Full wwPDB X-ray Structure Validation Report (i)

Mar 4, 2024 – 01:45 AM EST

PDB ID	:	4KDQ
Title	:	Crystal structure of the hemagglutinin of A/Xinjiang/1/2006 virus
Authors	:	Lu, X.; Shi, Y.; Zhang, W.; Zhang, Y.; Qi, J.; Gao, G.F.
Deposited on	:	2013-04-25
Resolution	:	2.60 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

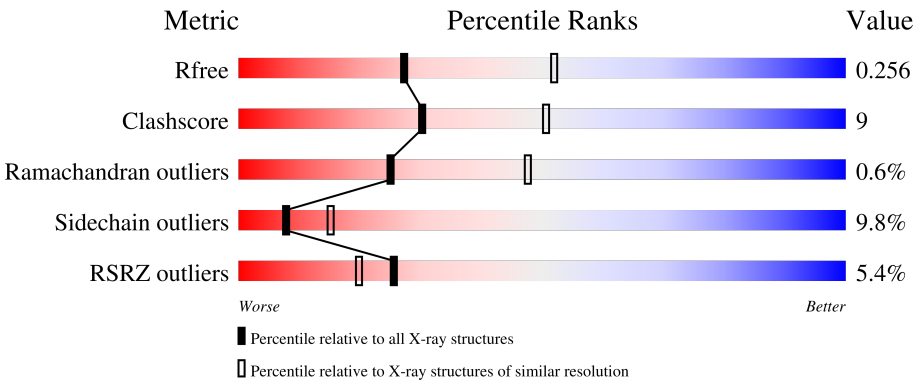
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 of 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 <=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	321	% 78% 19% •
1	C	321	% 79% 19% •
1	E	321	4% 77% 20% •
2	B	164	12% 80% 18% •
2	D	164	2% 79% 20% •

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Mol	Chain	Length	Quality of chain
2	F	164	23% 79% 20%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 11805 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

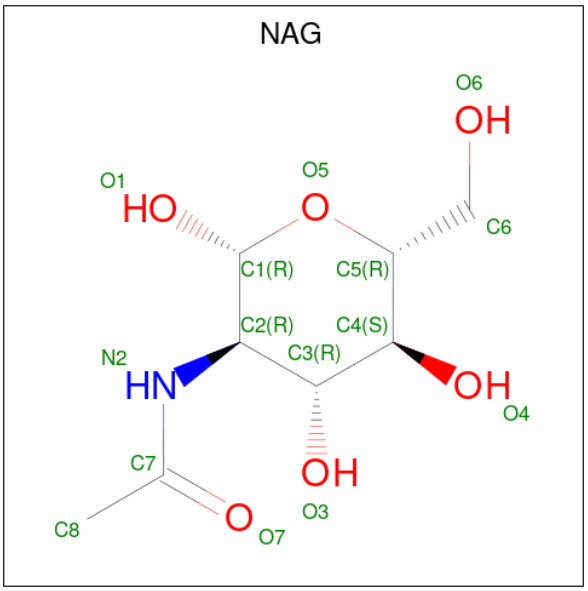
- Molecule 1 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	321	2549	1605	444	486	14	0	0	0
1	C	321	2549	1605	444	486	14	0	0	0
1	E	321	2549	1605	444	486	14	0	0	0

- Molecule 2 is a protein called Hemagglutinin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	164	1329	827	230	264	8	0	0	0
2	D	164	1329	827	230	264	8	0	0	0
2	F	164	1329	827	230	264	8	0	0	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	23	23	23	0	0
			Total	O		
4	C	16	16	16	0	0
			Total	O		
4	E	15	15	15	0	0
			Total	O		
4	B	8	8	8	0	0
			Total	O		
4	D	7	7	7	0	0

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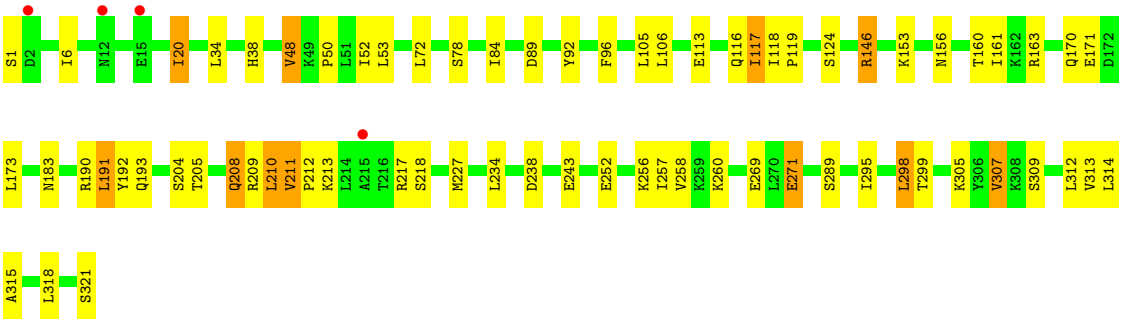
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	F	4	4	4	0	0

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.

