0/1918
All	All	0.45	3/11729 (0.0%)	0.69	3/15924 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	119	GLU	CB-CG	-5.29	1.42	1.52
1	D	119	GLU	CB-CG	-5.07	1.42	1.52
1	A	119	GLU	CB-CG	-5.07	1.42	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	54	ASN	N-CA-C	7.32	130.76	111.00
1	D	54	ASN	C-N-CD	6.18	141.37	128.40
1	D	53	ASN	N-CA-C	5.04	124.61	111.00

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	2425	0	2339	181	0
1	D	2432	0	2352	160	0
1	G	2426	0	2341	183	0
2	B	1398	0	1309	89	0
2	E	1401	0	1318	84	0
2	H	1404	0	1327	80	0
3	A	60	0	60	20	0
3	D	15	0	15	1	0
3	G	15	0	15	3	0
3	H	15	0	15	2	0
4	A	30	0	24	8	0
4	B	30	0	24	5	0
4	D	45	0	36	14	0
4	E	15	0	12	0	0
4	G	60	0	48	16	0
5	A	24	0	24	8	0
5	D	24	0	24	6	0
5	G	24	0	24	6	0
6	A	10	0	0	6	0
6	B	5	0	0	0	0
6	D	11	0	0	0	0
6	E	7	0	0	2	0
6	G	9	0	0	6	0
6	H	5	0	0	1	0
All	All	11890	0	11307	717	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 31.