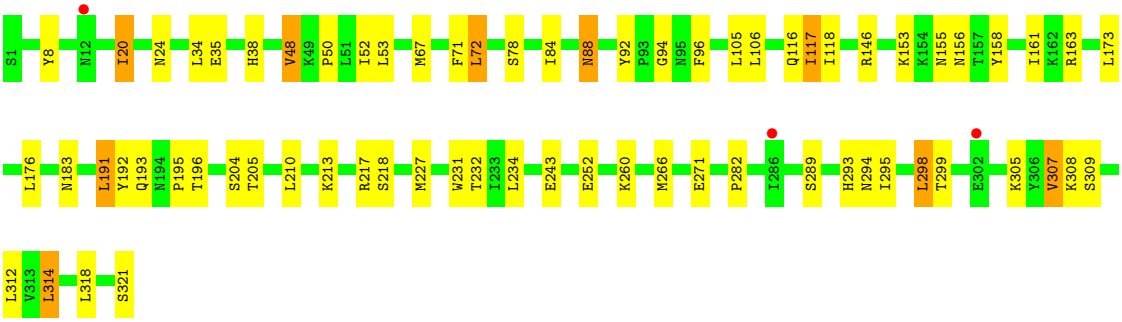
• Molecule 1: Hemagglutinin

Chain A:



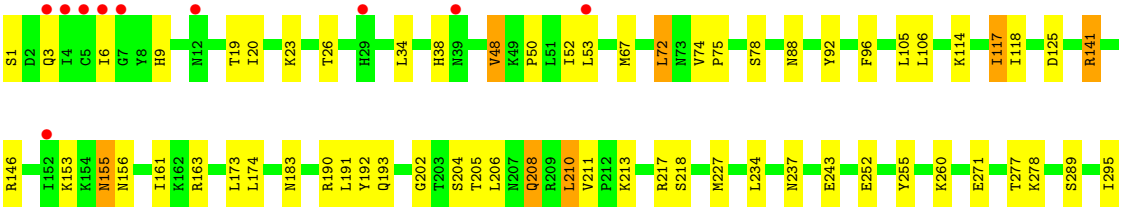
• Molecule 1: Hemagglutinin

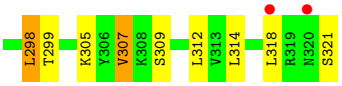
Chain C:



• Molecule 1: Hemagglutinin

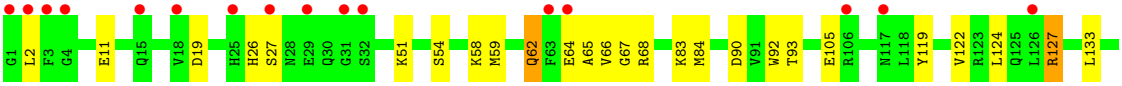
Chain E:

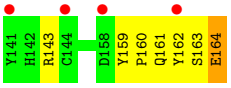




• Molecule 2: Hemagglutinin

Chain B:



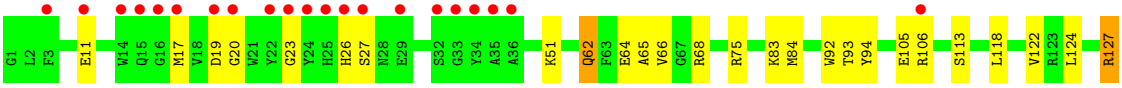


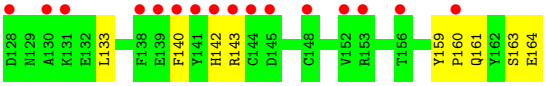
• Molecule 2: Hemagglutinin

Chain D:

• Molecule 2: Hemagglutinin

Chain F:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α, β, γ	72.05Å 72.05Å 365.86Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	36.89 – 2.60 36.89 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.8 (36.89-2.60) 99.8 (36.89-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.93 (at 2.61Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.233 , 0.262 0.227 , 0.256	Depositor DCC
R_{free} test set	3292 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	51.1	Xtriage
Anisotropy	0.429	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 32.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.035 for -h,-k,l 0.057 for h,-h-k,-l 0.039 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	11805	wwPDB-VP
Average B, all atoms (Å^2)	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.05% 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, 0.333 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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	A	0.37	0/2609	0.53	0/3545
1	C	0.39	0/2609	0.54	0/3545
1	E	0.35	0/2609	0.52	0/3545
2	B	0.31	0/1356	0.45	0/1825
2	D	0.33	0/1356	0.45	0/1825
2	F	0.29	0/1356	0.45	0/1825
All	All	0.35	0/11895	0.50	0/16110

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2549	0	2489	56	1
1	C	2549	0	2489	59	0
1	E	2549	0	2488	42	1
2	B	1329	0	1230	29	0
2	D	1329	0	1230	30	0
2	F	1329	0	1230	26	0
3	A	28	0	26	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	28	0	26	1	0
3	E	42	0	39	4	0
4	A	23	0	0	33	0
4	B	8	0	0	10	0
4	C	16	0	0	30	0
4	D	7	0	0	13	0
4	E	15	0	0	15	0
4	F	4	0	0	11	0
All	All	11805	0	11247	213	1

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 9.