All (717) 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:165:ASN:OD1	3:A:333:NAG:H1	1.40	1.19
2:B:125:GLN:HE22	2:B:155:GLY:HA2	1.09	1.18
4:D:333:NDG:O4	5:D:334:MAN:H1	1.51	1.10
3:A:333:NAG:H4	4:G:330:NDG:C1	1.83	1.08
4:D:333:NDG:C1	3:G:335:NAG:H4	1.86	1.04
3:A:335:NAG:H4	5:A:336:MAN:H1	1.42	1.01
2:B:125:GLN:NE2	2:B:155:GLY:HA2	1.77	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:29:ILE:HD11	2:B:102:LEU:HD12	1.44	0.95
1:A:201:ARG:HA	6:A:345:HOH:O	1.69	0.93
1:A:214:ILE:HG12	6:A:345:HOH:O	1.69	0.92
1:G:44:GLN:HG2	1:G:292:LYS:HD3	1.51	0.92
2:E:169:ASN:HA	2:E:172:GLN:HE21	1.37	0.90
1:A:81:ASN:ND2	1:A:119:GLU:HA	1.87	0.90
1:G:275:ASP:CG	1:G:276:THR:H	1.75	0.90
1:A:165:ASN:OD1	3:A:333:NAG:C1	2.23	0.87
1:G:248:ASN:HD22	1:G:248:ASN:H	1.21	0.87
2:B:144:CYS:SG	2:B:149:ILE:HD12	2.15	0.86
2:H:150:GLU:HG3	3:H:341:NAG:O1	1.76	0.84
3:A:335:NAG:H4	5:A:336:MAN:C1	2.06	0.84
4:A:334:NDG:O4	4:B:222:NDG:C1	2.26	0.84
3:A:335:NAG:C4	5:A:336:MAN:H1	2.07	0.84
1:D:165:ASN:HD21	4:D:332:NDG:C1	1.91	0.83
1:A:111:LEU:HD12	1:A:112:VAL:N	1.92	0.83
2:B:57:GLU:HG3	2:B:57:GLU:O	1.77	0.83
1:G:161:TYR:HB3	1:G:197:GLN:HE22	1.43	0.83
3:A:335:NAG:H82	4:D:332:NDG:H6C1	1.61	0.82
1:D:89:GLU:HG3	1:D:267:ILE:HD11	1.63	0.81
2:E:12:ASN:HD22	2:E:12:ASN:N	1.76	0.80
2:H:57:GLU:HG3	2:H:57:GLU:O	1.80	0.80
1:A:27:LYS:HE2	2:E:54:ARG:HH12	1.45	0.80
3:A:333:NAG:H4	4:G:330:NDG:O5	1.80	0.80
1:G:189:GLN:O	1:G:193:ASN:HB2	1.82	0.80
2:H:41:THR:O	2:H:45:ILE:HG13	1.82	0.80
1:G:81:ASN:HD21	4:G:334:NDG:C7	1.94	0.80
1:D:165:ASN:ND2	4:D:332:NDG:C1	2.45	0.79
2:E:57:GLU:HG3	2:E:57:GLU:O	1.84	0.78
1:A:170:ASN:OD1	1:A:176:LYS:HE3	1.83	0.78
1:G:316:LEU:HD23	2:H:52:LEU:HD13	1.65	0.78
1:D:43:VAL:HA	1:D:294:PHE:O	1.84	0.78
1:A:285:ASN:HD21	4:A:334:NDG:C1	1.98	0.77
1:G:67:ILE:HG13	1:G:105:TYR:CZ	2.21	0.76
1:G:39:ALA:O	4:G:333:NDG:H2	1.86	0.75
2:B:54:ARG:HG3	6:G:339:HOH:O	1.85	0.75
1:G:24:THR:OG1	4:G:333:NDG:H6C2	1.86	0.75
2:E:134:GLY:HA2	2:H:124:ARG:HD3	1.67	0.75
2:E:125:GLN:HE21	2:E:157:TYR:HB3	1.50	0.75
1:G:102:ILE:HG12	1:G:232:ILE:HB	1.66	0.75
1:D:169:PRO:CA	1:D:242:VAL:HG23	2.17	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:133:MET:SD	2:H:139:LYS:HB2	2.26	0.75
1:G:275:ASP:CG	1:G:276:THR:N	2.38	0.75
5:G:331:MAN:H2	5:G:332:MAN:H1	1.69	0.75
1:D:98:TYR:CD2	1:D:230:ILE:HD13	2.22	0.74
1:A:185:PRO:HG2	1:A:191:GLN:OE1	1.87	0.74
2:E:72:GLU:HG2	1:G:238:LYS:NZ	2.02	0.74
3:A:333:NAG:H61	4:G:330:NDG:C1	2.18	0.73
1:G:11:ALA:HB3	2:H:140:ILE:HB	1.69	0.73
1:G:38:ASN:HD22	1:G:39:ALA:N	1.85	0.73
1:D:148:PHE:HB2	1:D:151:LEU:HD12	1.71	0.73
1:G:38:ASN:ND2	1:G:39:ALA:N	2.36	0.73
1:D:109:ARG:NH1	1:D:267:ILE:HD13	2.04	0.72
1:G:71:LEU:HD23	1:G:179:ILE:HD11	1.72	0.72
1:D:248:ASN:HD22	1:D:248:ASN:H	1.36	0.72
5:D:334:MAN:O2	5:D:335:MAN:H5	1.90	0.72
2:E:144:CYS:SG	2:E:149:ILE:HD12	2.30	0.72
1:A:304:ALA:HB2	2:B:61:GLU:HG2	1.72	0.71
1:D:52:CYS:HB2	1:D:279:SER:HB3	1.72	0.71
1:G:109:ARG:NH1	1:G:267:ILE:HD13	2.06	0.71
3:A:335:NAG:O1	4:D:332:NDG:O4	2.08	0.70
1:A:71:LEU:HD23	1:A:179:ILE:HD11	1.74	0.70
2:H:151:SER:HA	2:H:156:THR:HG23	1.74	0.70
1:A:96:ASN:HA	1:A:224:ARG:HE	1.56	0.69
1:A:42:LEU:HD22	1:A:293:PRO:HG2	1.75	0.69
1:G:292:LYS:O	1:G:306:PRO:HB3	1.91	0.69
1:A:180:TRP:HB3	1:A:254:PRO:HG3	1.74	0.69
1:A:214:ILE:HA	6:A:345:HOH:O	1.92	0.69
1:A:15:LEU:HD22	2:B:119:PHE:HA	1.73	0.69
1:A:17:HIS:HA	2:B:21:TRP:O	1.91	0.69
1:G:291:ASP:OD1	1:G:292:LYS:HG3	1.93	0.69
2:E:37:ASP:OD2	2:E:40:SER:HB2	1.92	0.69
1:D:66:LEU:HD21	1:D:112:VAL:HG12	1.75	0.69
1:A:185:PRO:HB2	1:A:217:ILE:HG13	1.75	0.69
5:G:331:MAN:C2	5:G:332:MAN:H1	2.23	0.69
2:H:169:ASN:HA	2:H:172:GLN:NE2	2.08	0.69
1:A:30:THR:O	2:E:50:ARG:HD2	1.94	0.68
1:G:151:LEU:HA	6:G:341:HOH:O	1.91	0.68
1:G:183:HIS:HB2	1:G:252:ILE:HD11	1.75	0.68
1:G:293:PRO:HB2	1:G:294:PHE:CE1	2.28	0.68
1:D:90:ARG:HD2	1:D:90:ARG:N	2.08	0.68
1:G:325:GLU:HG2	2:H:12:ASN:HD22	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:G:330:NDG:O4	5:G:331:MAN:H1	1.94	0.68
1:D:167:THR:OG1	4:D:332:NDG:H6C2	1.94	0.67
1:D:29:ILE:HD11	2:E:102:LEU:HD12	1.74	0.67
1:A:71:LEU:CD2	1:A:179:ILE:HD11	2.24	0.67
1:G:220:ARG:HB2	1:G:227:PRO:O	1.94	0.67
1:G:255:ARG:HG3	6:G:341:HOH:O	1.93	0.67
1:D:165:ASN:OD1	4:D:332:NDG:O1	2.13	0.67
2:H:71:SER:C	2:H:72:GLU:HG3	2.15	0.67
1:A:175:ASP:OD1	1:A:239:PRO:HD3	1.95	0.67
1:A:184:HIS:HB3	1:A:220:ARG:HH21	1.60	0.67
2:B:158:ASP:HB3	2:B:161:ILE:HD12	1.76	0.66
4:D:333:NDG:C1	3:G:335:NAG:C4	2.69	0.66
1:A:12:THR:HG23	2:B:133:MET:HE3	1.78	0.66
2:B:131:GLU:OE2	2:B:170:ARG:HD2	1.96	0.66
2:B:28:ASN:HD22	2:B:145:ASP:HA	1.60	0.66
2:B:169:ASN:HA	2:B:172:GLN:HE21	1.61	0.66
1:A:183:HIS:HB2	1:A:252:ILE:HD11	1.77	0.65
4:A:331:NDG:O4	3:A:332:NAG:H1	1.96	0.65
1:D:169:PRO:N	1:D:242:VAL:HG23	2.11	0.65
2:B:77:ILE:HG23	2:B:78:GLN:N	2.10	0.65
2:B:54:ARG:HD3	1:G:32:ASP:HB3	1.78	0.65
1:A:96:ASN:HA	1:A:224:ARG:NE	2.11	0.65
1:G:290:ASN:C	1:G:290:ASN:HD22	1.99	0.65
2:B:11:GLU:HA	2:B:11:GLU:OE1	1.95	0.65
1:A:129:GLY:HA3	1:A:162:PRO:HG2	1.79	0.65
1:D:81:ASN:N	1:D:81:ASN:HD22	1.93	0.64
1:A:220:ARG:HD2	1:A:229:ARG:HG3	1.79	0.64
1:A:104:ASP:CG	1:A:107:SER:HB2	2.18	0.64
1:A:27:LYS:HE2	2:E:54:ARG:NH1	2.12	0.64
1:A:29:ILE:H	2:B:105:GLN:HE21	1.44	0.64
1:G:71:LEU:CD2	1:G:179:ILE:HD11	2.27	0.64
1:D:44:GLN:HG2	1:D:292:LYS:HD2	1.79	0.63
1:G:121:ILE:HD12	1:G:257:TYR:OH	1.98	0.63
1:D:54:ASN:O	1:D:55:PRO:C	2.29	0.63
2:E:51:LYS:HE3	2:E:107:THR:OG1	1.98	0.63
1:D:97:CYS:O	1:D:224:ARG:NH1	2.31	0.63
1:D:180:TRP:HB3	1:D:254:PRO:HG3	1.79	0.63
1:A:166:VAL:HG22	1:A:245:ILE:HB	1.81	0.63
1:D:169:PRO:HA	1:D:242:VAL:HG23	1.80	0.62
1:A:12:THR:HG23	2:B:133:MET:CE	2.30	0.62
1:G:161:TYR:HB3	1:G:197:GLN:NE2	2.13	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:220:ARG:CB	1:G:229:ARG:HH11	2.13	0.62
1:A:170:ASN:HD22	1:A:238:LYS:C	2.02	0.62
1:G:86:LEU:HD21	1:G:268:MET:HE3	1.82	0.62
2:H:21:TRP:H	2:H:41:THR:CG2	2.13	0.62
1:A:84:TRP:CE2	1:A:116:GLY:HA2	2.33	0.62
1:G:161:TYR:CE1	1:G:195:TYR:HD2	2.18	0.62
1:G:81:ASN:ND2	4:G:334:NDG:C1	2.62	0.62
2:H:35:ALA:HB2	2:H:153:ARG:NH1	2.14	0.62
1:D:97:CYS:H	1:D:224:ARG:NH1	1.98	0.62
3:A:333:NAG:C4	4:G:330:NDG:C1	2.70	0.62
2:H:151:SER:O	2:H:156:THR:HG23	1.99	0.62
1:A:125:PHE:O	1:A:126:THR:HG23	1.99	0.62
1:A:302:TYR:HE2	2:B:63:PHE:HB3	1.64	0.62
1:D:169:PRO:HA	1:D:242:VAL:HA	1.80	0.62
1:D:264:LYS:HB2	2:E:63:PHE:CG	2.35	0.62
1:D:279:SER:OG	1:D:287:SER:HB3	2.00	0.61
2:H:125:GLN:HE21	2:H:157:TYR:HB3	1.64	0.61
1:D:175:ASP:OD1	1:D:239:PRO:HD3	2.01	0.61
2:B:26:HIS:CE1	2:B:33:GLY:HA3	2.36	0.61
3:A:335:NAG:H1	4:D:332:NDG:H4	1.83	0.61
2:H:71:SER:O	2:H:72:GLU:HG3	2.00	0.61
2:E:43:ALA:O	2:E:47:GLN:HG3	2.00	0.61
1:D:316:LEU:HD23	2:E:52:LEU:HD13	1.83	0.61
2:E:12:ASN:ND2	2:E:12:ASN:N	2.49	0.61
1:G:15:LEU:HD23	2:H:118:LEU:HG	1.82	0.61
1:A:217:ILE:HD12	1:A:217:ILE:N	2.16	0.60
2:H:131:GLU:OE2	2:H:170:ARG:HD2	2.01	0.60
1:D:27:LYS:HB3	2:H:54:ARG:NH1	2.17	0.60
2:E:11:GLU:C	2:E:12:ASN:HD22	2.03	0.60
1:A:248:ASN:HD22	1:A:248:ASN:H	1.48	0.60
1:A:81:ASN:ND2	4:A:331:NDG:C1	2.65	0.60
2:H:19:ASP:OD1	2:H:19:ASP:N	2.35	0.60
1:D:326:LYS:N	2:E:12:ASN:OD1	2.31	0.60
2:B:102:LEU:HD21	2:E:102:LEU:HD23	1.83	0.60
1:G:220:ARG:HB3	1:G:229:ARG:NH1	2.17	0.60
1:G:53:ASN:HB3	1:G:275:ASP:O	2.02	0.60
2:B:77:ILE:HG23	2:B:78:GLN:H	1.67	0.59
1:G:220:ARG:CB	1:G:229:ARG:NH1	2.65	0.59
1:A:182:VAL:HG11	1:A:213:ILE:HG21	1.85	0.59
2:B:98:LEU:HD12	2:B:102:LEU:HD13	1.83	0.59
1:G:316:LEU:HD23	2:H:52:LEU:CD1	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:110:LEU:HD23	2:B:110:LEU:C	2.23	0.59
1:D:111:LEU:HD12	1:D:111:LEU:C	2.22	0.59
1:A:86:LEU:HD21	1:A:268:MET:HE3	1.83	0.59
2:B:102:LEU:HD23	2:H:102:LEU:HD21	1.85	0.59
2:E:91:LEU:O	2:E:94:TYR:HB3	2.03	0.59
2:B:149:ILE:HG22	2:B:150:GLU:N	2.17	0.58
1:A:38:ASN:ND2	3:A:330:NAG:H1	2.18	0.58
1:A:300:ILE:HD11	2:B:69:GLU:HG3	1.85	0.58
2:E:3:PHE:CE1	2:E:113:SER:HB2	2.39	0.58
1:G:38:ASN:HD22	1:G:38:ASN:C	2.06	0.58
1:G:311:GLN:NE2	2:H:93:SER:HB3	2.18	0.58
1:G:29:ILE:HG22	1:G:30:THR:HG23	1.85	0.58
1:G:56:HIS:O	1:G:58:ILE:HG13	2.03	0.58
1:D:220:ARG:HD2	1:D:229:ARG:HG2	1.84	0.58
1:G:220:ARG:HB2	1:G:229:ARG:HH11	1.67	0.58
1:G:42:LEU:O	1:G:292:LYS:HB3	2.03	0.58
1:D:30:THR:HG22	2:H:51:LYS:HB2	1.86	0.58
1:G:248:ASN:N	1:G:248:ASN:HD22	1.96	0.58
1:A:63:ALA:HA	1:A:93:ALA:HA	1.85	0.58
1:A:102:ILE:HG12	1:A:232:ILE:HB	1.86	0.58
1:A:184:HIS:HB3	1:A:220:ARG:NH2	2.19	0.57
1:A:312:ASN:OD1	1:A:313:THR:HG22	2.04	0.57
1:D:120:PHE:CE2	1:D:150:ARG:HD2	2.39	0.57
1:G:183:HIS:O	1:G:185:PRO:HD3	2.04	0.57
1:G:98:TYR:CD2	1:G:99:PRO:HD2	2.39	0.57
1:G:24:THR:CG2	4:G:333:NDG:H6C2	2.35	0.57
2:B:154:ASN:HD21	4:B:223:NDG:C1	2.16	0.57
1:G:81:ASN:ND2	4:G:334:NDG:C7	2.66	0.57
1:A:111:LEU:HD12	1:A:111:LEU:C	2.25	0.57
1:A:302:TYR:CZ	2:B:63:PHE:HD2	2.23	0.57
2:E:100:VAL:HG23	2:E:101:ALA:N	2.20	0.57
2:E:150:GLU:HA	2:E:150:GLU:OE2	2.04	0.57
2:E:131:GLU:OE2	2:E:170:ARG:HD2	2.04	0.57
1:G:99:PRO:HG3	1:G:223:VAL:HG12	1.87	0.57
1:D:167:THR:HG23	1:D:244:VAL:CG2	2.35	0.57
2:E:52:LEU:O	2:E:56:ILE:HG22	2.04	0.57
1:A:125:PHE:HD1	1:A:127:TRP:H	1.53	0.56
1:A:280:GLU:HA	1:A:280:GLU:OE1	2.05	0.56
1:G:170:ASN:HA	1:G:176:LYS:NZ	2.19	0.56
2:E:72:GLU:CG	1:G:238:LYS:NZ	2.68	0.56
5:G:331:MAN:O2	5:G:332:MAN:H1	2.03	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:281:CYS:HB2	1:G:304:ALA:O	2.04	0.56
2:H:68:LYS:HE2	2:H:85:GLU:OE1	2.05	0.56
1:G:288:ILE:HG21	1:G:297:VAL:HG21	1.88	0.56
1:A:132:GLN:HG2	1:A:154:LEU:CD2	2.36	0.56
1:A:81:ASN:CG	4:A:331:NDG:C1	2.74	0.56
1:A:54:ASN:HA	1:A:56:HIS:N	2.20	0.56
1:G:109:ARG:NH1	1:G:267:ILE:CD1	2.68	0.56
1:D:301:THR:HB	1:D:305:CYS:SG	2.46	0.56
2:E:169:ASN:HA	2:E:172:GLN:NE2	2.14	0.56
1:A:71:LEU:O	1:A:148:PHE:HB3	2.05	0.56
2:B:100:VAL:HG23	2:B:101:ALA:N	2.20	0.56
2:B:121:LYS:HD2	2:B:121:LYS:O	2.06	0.55
1:G:15:LEU:CD2	2:H:118:LEU:HG	2.37	0.55
1:A:159:SER:O	1:A:160:ALA:HB2	2.06	0.55
2:B:54:ARG:NH1	1:G:27:LYS:HE2	2.22	0.55
1:G:217:ILE:HD12	1:G:217:ILE:N	2.22	0.55
1:G:266:SER:OG	1:G:267:ILE:N	2.38	0.55
1:A:222:TRP:CZ3	5:A:336:MAN:O1	2.59	0.55
1:D:304:ALA:HB2	2:E:61:GLU:HG2	1.88	0.55
1:A:275:ASP:CG	1:A:276:THR:N	2.60	0.55
2:B:150:GLU:OE2	2:B:150:GLU:HA	2.07	0.55
1:A:42:LEU:HD22	1:A:293:PRO:CG	2.37	0.55
1:A:304:ALA:HB2	2:B:61:GLU:CG	2.37	0.55
1:A:74:PRO:HA	1:A:141:ARG:HH21	1.72	0.55
1:A:189:GLN:O	1:A:193:ASN:HB2	2.06	0.55
2:B:98:LEU:CD1	2:B:102:LEU:HD13	2.36	0.55
2:E:40:SER:O	2:E:43:ALA:HB3	2.05	0.55
1:A:302:TYR:CE2	2:B:63:PHE:HB3	2.42	0.55
2:H:151:SER:CA	2:H:156:THR:HG23	2.37	0.55
1:A:274:ILE:HG12	1:A:274:ILE:O	2.05	0.54
2:H:125:GLN:NE2	2:H:155:GLY:HA2	2.21	0.54
1:A:134:GLY:HA3	1:A:153:TRP:HB3	1.89	0.54
2:B:54:ARG:HA	2:B:58:LYS:NZ	2.23	0.54
1:D:102:ILE:HG12	1:D:232:ILE:HB	1.89	0.54
1:G:221:PRO:HA	4:G:330:NDG:O7	2.07	0.54
1:A:238:LYS:NZ	2:H:72:GLU:HG2	2.23	0.54
1:A:38:ASN:HD21	3:A:330:NAG:H1	1.73	0.54
1:D:148:PHE:CB	1:D:151:LEU:HD12	2.36	0.54
1:D:15:LEU:HD22	2:E:119:PHE:HA	1.90	0.54
1:G:17:HIS:HB2	1:G:320:MET:SD	2.48	0.54
1:G:165:ASN:CG	3:G:335:NAG:O1	2.46	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:38:ASN:OD1	4:D:330:NDG:O1	2.25	0.54
1:A:222:TRP:NE1	1:A:227:PRO:HG3	2.23	0.54
1:D:119:GLU:HB2	1:D:259:LYS:HG2	1.90	0.54
1:G:325:GLU:HG2	2:H:12:ASN:ND2	2.23	0.54
2:E:125:GLN:NE2	2:E:157:TYR:HB3	2.21	0.53
2:E:74:GLU:HG3	2:E:78:GLN:NE2	2.23	0.53
1:A:216:ASN:CB	1:D:212:THR:HG21	2.38	0.53
1:G:71:LEU:HD23	1:G:179:ILE:CD1	2.38	0.53
1:A:43:VAL:HA	1:A:294:PHE:O	2.08	0.53
1:G:39:ALA:HB2	1:G:317:ALA:HA	1.89	0.53
4:D:333:NDG:O4	5:D:334:MAN:C1	2.42	0.53
1:A:44:GLN:NE2	1:A:289:PRO:HD2	2.24	0.53
1:A:72:GLY:HA3	1:A:149:SER:OG	2.09	0.53
1:D:12:THR:O	2:E:26:HIS:HA	2.08	0.53
1:D:38:ASN:ND2	1:D:39:ALA:N	2.57	0.53
1:D:291:ASP:O	2:E:56:ILE:HG13	2.09	0.53
2:B:127:ARG:NH1	2:H:131:GLU:OE1	2.40	0.53
1:A:26:VAL:O	1:A:34:ILE:HG22	2.08	0.53
1:A:304:ALA:CB	2:B:61:GLU:HG2	2.39	0.53
1:A:204:VAL:CG1	1:A:243:LEU:HD11	2.37	0.53
1:D:53:ASN:HD22	1:D:54:ASN:N	2.07	0.53
2:E:77:ILE:HG23	2:E:78:GLN:N	2.23	0.53
2:H:169:ASN:HA	2:H:172:GLN:HE21	1.74	0.53
1:A:82:GLU:HG3	1:A:83:THR:H	1.74	0.53
2:B:87:THR:O	2:B:91:LEU:HD22	2.08	0.53
1:D:28:THR:N	1:D:31:ASP:O	2.31	0.53
2:B:57:GLU:C	2:B:58:LYS:HG3	2.29	0.53
1:A:228:GLY:O	1:A:229:ARG:HG2	2.08	0.52
2:B:158:ASP:HB3	2:B:161:ILE:CD1	2.39	0.52
1:G:150:ARG:C	1:G:255:ARG:HD2	2.29	0.52
1:G:165:ASN:C	1:G:165:ASN:HD22	2.12	0.52
1:A:285:ASN:ND2	4:A:334:NDG:C1	2.71	0.52
1:D:117:THR:HG21	1:D:261:ARG:HD2	1.91	0.52
1:D:129:GLY:HA3	1:D:162:PRO:HG2	1.91	0.52
2:E:22:TYR:HE2	2:E:115:MET:HB2	1.74	0.52
1:A:43:VAL:HG23	6:A:347:HOH:O	2.08	0.52
2:B:150:GLU:HG3	4:B:223:NDG:O5	2.10	0.52
1:D:183:HIS:O	1:D:185:PRO:HD3	2.10	0.52
2:H:123:ARG:HB3	2:H:123:ARG:HH11	1.75	0.52
2:B:114:GLU:OE2	2:B:117:LYS:HD2	2.10	0.52
1:D:304:ALA:CA	2:E:61:GLU:HG2	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:131:GLU:CG	2:B:170:ARG:HH11	2.22	0.52
2:B:48:ILE:HG12	2:B:107:THR:HG23	1.90	0.52
1:D:119:GLU:HB2	1:D:259:LYS:CG	2.40	0.52
1:D:180:TRP:CD2	1:D:204:VAL:HG21	2.45	0.52
1:D:295:GLN:NE2	1:D:308:TYR:HD1	2.08	0.52
2:H:28:ASN:ND2	2:H:145:ASP:HA	2.25	0.52
1:A:233:TYR:CD1	1:A:233:TYR:N	2.76	0.52
2:E:132:ASP:OD2	2:H:124:ARG:NE	2.40	0.52
1:D:98:TYR:CD2	1:D:99:PRO:HD2	2.44	0.52
1:G:323:VAL:HG21	2:H:7:ALA:HB2	1.92	0.52
1:A:203:THR:HG23	1:A:212:THR:HB	1.92	0.52
1:G:293:PRO:HB2	1:G:294:PHE:CD1	2.45	0.52
1:G:84:TRP:CE2	1:G:116:GLY:HA2	2.45	0.52
1:G:264:LYS:HB2	2:H:63:PHE:CG	2.45	0.52
2:B:126:LEU:HD21	2:B:152:ILE:HD13	1.91	0.52
1:G:228:GLY:C	1:G:229:ARG:HD2	2.31	0.52
1:A:67:ILE:HG13	1:A:105:TYR:CZ	2.45	0.51
1:D:167:THR:HG22	1:D:242:VAL:CG2	2.40	0.51
2:H:126:LEU:HD21	2:H:152:ILE:HD13	1.91	0.51
1:D:36:VAL:HG23	1:D:38:ASN:H	1.75	0.51
1:G:325:GLU:OE2	2:H:15:GLU:HG3	2.09	0.51
1:A:170:ASN:ND2	1:A:239:PRO:HA	2.24	0.51
1:A:275:ASP:CG	1:A:276:THR:H	2.13	0.51
1:A:279:SER:OG	1:A:287:SER:HB3	2.11	0.51
1:A:92:ASN:HD22	1:A:93:ALA:N	2.07	0.51
2:E:85:GLU:O	2:E:89:ILE:HG13	2.11	0.51
1:G:154:LEU:HD12	1:G:251:LEU:HD23	1.92	0.51
1:G:42:LEU:HD11	1:G:316:LEU:HB2	1.92	0.51
1:G:99:PRO:HG3	1:G:223:VAL:CG1	2.40	0.51
1:D:55:PRO:HG3	1:D:278:ILE:HG23	1.91	0.51
1:D:295:GLN:HE21	1:D:308:TYR:HB2	1.74	0.51
1:D:310:LYS:NZ	2:E:90:ASP:OD1	2.42	0.51
1:G:81:ASN:HD21	4:G:334:NDG:C1	2.24	0.51
1:A:203:THR:HG21	1:G:220:ARG:NH1	2.25	0.51
5:D:334:MAN:HO2	5:D:335:MAN:H5	1.74	0.51
1:G:31:ASP:N	6:G:339:HOH:O	2.42	0.51
1:D:221:PRO:O	1:D:229:ARG:NH2	2.40	0.51
1:D:99:PRO:CB	1:D:229:ARG:HE	2.24	0.51
1:A:236:ILE:N	1:A:236:ILE:HD12	2.26	0.51
1:A:29:ILE:O	1:A:29:ILE:HG22	2.10	0.51
1:D:99:PRO:HG3	1:D:223:VAL:CG1	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:11:GLU:OE2	2:H:11:GLU:HA	2.11	0.51
1:D:53:ASN:HB3	1:D:275:ASP:O	2.11	0.51
1:D:311:GLN:HG3	1:D:314:LEU:HD11	1.92	0.51
2:H:135:ASN:OD1	2:H:137:CYS:SG	2.69	0.51
2:B:135:ASN:OD1	2:B:137:CYS:HB2	2.11	0.50
1:G:290:ASN:ND2	1:G:290:ASN:O	2.44	0.50
2:H:21:TRP:H	2:H:41:THR:HG23	1.74	0.50
2:H:46:ASP:O	2:H:50:ARG:HG3	2.11	0.50
1:A:228:GLY:C	1:A:229:ARG:HG2	2.32	0.50
1:G:220:ARG:HD2	1:G:229:ARG:HD3	1.93	0.50
3:A:335:NAG:H4	5:A:336:MAN:O1	2.09	0.50
1:D:54:ASN:C	1:D:56:HIS:N	2.58	0.50
1:D:58:ILE:HD11	1:D:282:ILE:CD1	2.41	0.50
2:E:57:GLU:C	2:E:58:LYS:HG3	2.30	0.50
1:G:108:LEU:O	1:G:112:VAL:HG23	2.10	0.50
2:E:8:GLY:O	2:E:10:ILE:N	2.45	0.50
2:B:158:ASP:OD1	2:B:161:ILE:HG13	2.12	0.50
1:D:264:LYS:HB2	2:E:63:PHE:CD1	2.46	0.50
1:D:80:GLN:O	1:D:81:ASN:HB2	2.10	0.50
1:A:235:THR:C	1:A:236:ILE:HD12	2.32	0.50
2:B:121:LYS:HD2	2:B:121:LYS:C	2.32	0.50
2:E:9:PHE:CD1	2:E:10:ILE:HG13	2.47	0.50
1:G:127:TRP:CZ2	1:G:253:ALA:HB1	2.46	0.50
1:A:283:THR:C	1:A:285:ASN:H	2.15	0.50
1:G:90:ARG:HH22	1:G:274:ILE:HG13	1.77	0.50
2:B:125:GLN:HE22	2:B:155:GLY:CA	2.00	0.50
1:D:42:LEU:O	1:D:293:PRO:HD2	2.11	0.50
1:D:97:CYS:SG	1:D:98:TYR:N	2.84	0.50
1:G:180:TRP:HB3	1:G:254:PRO:HG3	1.94	0.50
1:G:63:ALA:HA	1:G:93:ALA:HA	1.93	0.49
1:G:89:GLU:HG3	1:G:267:ILE:HD11	1.93	0.49
1:G:325:GLU:HG2	2:H:13:GLY:O	2.12	0.49
1:G:48:THR:HG23	1:G:287:SER:O	2.12	0.49
1:A:195:TYR:CE2	1:A:250:ASN:HA	2.47	0.49
1:A:290:ASN:HD22	1:A:290:ASN:H	1.60	0.49
1:A:80:GLN:O	1:A:81:ASN:HB2	2.12	0.49
1:G:44:GLN:O	1:G:295:GLN:HA	2.12	0.49
1:G:297:VAL:O	4:G:336:NDG:H8C1	2.12	0.49
2:H:110:LEU:HD23	2:H:110:LEU:C	2.32	0.49
1:G:304:ALA:HB2	2:H:61:GLU:HG2	1.95	0.49
1:A:96:ASN:ND2	1:A:96:ASN:C	2.64	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:222:TRP:CD1	1:G:227:PRO:HG3	2.48	0.49
1:A:134:GLY:CA	1:A:153:TRP:HB3	2.43	0.49
1:A:220:ARG:NH1	1:D:203:THR:HG21	2.28	0.49
1:D:60:ASP:HB3	1:D:62:ARG:NH1	2.27	0.49
2:H:35:ALA:CB	2:H:153:ARG:NH1	2.75	0.49
2:H:110:LEU:HD23	2:H:110:LEU:O	2.12	0.49
1:G:175:ASP:OD1	1:G:239:PRO:HD3	2.13	0.49
1:A:163:VAL:O	1:A:163:VAL:HG12	2.13	0.49
1:D:71:LEU:HD11	1:D:232:ILE:CD1	2.43	0.49
2:H:126:LEU:HD13	2:H:130:ALA:CB	2.43	0.49
3:A:335:NAG:C1	4:D:332:NDG:HC	2.23	0.49
2:E:54:ARG:HA	2:E:58:LYS:NZ	2.28	0.49
1:G:295:GLN:NE2	1:G:308:TYR:HB2	2.28	0.49
1:D:59:LEU:HD22	1:D:82:GLU:CG	2.43	0.48
1:A:279:SER:CB	1:A:287:SER:HB3	2.43	0.48
1:D:177:LEU:HD13	1:D:236:ILE:HD11	1.95	0.48
1:D:26:VAL:CG1	1:D:27:LYS:N	2.76	0.48
2:E:121:LYS:HD2	2:E:121:LYS:O	2.12	0.48
1:G:222:TRP:CZ3	5:G:331:MAN:H3	2.48	0.48
1:D:97:CYS:N	1:D:224:ARG:HH11	2.11	0.48
1:A:138:ALA:HB1	1:A:224:ARG:HB2	1.96	0.48
1:A:222:TRP:CD1	1:A:227:PRO:HG3	2.47	0.48
3:A:335:NAG:H1	4:D:332:NDG:C4	2.44	0.48
1:A:186:SER:HA	1:A:218:GLY:O	2.13	0.48
2:B:125:GLN:NE2	2:B:155:GLY:CA	2.64	0.48
1:D:27:LYS:HB3	2:H:54:ARG:HH12	1.77	0.48
1:G:305:CYS:HA	1:G:306:PRO:HD3	1.67	0.48
2:B:131:GLU:CD	2:B:170:ARG:HH11	2.16	0.48
1:G:26:VAL:CG1	2:H:104:ASN:ND2	2.77	0.48
1:G:290:ASN:C	1:G:290:ASN:ND2	2.66	0.48
1:G:97:CYS:SG	1:G:98:TYR:N	2.83	0.48
2:E:120:GLU:OE1	2:E:123:ARG:NH1	2.47	0.48
1:G:86:LEU:HD22	1:G:302:TYR:CD1	2.48	0.48
1:G:170:ASN:ND2	1:G:239:PRO:HA	2.28	0.48
1:G:251:LEU:HD21	1:G:253:ALA:HB2	1.96	0.48
1:G:27:LYS:HG2	1:G:32:ASP:O	2.14	0.48
1:A:73:ASP:OD1	1:A:74:PRO:HD2	2.14	0.48
1:D:213:ILE:HG12	1:D:233:TYR:CZ	2.49	0.48
1:D:55:PRO:HG3	1:D:278:ILE:CG2	2.44	0.48
1:A:182:VAL:HG11	1:A:213:ILE:CG2	2.42	0.47
1:A:59:LEU:CD2	1:A:82:GLU:HG2	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:PHE:CD1	1:A:94:PHE:C	2.88	0.47
1:D:323:VAL:HG21	2:E:7:ALA:HB2	1.95	0.47
1:D:59:LEU:HD22	1:D:82:GLU:HG3	1.96	0.47
1:G:54:ASN:CG	1:G:55:PRO:HA	2.34	0.47
1:A:111:LEU:HD12	1:A:112:VAL:HG23	1.96	0.47
1:G:38:ASN:ND2	1:G:318:THR:OG1	2.47	0.47
1:D:294:PHE:HB3	1:D:309:VAL:HG22	1.95	0.47
1:G:95:SER:O	1:G:224:ARG:NH2	2.36	0.47
1:A:75:HIS:NE2	1:A:94:PHE:CE1	2.82	0.47
2:B:145:ASP:O	2:B:148:CYS:HB3	2.14	0.47
1:D:248:ASN:N	1:D:248:ASN:HD22	2.05	0.47
1:G:222:TRP:NE1	1:G:227:PRO:HG3	2.29	0.47
1:G:295:GLN:HE21	1:G:308:TYR:HB2	1.79	0.47
1:A:104:ASP:OD1	1:A:107:SER:HB2	2.14	0.47
2:B:3:PHE:HB2	2:B:112:ASP:OD2	2.14	0.47
1:D:99:PRO:HB2	1:D:229:ARG:HE	1.79	0.47
1:D:97:CYS:H	1:D:224:ARG:HH11	1.62	0.47
1:G:164:LEU:HB2	1:G:247:SER:O	2.15	0.47
2:H:114:GLU:OE2	2:H:117:LYS:HD2	2.14	0.47
1:A:55:PRO:HD3	1:A:278:ILE:HG23	1.96	0.47
1:G:86:LEU:HD22	1:G:302:TYR:CG	2.49	0.47
1:A:216:ASN:HB2	1:D:212:THR:HG21	1.95	0.47
2:E:9:PHE:CE1	2:E:10:ILE:HG13	2.49	0.47
1:G:179:ILE:O	1:G:179:ILE:HG12	2.13	0.47
1:D:26:VAL:HG12	1:D:27:LYS:N	2.29	0.47
6:A:340:HOH:O	1:G:216:ASN:HB3	2.14	0.47
1:G:222:TRP:CE2	4:G:330:NDG:H4	2.49	0.47
1:A:204:VAL:HG13	1:A:243:LEU:HD11	1.97	0.47
2:H:28:ASN:HD22	2:H:145:ASP:HA	1.80	0.47
1:A:230:ILE:HD12	1:A:252:ILE:HG12	1.97	0.47
2:B:141:TYR:CG	2:B:170:ARG:HG2	2.50	0.47
2:B:17:MET:O	2:B:18:ILE:HD13	2.15	0.47
1:D:81:ASN:CG	3:D:331:NAG:HO1	2.10	0.47
1:G:220:ARG:HB2	1:G:229:ARG:NH1	2.27	0.47
2:H:37:ASP:OD2	2:H:40:SER:HB2	2.15	0.47
1:D:53:ASN:CG	1:D:276:THR:HA	2.35	0.46
1:G:67:ILE:HG13	1:G:105:TYR:OH	2.15	0.46
2:H:129:ASN:OD1	2:H:129:ASN:N	2.47	0.46
1:A:251:LEU:HD12	1:A:252:ILE:N	2.30	0.46
2:B:154:ASN:ND2	4:B:223:NDG:C1	2.78	0.46
1:D:165:ASN:C	1:D:165:ASN:ND2	2.68	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:111:LEU:HD12	1:D:112:VAL:N	2.30	0.46
2:H:70:PHE:CD1	2:H:70:PHE:N	2.83	0.46
1:D:85:ASP:O	1:D:265:SER:HA	2.16	0.46
2:E:37:ASP:OD2	2:E:40:SER:CB	2.63	0.46
1:G:180:TRP:CE2	1:G:204:VAL:HG21	2.51	0.46
1:A:255:ARG:HG2	1:A:255:ARG:NH1	2.31	0.46
1:A:54:ASN:HA	1:A:56:HIS:H	1.79	0.46
1:D:180:TRP:N	1:D:180:TRP:CD1	2.83	0.46
1:G:34:ILE:HG12	1:G:35:GLU:N	2.31	0.46
1:A:255:ARG:HG2	1:A:255:ARG:HH11	1.80	0.46
1:A:90:ARG:HH11	1:A:271:ASP:HA	1.80	0.46
2:B:49:ASN:O	2:B:52:LEU:HB3	2.15	0.46
1:D:27:LYS:HE2	2:H:54:ARG:CZ	2.46	0.46
1:D:167:THR:HG22	1:D:242:VAL:HG21	1.98	0.46
1:G:311:GLN:HG2	1:G:311:GLN:H	1.50	0.46
1:A:54:ASN:ND2	1:A:55:PRO:HA	2.30	0.46
1:D:220:ARG:HD2	1:D:229:ARG:CG	2.45	0.46
2:E:70:PHE:CD1	2:E:70:PHE:N	2.84	0.46
1:D:220:ARG:HH11	1:G:210:GLN:HG3	1.80	0.46
1:G:90:ARG:HD3	1:G:270:SER:O	2.16	0.46
1:A:288:ILE:HG21	1:A:297:VAL:HG21	1.98	0.45
1:D:325:GLU:HA	2:E:12:ASN:HB3	1.97	0.45
2:E:8:GLY:C	2:E:10:ILE:N	2.69	0.45
1:G:295:GLN:NE2	1:G:308:TYR:HD1	2.14	0.45
2:E:60:ASN:C	2:E:60:ASN:HD22	2.17	0.45
1:A:291:ASP:OD1	1:A:292:LYS:HG3	2.17	0.45
1:A:324:PRO:O	1:A:325:GLU:CB	2.64	0.45
1:G:228:GLY:O	1:G:229:ARG:HD2	2.16	0.45
1:G:34:ILE:CG1	1:G:35:GLU:N	2.79	0.45
1:A:234:TRP:HD1	1:A:236:ILE:CD1	2.29	0.45
1:A:291:ASP:O	2:B:56:ILE:HG13	2.16	0.45
1:D:58:ILE:HD11	1:D:282:ILE:HD13	1.98	0.45
1:D:120:PHE:CD2	1:D:150:ARG:HD2	2.51	0.45
1:G:125:PHE:CE1	1:G:254:PRO:HB2	2.52	0.45
1:A:229:ARG:HG2	1:A:229:ARG:HH11	1.81	0.45
1:A:82:GLU:HG3	1:A:83:THR:N	2.32	0.45
1:D:165:ASN:C	1:D:165:ASN:HD22	2.20	0.45
1:D:60:ASP:OD2	1:D:90:ARG:NH1	2.50	0.45
1:G:38:ASN:ND2	1:G:38:ASN:C	2.69	0.45
1:D:222:TRP:NE1	1:D:227:PRO:HG3	2.31	0.45
1:D:87:PHE:O	1:D:267:ILE:HG13	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:186:SER:HA	1:G:218:GLY:O	2.17	0.45
1:G:220:ARG:O	1:G:227:PRO:HA	2.16	0.45
2:B:27:GLN:HE21	2:B:27:GLN:HB3	1.51	0.45
1:D:137:SER:HA	1:D:145:ASN:OD1	2.17	0.45
2:E:19:ASP:OD1	2:E:19:ASP:N	2.47	0.45
1:A:27:LYS:HG2	1:A:32:ASP:O	2.17	0.45
1:D:12:THR:HG23	2:E:133:MET:CE	2.47	0.45
1:D:66:LEU:HD21	1:D:112:VAL:CG1	2.44	0.45
1:G:147:PHE:CE2	1:G:151:LEU:HB2	2.51	0.45
1:A:217:ILE:CD1	1:A:217:ILE:N	2.80	0.45
1:A:314:LEU:HB2	6:A:347:HOH:O	2.17	0.45
1:A:53:ASN:OD1	1:A:276:THR:HA	2.17	0.45
1:G:161:TYR:HE1	1:G:195:TYR:HD2	1.62	0.45
1:G:181:GLY:O	1:G:252:ILE:HB	2.17	0.45
1:A:283:THR:C	1:A:285:ASN:N	2.70	0.44
1:D:67:ILE:O	1:D:70:LEU:HB3	2.17	0.44
2:E:121:LYS:HD2	2:E:121:LYS:C	2.37	0.44
2:H:156:THR:HG21	3:H:341:NAG:H1	1.99	0.44
1:A:108:LEU:O	1:A:109:ARG:C	2.55	0.44
1:A:89:GLU:HG3	1:A:267:ILE:HD11	2.00	0.44
1:D:109:ARG:NH1	1:D:267:ILE:CD1	2.78	0.44
1:D:19:ALA:O	2:E:15:GLU:HA	2.17	0.44
1:D:324:PRO:O	1:D:325:GLU:CB	2.65	0.44
5:D:334:MAN:O2	5:D:335:MAN:C5	2.62	0.44
1:D:41:GLU:HG2	1:D:315:LYS:NZ	2.32	0.44
1:A:302:TYR:CE2	2:B:63:PHE:HD2	2.35	0.44
1:D:167:THR:HG23	1:D:244:VAL:HG22	1.98	0.44
2:E:77:ILE:CG2	2:E:78:GLN:N	2.80	0.44
1:D:304:ALA:CB	2:E:61:GLU:HG2	2.48	0.44
1:G:159:SER:O	1:G:160:ALA:HB2	2.18	0.44
1:G:195:TYR:O	1:G:196:VAL:HB	2.18	0.44
1:A:253:ALA:HA	1:A:254:PRO:HD3	1.77	0.44
2:B:158:ASP:CG	2:B:161:ILE:HG13	2.37	0.44
2:B:169:ASN:HA	2:B:172:GLN:NE2	2.31	0.44
1:D:186:SER:HB3	1:D:227:PRO:HB2	1.99	0.44
1:D:203:THR:OG1	1:D:212:THR:HB	2.18	0.44
1:D:29:ILE:HD11	2:E:102:LEU:CD1	2.44	0.44
1:G:213:ILE:HG22	1:G:214:ILE:N	2.32	0.44
1:G:252:ILE:HG22	1:G:252:ILE:O	2.18	0.44
1:G:47:SER:HA	1:G:288:ILE:HG22	1.99	0.44
1:G:67:ILE:O	1:G:70:LEU:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:71:SER:C	2:B:72:GLU:HG3	2.37	0.44
1:D:307:LYS:HE2	2:E:60:ASN:HD21	1.81	0.44
2:E:8:GLY:C	2:E:10:ILE:H	2.21	0.44
1:G:264:LYS:HB2	2:H:63:PHE:CD1	2.53	0.44
1:G:253:ALA:HA	1:G:254:PRO:HD3	1.70	0.44
1:G:291:ASP:OD1	1:G:292:LYS:HD2	2.17	0.44
1:D:189:GLN:O	1:D:193:ASN:HB2	2.18	0.44
2:B:131:GLU:CG	2:B:170:ARG:NH1	2.81	0.44
1:G:132:GLN:HG2	1:G:154:LEU:CD2	2.48	0.44
1:A:111:LEU:CD1	1:A:112:VAL:HG23	2.48	0.43
2:B:168:ASN:O	2:B:172:GLN:HB3	2.18	0.43
2:B:23:GLY:HA3	2:B:36:ALA:HA	2.00	0.43
1:D:167:THR:HG23	1:D:244:VAL:HG23	2.00	0.43
1:D:221:PRO:HG3	1:G:244:VAL:CG2	2.48	0.43
1:G:300:ILE:HD11	2:H:69:GLU:HG3	2.00	0.43
1:G:67:ILE:O	1:G:70:LEU:HB3	2.17	0.43
2:E:2:LEU:HB3	2:H:3:PHE:CZ	2.53	0.43
1:A:125:PHE:HB2	1:A:127:TRP:CD1	2.54	0.43
1:A:92:ASN:C	1:A:92:ASN:HD22	2.19	0.43
2:B:168:ASN:ND2	2:B:168:ASN:O	2.50	0.43
1:G:248:ASN:H	1:G:248:ASN:ND2	2.02	0.43
1:G:76:CYS:C	1:G:78:VAL:H	2.20	0.43
1:A:272:ALA:HA	1:A:273:PRO:HD3	1.90	0.43
1:D:77:ASP:OD2	1:D:141:ARG:NH1	2.51	0.43
1:D:98:TYR:CE2	1:D:230:ILE:HD13	2.52	0.43
1:A:212:THR:HG21	1:G:216:ASN:HB2	2.00	0.43
1:A:165:ASN:HA	1:A:245:ILE:O	2.18	0.43
1:A:119:GLU:O	1:A:258:PHE:HA	2.19	0.43
1:A:29:ILE:HD11	2:B:102:LEU:CD1	2.31	0.43
2:B:77:ILE:CG2	2:B:78:GLN:N	2.79	0.43
1:D:166:VAL:HG12	1:D:167:THR:N	2.34	0.43
1:G:26:VAL:HG12	1:G:27:LYS:O	2.18	0.43
1:G:310:LYS:HE2	2:H:90:ASP:OD1	2.18	0.43
1:D:294:PHE:HA	1:D:307:LYS:O	2.18	0.43
1:G:172:ASP:HB3	1:G:174:PHE:CE2	2.54	0.43
2:H:21:TRP:CG	2:H:41:THR:HG23	2.54	0.43
1:A:121:ILE:HG22	1:A:121:ILE:O	2.19	0.43
1:A:96:ASN:HD22	1:A:96:ASN:C	2.22	0.43
1:G:84:TRP:HZ3	1:G:118:LEU:HG	1.84	0.43
1:G:322:ASN:O	1:G:324:PRO:HD3	2.19	0.43
1:G:323:VAL:CG2	2:H:7:ALA:HB2	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:116:GLY:HA3	1:A:265:SER:OG	2.19	0.43
1:A:41:GLU:HG2	1:A:315:LYS:NZ	2.34	0.43
1:A:73:ASP:OD1	1:A:96:ASN:ND2	2.52	0.43
2:B:15:GLU:O	2:B:18:ILE:HD11	2.18	0.43
1:D:84:TRP:CE2	1:D:116:GLY:HA2	2.53	0.43
2:E:87:THR:HG23	2:H:88:LYS:HG3	2.00	0.43
1:G:72:GLY:HA3	1:G:149:SER:OG	2.18	0.43
1:A:137:SER:HA	1:A:145:ASN:OD1	2.18	0.43
1:A:67:ILE:HG13	1:A:105:TYR:CE1	2.54	0.43
1:D:132:GLN:HG2	1:D:154:LEU:CD2	2.49	0.43
1:D:53:ASN:OD1	1:D:276:THR:HA	2.19	0.43
1:G:224:ARG:NH1	1:G:224:ARG:HG3	2.34	0.43
1:G:98:TYR:CE1	1:G:226:GLN:HG3	2.54	0.43
1:G:44:GLN:N	1:G:292:LYS:HZ2	2.17	0.43
2:H:125:GLN:HE22	2:H:152:ILE:HA	1.83	0.43
2:H:127:ARG:HB3	2:H:128:GLU:H	1.53	0.43
1:A:210:GLN:HE21	1:A:210:GLN:HB3	1.54	0.43
1:G:291:ASP:OD1	1:G:292:LYS:CG	2.65	0.43
1:G:325:GLU:OE2	2:H:15:GLU:CG	2.67	0.43
1:A:52:CYS:SG	1:A:279:SER:HB2	2.59	0.42
5:A:336:MAN:O2	5:A:337:MAN:O1	1.94	0.42
2:B:91:LEU:HD13	2:E:92:TRP:CE2	2.54	0.42
1:A:214:ILE:HA	1:A:215:PRO:HD3	1.94	0.42
2:B:168:ASN:ND2	2:B:168:ASN:C	2.72	0.42
5:D:334:MAN:C2	5:D:335:MAN:H1	2.49	0.42
2:E:5:ALA:O	2:E:10:ILE:HB	2.19	0.42
2:E:1:GLY:HA2	2:E:109:ASP:OD1	2.19	0.42
1:A:20:VAL:N	1:A:322:ASN:OD1	2.49	0.42
2:B:133:MET:HE2	2:B:138:PHE:C	2.39	0.42
1:D:220:ARG:HB2	1:D:227:PRO:O	2.19	0.42
1:D:311:GLN:HE21	1:D:314:LEU:HD11	1.84	0.42
1:G:214:ILE:HA	1:G:215:PRO:HD3	1.91	0.42
1:G:320:MET:CE	2:H:21:TRP:HB3	2.49	0.42
1:G:67:ILE:HG13	1:G:105:TYR:CE1	2.54	0.42
1:A:29:ILE:O	1:A:29:ILE:CG2	2.68	0.42
1:A:34:ILE:O	1:A:34:ILE:HG23	2.20	0.42
2:B:18:ILE:O	2:B:18:ILE:HG22	2.19	0.42
1:D:69:ALA:HA	1:D:76:CYS:HB3	2.02	0.42
1:G:312:ASN:OD1	1:G:313:THR:HG22	2.19	0.42
1:A:168:MET:C	1:A:242:VAL:HG23	2.40	0.42
2:H:4:GLY:HA2	6:H:345:HOH:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:335:NAG:C4	5:A:336:MAN:C1	2.82	0.42
1:D:149:SER:O	1:D:255:ARG:HD2	2.20	0.42
1:D:53:ASN:ND2	1:D:54:ASN:N	2.68	0.42
2:B:25:ARG:NE	2:B:34:GLN:OE1	2.37	0.42
1:G:301:THR:HB	1:G:305:CYS:SG	2.60	0.42
2:H:66:ILE:HG13	2:H:67:GLU:O	2.20	0.42
2:B:122:THR:O	2:B:123:ARG:C	2.58	0.42
1:D:304:ALA:HA	2:E:61:GLU:HG2	2.02	0.42
1:G:311:GLN:HE21	2:H:93:SER:HB3	1.84	0.42
1:A:138:ALA:HB2	1:A:226:GLN:HG2	2.02	0.42
2:B:100:VAL:CG2	2:B:101:ALA:N	2.82	0.42
1:D:29:ILE:O	1:D:29:ILE:HG22	2.18	0.42
1:D:67:ILE:HA	1:D:67:ILE:HD13	1.89	0.42
2:B:150:GLU:O	2:B:154:ASN:ND2	2.53	0.41
2:B:168:ASN:HD22	2:B:168:ASN:C	2.22	0.41
2:B:61:GLU:O	2:B:62:LYS:HD3	2.20	0.41
1:A:108:LEU:HD12	1:A:111:LEU:HD11	2.02	0.41
1:D:55:PRO:HD3	1:D:278:ILE:HA	2.02	0.41
2:E:149:ILE:HG22	2:E:150:GLU:N	2.35	0.41
2:E:152:ILE:HA	2:E:157:TYR:HB2	2.01	0.41
2:E:20:GLY:HA3	2:E:36:ALA:HB1	2.00	0.41
2:E:68:LYS:HA	6:E:242:HOH:O	2.20	0.41
1:G:184:HIS:HB3	1:G:220:ARG:NH2	2.35	0.41
1:D:219:SER:H	1:G:246:ASN:ND2	2.18	0.41
1:A:300:ILE:O	1:A:301:THR:CG2	2.68	0.41
1:A:62:ARG:HH11	1:A:62:ARG:HG2	1.85	0.41
1:D:284:PRO:CG	1:D:300:ILE:HB	2.51	0.41
1:D:99:PRO:HB3	1:D:229:ARG:NE	2.35	0.41
1:D:98:TYR:HA	1:D:99:PRO:HD3	1.92	0.41
2:E:57:GLU:CG	2:E:57:GLU:O	2.61	0.41
2:H:126:LEU:HD13	2:H:130:ALA:HB3	2.02	0.41
1:A:58:ILE:HD11	1:A:282:ILE:CD1	2.51	0.41
1:A:97:CYS:SG	1:A:98:TYR:N	2.93	0.41
1:D:26:VAL:CG1	2:E:104:ASN:ND2	2.83	0.41
2:E:148:CYS:O	2:E:152:ILE:HG13	2.21	0.41
1:A:101:ASP:O	1:A:231:SER:HA	2.21	0.41
1:A:169:PRO:HA	1:A:242:VAL:HG23	2.02	0.41
1:A:49:GLY:O	1:A:273:PRO:HD2	2.21	0.41
1:D:26:VAL:HG11	2:E:104:ASN:CG	2.41	0.41
1:G:170:ASN:HD22	1:G:238:LYS:C	2.23	0.41
1:G:203:THR:HG23	1:G:212:THR:HB	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:284:PRO:HG2	1:D:300:ILE:HB	2.02	0.41
1:G:248:ASN:N	1:G:248:ASN:ND2	2.67	0.41
1:A:14:CYS:O	2:B:24:PHE:HA	2.20	0.41
2:B:71:SER:OG	2:B:72:GLU:OE2	2.39	0.41
1:A:125:PHE:CD1	1:A:126:THR:N	2.89	0.41
1:A:222:TRP:CE3	1:A:225:GLY:HA2	2.56	0.41
1:A:300:ILE:C	1:A:301:THR:HG23	2.42	0.41
4:A:334:NDG:H3	4:B:222:NDG:O1	2.20	0.41
2:B:119:PHE:CE1	2:B:136:GLY:HA2	2.55	0.41
1:D:172:ASP:O	1:D:239:PRO:HB3	2.20	0.41
1:D:27:LYS:HE2	2:H:54:ARG:NH2	2.36	0.41
1:D:67:ILE:HG13	1:D:105:TYR:CZ	2.56	0.41
1:D:99:PRO:CB	1:D:229:ARG:NE	2.83	0.41
2:E:61:GLU:O	2:E:62:LYS:HD3	2.21	0.41
1:A:26:VAL:CG1	1:A:27:LYS:N	2.83	0.41
1:A:53:ASN:O	1:A:54:ASN:HB3	2.20	0.41
2:E:158:ASP:HB3	2:E:161:ILE:HD12	2.02	0.41
6:E:248:HOH:O	1:G:208:ARG:CG	2.68	0.41
2:H:120:GLU:HG3	2:H:123:ARG:NH1	2.36	0.41
2:H:26:HIS:CE1	2:H:33:GLY:HA3	2.56	0.41
3:A:335:NAG:O3	5:A:336:MAN:C1	2.69	0.41
1:D:226:GLN:HA	1:D:227:PRO:HD3	1.84	0.41
1:D:313:THR:O	1:D:313:THR:HG23	2.21	0.41
1:G:212:THR:O	1:G:213:ILE:HD13	2.21	0.41
1:G:254:PRO:HA	6:G:341:HOH:O	2.21	0.41
1:G:295:GLN:HG3	1:G:306:PRO:O	2.21	0.41
1:G:304:ALA:HA	2:H:61:GLU:HA	2.03	0.41
1:A:57:ARG:O	1:A:85:ASP:HB2	2.22	0.40
1:D:44:GLN:HG2	1:D:292:LYS:CD	2.50	0.40
1:G:101:ASP:O	1:G:232:ILE:N	2.52	0.40
4:G:330:NDG:O4	5:G:331:MAN:C1	2.65	0.40
1:G:77:ASP:HA	6:G:343:HOH:O	2.19	0.40
2:H:151:SER:HA	2:H:156:THR:CG2	2.48	0.40
1:A:283:THR:O	1:A:285:ASN:N	2.54	0.40
1:A:285:ASN:HD21	4:A:334:NDG:C2	2.34	0.40
1:A:66:LEU:HG	1:A:66:LEU:O	2.22	0.40
2:B:102:LEU:HD21	2:E:102:LEU:CD2	2.48	0.40
2:B:122:THR:O	2:B:125:GLN:N	2.54	0.40
1:D:288:ILE:HA	1:D:289:PRO:HD3	1.84	0.40
1:D:324:PRO:O	1:D:325:GLU:HB2	2.21	0.40
1:D:99:PRO:HG3	1:D:223:VAL:HG12	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:42:GLN:HG3	2:E:46:ASP:OD2	2.22	0.40
1:G:121:ILE:HD12	1:G:257:TYR:CZ	2.56	0.40
1:G:292:LYS:HA	1:G:293:PRO:HD3	1.94	0.40
2:B:150:GLU:OE2	2:B:150:GLU:CA	2.69	0.40
2:E:74:GLU:HG3	2:E:78:GLN:HE21	1.86	0.40
1:G:170:ASN:ND2	1:G:238:LYS:C	2.75	0.40
1:A:20:VAL:HB	1:A:21:PRO:CD	2.52	0.40
2:H:117:LYS:O	2:H:121:LYS:HB2	2.22	0.40
1:A:220:ARG:HH12	1:D:203:THR:HG21	1.86	0.40
1:D:121:ILE:HD12	1:D:257:TYR:CE1	2.57	0.40
2:E:100:VAL:CG2	2:E:101:ALA:N	2.85	0.40
1:G:51:ILE:HG22	1:G:58:ILE:CD1	2.51	0.40
1:D:27:LYS:CB	2:H:54:ARG:HH12	2.35	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%)	268 (85%)	40 (13%)	8 (2%)	5	21
1	D	316/329 (96%)	283 (90%)	30 (10%)	3 (1%)	17	48
1	G	316/329 (96%)	276 (87%)	35 (11%)	5 (2%)	9	32
2	B	170/221 (77%)	145 (85%)	24 (14%)	1 (1%)	25	58
2	E	170/221 (77%)	153 (90%)	13 (8%)	4 (2%)	6	22
2	H	170/221 (77%)	150 (88%)	18 (11%)	2 (1%)	13	40
All	All	1458/1650 (88%)	1275 (87%)	160 (11%)	23 (2%)	9	32

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	324	PRO
1	A	325	GLU
1	D	324	PRO
1	D	325	GLU
1	G	133	ASN
2	H	63	PHE
1	A	21	PRO
1	A	119	GLU
2	E	11	GLU
1	G	74	PRO
1	G	75	HIS
2	H	76	ARG
1	D	54	ASN
2	E	29	SER
2	E	57	GLU
1	A	66	LEU
1	A	74	PRO
2	B	161	ILE
1	A	62	ARG
2	E	9	PHE
1	A	297	VAL
1	G	21	PRO
1	G	221	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	268/288 (93%)	248 (92%)	20 (8%)	13	37
1	D	270/288 (94%)	247 (92%)	23 (8%)	10	31
1	G	268/288 (93%)	249 (93%)	19 (7%)	14	40
2	B	145/190 (76%)	135 (93%)	10 (7%)	15	41
2	E	146/190 (77%)	134 (92%)	12 (8%)	11	32
2	H	147/190 (77%)	138 (94%)	9 (6%)	18	48
All	All	1244/1434 (87%)	1151 (92%)	93 (8%)	13	37

All (93) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	HIS
1	A	44	GLN
1	A	74	PRO
1	A	92	ASN
1	A	96	ASN
1	A	101	ASP
1	A	107	SER
1	A	161	TYR
1	A	179	ILE
1	A	182	VAL
1	A	197	GLN
1	A	210	GLN
1	A	248	ASN
1	A	261	ARG
1	A	274	ILE
1	A	280	GLU
1	A	283	THR
1	A	290	ASN
1	A	296	ASN
1	A	311	GLN
2	B	27	GLN
2	B	49	ASN
2	B	60	ASN
2	B	64	HIS
2	B	72	GLU
2	B	91	LEU
2	B	120	GLU
2	B	121	LYS
2	B	127	ARG
2	B	168	ASN
1	D	18	HIS
1	D	38	ASN
1	D	44	GLN
1	D	45	SER
1	D	53	ASN
1	D	55	PRO
1	D	81	ASN
1	D	90	ARG
1	D	92	ASN
1	D	96	ASN
1	D	101	ASP
1	D	155	THR

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Mol	Chain	Res	Type
1	D	165	ASN
1	D	167	THR
1	D	182	VAL
1	D	210	GLN
1	D	220	ARG
1	D	231	SER
1	D	248	ASN
1	D	261	ARG
1	D	277	CYS
1	D	318	THR
1	D	324	PRO
2	E	12	ASN
2	E	19	ASP
2	E	27	GLN
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	123	ARG
2	E	127	ARG
2	E	168	ASN
1	G	18	HIS
1	G	29	ILE
1	G	38	ASN
1	G	40	THR
1	G	44	GLN
1	G	74	PRO
1	G	92	ASN
1	G	96	ASN
1	G	155	THR
1	G	165	ASN
1	G	179	ILE
1	G	182	VAL
1	G	210	GLN
1	G	248	ASN
1	G	261	ARG
1	G	284	PRO
1	G	290	ASN
1	G	296	ASN
1	G	311	GLN

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Mol	Chain	Res	Type
2	H	19	ASP
2	H	49	ASN
2	H	60	ASN
2	H	102	LEU
2	H	114	GLU
2	H	120	GLU
2	H	121	LYS
2	H	129	ASN
2	H	156	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (62) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	HIS
1	A	38	ASN
1	A	44	GLN
1	A	54	ASN
1	A	81	ASN
1	A	92	ASN
1	A	96	ASN
1	A	170	ASN
1	A	193	ASN
1	A	210	GLN
1	A	211	GLN
1	A	216	ASN
1	A	248	ASN
1	A	285	ASN
1	A	290	ASN
2	B	27	GLN
2	B	60	ASN
2	B	105	GLN
2	B	154	ASN
2	B	168	ASN
2	B	169	ASN
2	B	172	GLN
1	D	44	GLN
1	D	53	ASN
1	D	54	ASN
1	D	92	ASN
1	D	96	ASN
1	D	165	ASN
1	D	171	ASN

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Mol	Chain	Res	Type
1	D	210	GLN
1	D	248	ASN
1	D	296	ASN
2	E	12	ASN
2	E	27	GLN
2	E	60	ASN
2	E	105	GLN
2	E	125	GLN
2	E	146	ASN
2	E	168	ASN
2	E	172	GLN
1	G	18	HIS
1	G	38	ASN
1	G	44	GLN
1	G	81	ASN
1	G	92	ASN
1	G	96	ASN
1	G	170	ASN
1	G	171	ASN
1	G	197	GLN
1	G	210	GLN
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	125	GLN
2	H	168	ASN
2	H	172	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

25 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	NDG	A	334	-	15,15,15	0.76	1 (6%)	21,21,21	1.07	2 (9%)
5	MAN	G	331	-	12,12,12	0.57	0	17,17,17	0.92	0
4	NDG	G	333	-	15,15,15	0.68	0	21,21,21	0.91	1 (4%)
3	NAG	A	333	-	15,15,15	0.54	0	21,21,21	1.49	3 (14%)
5	MAN	A	337	-	12,12,12	0.66	0	17,17,17	0.93	0
3	NAG	A	332	-	15,15,15	1.34	1 (6%)	21,21,21	2.39	2 (9%)
3	NAG	H	341	-	15,15,15	0.47	0	21,21,21	1.28	1 (4%)
4	NDG	B	223	-	15,15,15	0.62	0	21,21,21	0.72	1 (4%)
5	MAN	D	334	-	12,12,12	0.73	0	17,17,17	1.77	3 (17%)
4	NDG	G	336	-	15,15,15	0.70	0	21,21,21	0.76	0
5	MAN	D	335	-	12,12,12	0.52	0	17,17,17	0.48	0
4	NDG	D	333	-	15,15,15	1.06	2 (13%)	21,21,21	1.24	3 (14%)
5	MAN	G	332	-	12,12,12	0.47	0	17,17,17	0.41	0
4	NDG	D	332	-	15,15,15	1.62	1 (6%)	21,21,21	1.79	6 (28%)
3	NAG	D	331	-	15,15,15	0.60	0	21,21,21	1.66	3 (14%)
4	NDG	G	330	-	15,15,15	0.82	1 (6%)	21,21,21	0.95	0
4	NDG	D	330	-	15,15,15	0.81	0	21,21,21	0.86	0
3	NAG	G	335	-	15,15,15	0.67	0	21,21,21	1.85	6 (28%)
4	NDG	A	331	-	15,15,15	1.12	2 (13%)	21,21,21	1.00	1 (4%)
4	NDG	E	241	-	15,15,15	0.50	0	21,21,21	0.58	0
4	NDG	B	222	-	15,15,15	0.60	0	21,21,21	0.85	0
3	NAG	A	330	-	15,15,15	0.83	1 (6%)	21,21,21	2.39	4 (19%)
4	NDG	G	334	-	15,15,15	0.67	0	21,21,21	0.87	1 (4%)
5	MAN	A	336	-	12,12,12	0.99	1 (8%)	17,17,17	0.65	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	A	335	-	15,15,15	0.70	0	21,21,21	1.93	5 (23%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	MAN	A	337	-	-	2/2/22/22	0/1/1/1
5	MAN	G	331	-	1/1/5/5	2/2/22/22	0/1/1/1
4	NDG	G	333	-	-	6/6/26/26	0/1/1/1
3	NAG	A	333	-	-	4/6/26/26	0/1/1/1
4	NDG	A	334	-	-	2/6/26/26	0/1/1/1
3	NAG	A	332	-	-	3/6/26/26	0/1/1/1
3	NAG	H	341	-	-	6/6/26/26	0/1/1/1
4	NDG	B	223	-	-	4/6/26/26	0/1/1/1
5	MAN	D	334	-	1/1/5/5	1/2/22/22	0/1/1/1
4	NDG	G	336	-	-	4/6/26/26	0/1/1/1
5	MAN	D	335	-	1/1/5/5	2/2/22/22	0/1/1/1
4	NDG	D	333	-	-	4/6/26/26	0/1/1/1
5	MAN	G	332	-	1/1/5/5	1/2/22/22	0/1/1/1
4	NDG	D	332	-	-	2/6/26/26	0/1/1/1
3	NAG	D	331	-	-	4/6/26/26	0/1/1/1
4	NDG	G	330	-	-	2/6/26/26	0/1/1/1
4	NDG	D	330	-	-	6/6/26/26	0/1/1/1
3	NAG	G	335	-	-	4/6/26/26	0/1/1/1
4	NDG	A	331	-	-	5/6/26/26	0/1/1/1
4	NDG	E	241	-	-	2/6/26/26	0/1/1/1
4	NDG	B	222	-	-	4/6/26/26	0/1/1/1
3	NAG	A	330	-	-	4/6/26/26	0/1/1/1
4	NDG	G	334	-	-	2/6/26/26	0/1/1/1
5	MAN	A	336	-	-	2/2/22/22	0/1/1/1
3	NAG	A	335	-	-	2/6/26/26	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	332	NDG	C1-C2	-5.51	1.46	1.52
3	A	332	NAG	C1-C2	4.73	1.58	1.52
4	A	331	NDG	C4-C5	3.09	1.59	1.53
4	D	333	NDG	C1-C2	-2.72	1.49	1.52
3	A	330	NAG	C1-C2	2.24	1.55	1.52
4	A	331	NDG	C1-C2	-2.19	1.50	1.52
4	D	333	NDG	C4-C5	2.14	1.57	1.53
4	G	330	NDG	C4-C5	2.13	1.57	1.53
5	A	336	MAN	C1-C2	-2.10	1.47	1.52
4	A	334	NDG	C1-C2	2.01	1.55	1.52

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	330	NAG	O5-C1-C2	8.62	118.18	109.52
3	A	332	NAG	O5-C1-C2	8.47	118.03	109.52
3	A	335	NAG	C4-C3-C2	5.71	118.70	110.34
3	A	332	NAG	C1-C2-C3	5.68	118.28	110.54
4	D	332	NDG	C4-C3-C2	5.14	117.88	110.34
5	D	334	MAN	O5-C1-C2	4.93	119.08	110.28
3	G	335	NAG	C4-C3-C2	4.92	117.55	110.34
3	D	331	NAG	O5-C1-C2	4.87	114.41	109.52
3	H	341	NAG	C1-C2-C3	-4.64	104.22	110.54
3	A	330	NAG	C1-C2-C3	4.20	116.27	110.54
3	A	333	NAG	C4-C3-C2	3.63	115.66	110.34
5	D	334	MAN	C1-C2-C3	3.57	117.73	110.31
3	D	331	NAG	C1-C2-N2	-3.39	106.80	110.73
3	G	335	NAG	C3-C4-C5	3.21	115.96	110.24
4	D	332	NDG	C1-C2-N2	-3.21	107.01	110.73
3	A	333	NAG	C3-C4-C5	3.17	115.90	110.24
3	A	335	NAG	O5-C1-C2	3.12	112.65	109.52
3	A	330	NAG	C1-O5-C5	2.99	119.30	113.66
3	A	335	NAG	C1-C2-N2	-2.92	107.34	110.73
4	D	333	NDG	C8-C7-N2	2.79	120.82	116.10
4	D	332	NDG	O5-C1-C2	2.76	112.29	109.52
3	D	331	NAG	C1-C2-C3	2.74	114.29	110.54
3	G	335	NAG	C1-C2-C3	2.63	114.14	110.54
4	G	334	NDG	O5-C1-C2	2.59	112.12	109.52
3	A	333	NAG	C1-C2-N2	-2.57	107.75	110.73
4	A	334	NDG	C4-C3-C2	-2.48	106.71	110.34
3	G	335	NAG	C8-C7-N2	2.44	120.23	116.10
3	A	335	NAG	C1-C2-C3	2.42	113.84	110.54
4	G	333	NDG	C4-C3-C2	-2.34	106.91	110.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	335	NAG	C2-N2-C7	-2.31	117.56	123.18
3	A	330	NAG	C3-C4-C5	-2.31	106.13	110.24
5	D	334	MAN	C1-O5-C5	2.29	117.99	113.66
4	D	332	NDG	C3-C4-C5	2.29	114.33	110.24
4	A	331	NDG	O5-C5-C4	2.27	113.82	109.69
4	A	334	NDG	C1-C2-C3	-2.27	107.45	110.54
4	D	333	NDG	C2-N2-C7	-2.20	117.82	123.18
4	D	333	NDG	C6-C5-C4	-2.13	108.01	113.00
3	A	335	NAG	C3-C4-C5	2.10	113.98	110.24
4	D	332	NDG	C3-C2-N2	-2.08	106.68	110.62
4	D	332	NDG	C8-C7-N2	2.06	119.59	116.10
4	B	223	NDG	C2-N2-C7	-2.02	118.28	123.18
3	G	335	NAG	C1-C2-N2	-2.01	108.40	110.73

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	G	331	MAN	C1
5	D	335	MAN	C1
5	G	332	MAN	C1
5	D	334	MAN	C1

All (80) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	334	NDG	C8-C7-N2-C2
4	A	334	NDG	O7-C7-N2-C2
4	G	333	NDG	C1-C2-N2-C7
4	G	333	NDG	C8-C7-N2-C2
4	G	333	NDG	O7-C7-N2-C2
3	A	333	NAG	C8-C7-N2-C2
3	A	333	NAG	O7-C7-N2-C2
3	A	332	NAG	C8-C7-N2-C2
3	A	332	NAG	O7-C7-N2-C2
3	H	341	NAG	C1-C2-N2-C7
3	H	341	NAG	C8-C7-N2-C2
3	H	341	NAG	O7-C7-N2-C2
4	B	223	NDG	O7-C7-N2-C2
4	G	336	NDG	C8-C7-N2-C2
4	G	336	NDG	O7-C7-N2-C2
4	D	332	NDG	C8-C7-N2-C2
4	D	332	NDG	O7-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
3	D	331	NAG	C1-C2-N2-C7
3	D	331	NAG	C8-C7-N2-C2
3	D	331	NAG	O7-C7-N2-C2
4	D	330	NDG	C3-C2-N2-C7
4	D	330	NDG	C8-C7-N2-C2
4	D	330	NDG	O7-C7-N2-C2
4	A	331	NDG	C1-C2-N2-C7
4	A	331	NDG	C8-C7-N2-C2
4	A	331	NDG	O7-C7-N2-C2
4	B	222	NDG	C8-C7-N2-C2
4	B	222	NDG	O7-C7-N2-C2
3	A	330	NAG	C8-C7-N2-C2
3	A	330	NAG	O7-C7-N2-C2
4	B	223	NDG	C8-C7-N2-C2
3	A	333	NAG	O5-C5-C6-O6
5	D	335	MAN	O5-C5-C6-O6
4	G	330	NDG	O5-C5-C6-O6
4	A	331	NDG	O5-C5-C6-O6
4	G	334	NDG	C8-C7-N2-C2
4	G	334	NDG	O7-C7-N2-C2
3	A	330	NAG	O5-C5-C6-O6
4	A	331	NDG	C4-C5-C6-O6
5	G	331	MAN	C4-C5-C6-O6
3	H	341	NAG	O5-C5-C6-O6
4	B	223	NDG	O5-C5-C6-O6
5	D	335	MAN	C4-C5-C6-O6
4	G	330	NDG	C4-C5-C6-O6
5	G	331	MAN	O5-C5-C6-O6
5	A	336	MAN	O5-C5-C6-O6
3	A	333	NAG	C4-C5-C6-O6
3	A	330	NAG	C4-C5-C6-O6
3	H	341	NAG	C4-C5-C6-O6
4	D	333	NDG	C8-C7-N2-C2
4	B	223	NDG	C4-C5-C6-O6
5	A	336	MAN	C4-C5-C6-O6
4	D	333	NDG	O7-C7-N2-C2
4	D	330	NDG	C4-C5-C6-O6
3	G	335	NAG	O5-C5-C6-O6
3	A	335	NAG	O5-C5-C6-O6
4	G	333	NDG	C4-C5-C6-O6
3	G	335	NAG	C4-C5-C6-O6
4	B	222	NDG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
4	G	333	NDG	O5-C5-C6-O6
3	A	335	NAG	C4-C5-C6-O6
4	G	336	NDG	C3-C2-N2-C7
4	G	336	NDG	C1-C2-N2-C7
5	D	334	MAN	O5-C5-C6-O6
5	A	337	MAN	C4-C5-C6-O6
4	D	333	NDG	C4-C5-C6-O6
3	D	331	NAG	C3-C2-N2-C7
5	G	332	MAN	O5-C5-C6-O6
4	D	330	NDG	O5-C5-C6-O6
4	B	222	NDG	O5-C5-C6-O6
3	H	341	NAG	C3-C2-N2-C7
3	G	335	NAG	C8-C7-N2-C2
4	D	333	NDG	O5-C5-C6-O6
3	A	332	NAG	O5-C5-C6-O6
5	A	337	MAN	O5-C5-C6-O6
4	G	333	NDG	C3-C2-N2-C7
4	E	241	NDG	C4-C5-C6-O6
4	D	330	NDG	C1-C2-N2-C7
3	G	335	NAG	O7-C7-N2-C2
4	E	241	NDG	O5-C5-C6-O6

There are no ring outliers.

24 monomers are involved in 65 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	334	NDG	5	0
5	G	331	MAN	6	0
4	G	333	NDG	3	0
3	A	333	NAG	6	0
5	A	337	MAN	1	0
3	A	332	NAG	1	0
3	H	341	NAG	2	0
4	B	223	NDG	3	0
5	D	334	MAN	6	0
4	G	336	NDG	1	0
5	D	335	MAN	4	0
4	D	333	NDG	4	0
5	G	332	MAN	3	0
4	D	332	NDG	9	0
3	D	331	NAG	1	0
4	G	330	NDG	8	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	330	NDG	1	0
3	G	335	NAG	3	0
4	A	331	NDG	3	0
4	B	222	NDG	2	0
3	A	330	NAG	2	0
4	G	334	NDG	4	0
5	A	336	MAN	8	0
3	A	335	NAG	11	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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%)	0.14	10 (3%) 49 44	46, 71, 87, 98	0
1	D	318/329 (96%)	-0.06	4 (1%) 77 77	41, 59, 75, 95	0
1	G	318/329 (96%)	0.21	8 (2%) 57 55	47, 65, 82, 101	0
2	B	172/221 (77%)	0.06	5 (2%) 51 47	40, 64, 82, 100	0
2	E	172/221 (77%)	0.13	3 (1%) 70 69	41, 67, 85, 100	0
2	H	172/221 (77%)	0.26	5 (2%) 51 47	40, 66, 87, 101	0
All	All	1470/1650 (89%)	0.12	35 (2%) 59 56	40, 65, 84, 101	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	46	SER	4.7
2	B	57	GLU	4.3
2	H	27	GLN	4.1
2	H	29	SER	4.0
1	A	143	PRO	3.8
2	E	57	GLU	3.5
2	B	172	GLN	3.5
2	H	171	PHE	3.4
1	G	326	LYS	3.4
1	A	125	PHE	3.3
2	H	26	HIS	3.0
1	A	144	ALA	3.0
1	G	278	ILE	3.0
1	A	47	SER	3.0
1	G	270	SER	2.8
1	G	272	ALA	2.8
1	D	324	PRO	2.8
2	B	56	ILE	2.8
2	B	31	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
2	E	161	ILE	2.8
1	A	242	VAL	2.6
1	G	222	TRP	2.5
1	A	239	PRO	2.4
1	A	46	SER	2.4
1	D	32	ASP	2.4
1	G	20	VAL	2.4
2	H	144	CYS	2.4
1	A	207	ARG	2.4
1	D	278	ILE	2.2
2	E	172	GLN	2.2
1	A	142	GLY	2.2
1	D	171	ASN	2.1
2	B	171	PHE	2.1
1	A	274	ILE	2.1
1	G	279	SER	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](#)

There are no monosaccharides 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. 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	B-factors(Å ²)	Q<0.9
3	NAG	A	332	15/15	0.50	0.54	100,100,100,100	0
5	MAN	A	337	12/12	0.53	0.30	99,100,100,100	0
3	NAG	A	330	15/15	0.58	0.45	97,100,100,100	0
5	MAN	G	332	12/12	0.66	0.41	100,100,100,100	0
4	NDG	G	333	15/15	0.69	0.41	99,100,100,100	0
4	NDG	E	241	15/15	0.71	0.50	98,100,100,100	0
5	MAN	D	334	12/12	0.73	0.32	83,89,91,93	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	NDG	G	336	15/15	0.75	0.41	99,100,100,100	0
5	MAN	G	331	12/12	0.77	0.38	100,100,100,100	0
5	MAN	D	335	12/12	0.77	0.39	96,100,100,100	0
3	NAG	H	341	15/15	0.77	0.41	99,100,100,100	0
4	NDG	G	334	15/15	0.78	0.23	82,84,85,89	0
4	NDG	D	330	15/15	0.79	0.30	99,100,100,100	0
3	NAG	D	331	15/15	0.80	0.25	99,100,100,100	0
4	NDG	B	223	15/15	0.81	0.45	98,100,100,100	0
4	NDG	B	222	15/15	0.81	0.33	99,100,100,100	0
5	MAN	A	336	12/12	0.83	0.32	92,99,100,100	0
4	NDG	A	331	15/15	0.84	0.29	100,100,100,100	0
3	NAG	A	335	15/15	0.84	0.28	86,95,99,100	0
3	NAG	A	333	15/15	0.86	0.27	84,88,93,93	0
4	NDG	A	334	15/15	0.86	0.39	98,100,100,100	0
3	NAG	G	335	15/15	0.91	0.26	51,58,63,65	0
4	NDG	D	332	15/15	0.91	0.25	75,76,82,82	0
4	NDG	G	330	15/15	0.93	0.35	92,93,96,96	0
4	NDG	D	333	15/15	0.93	0.21	54,57,66,66	0

6.5 Other polymers [i](#)

There are no such residues in this entry.