All (213) 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:209:ARG:HD3	4:A:601:HOH:O	1.20	1.32
1:C:295:ILE:HB	4:C:608:HOH:O	1.14	1.31
1:C:84:ILE:HD11	4:C:615:HOH:O	1.13	1.30
1:C:24:ASN:HA	4:C:609:HOH:O	1.18	1.28
1:A:190:ARG:HD2	4:A:616:HOH:O	1.34	1.25
2:D:65:ALA:HA	4:D:203:HOH:O	1.34	1.23
1:C:196:THR:CB	4:C:611:HOH:O	1.86	1.20
1:C:293:HIS:HB2	4:C:616:HOH:O	1.43	1.18
2:B:68:ARG:HA	4:B:208:HOH:O	1.47	1.14
1:C:308:LYS:HD2	4:D:201:HOH:O	1.46	1.13
1:C:196:THR:N	4:C:611:HOH:O	1.81	1.12
1:C:196:THR:HB	4:C:611:HOH:O	1.46	1.10
1:C:266:MET:SD	4:C:607:HOH:O	2.09	1.08
1:C:293:HIS:ND1	4:C:608:HOH:O	1.86	1.08
2:D:59:MET:SD	4:F:203:HOH:O	2.08	1.07
1:C:72:LEU:N	4:C:606:HOH:O	1.84	1.06
1:A:89:ASP:HB3	4:A:609:HOH:O	1.53	1.05
1:A:256:LYS:N	4:A:620:HOH:O	1.91	1.02
2:F:75:ARG:NH1	4:F:201:HOH:O	1.91	1.00
1:A:170:GLN:HG2	4:A:617:HOH:O	1.59	0.98
1:C:294:ASN:N	4:C:616:HOH:O	1.91	0.98
3:E:502:NAG:O3	4:E:613:HOH:O	1.81	0.98
1:C:158:TYR:OH	4:C:601:HOH:O	1.81	0.97
2:D:24:TYR:OH	4:D:204:HOH:O	1.83	0.97
1:A:170:GLN:CB	4:A:617:HOH:O	2.11	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:146:ARG:O	4:A:614:HOH:O	1.82	0.96
1:A:170:GLN:CG	4:A:617:HOH:O	2.13	0.95
1:A:171:GLU:CD	4:A:602:HOH:O	2.04	0.94
1:A:160:THR:HG22	4:A:613:HOH:O	1.66	0.94
2:B:90:ASP:OD2	4:B:207:HOH:O	1.87	0.91
1:A:171:GLU:OE1	4:A:602:HOH:O	1.89	0.90
2:B:67:GLY:O	4:B:208:HOH:O	1.89	0.89
1:A:257:ILE:O	4:A:622:HOH:O	1.90	0.88
1:A:190:ARG:NH2	4:A:603:HOH:O	2.07	0.88
1:A:170:GLN:N	4:A:617:HOH:O	1.96	0.88
1:A:315:ALA:O	4:A:607:HOH:O	1.91	0.88
1:E:1:SER:HA	2:F:143:ARG:HH12	1.37	0.87
1:C:116:GLN:OE1	4:C:602:HOH:O	1.91	0.87
2:B:68:ARG:HG2	4:B:208:HOH:O	1.76	0.85
1:C:24:ASN:OD1	4:C:609:HOH:O	1.95	0.84
2:F:142:HIS:N	4:F:204:HOH:O	2.11	0.84
2:B:162:TYR:OH	4:B:204:HOH:O	1.96	0.84
2:D:65:ALA:O	4:D:203:HOH:O	1.94	0.84
2:D:153:ARG:NH2	4:D:202:HOH:O	2.12	0.83
1:A:313:VAL:O	4:A:619:HOH:O	1.97	0.82
2:F:113:SER:OG	4:F:202:HOH:O	1.96	0.82
1:C:293:HIS:CB	4:C:616:HOH:O	2.12	0.82
1:A:256:LYS:O	4:A:620:HOH:O	1.97	0.81
1:C:293:HIS:CA	4:C:616:HOH:O	2.28	0.81
2:B:68:ARG:CA	4:B:208:HOH:O	2.16	0.80
1:A:113:GLU:O	4:A:620:HOH:O	1.99	0.79
2:F:142:HIS:O	4:F:204:HOH:O	2.01	0.79
1:A:171:GLU:OE2	4:A:602:HOH:O	1.96	0.79
1:C:232:THR:OG1	4:C:603:HOH:O	1.86	0.79
1:A:271:GLU:OE1	4:A:604:HOH:O	2.00	0.78
2:D:90:ASP:OD2	4:D:206:HOH:O	2.01	0.78
1:A:256:LYS:CA	4:A:620:HOH:O	2.27	0.77
2:D:90:ASP:OD1	4:D:201:HOH:O	2.02	0.77
1:E:155:ASN:OD1	3:E:503:NAG:O7	2.03	0.76
1:C:266:MET:HB3	4:C:607:HOH:O	1.85	0.75
1:C:295:ILE:CB	4:C:608:HOH:O	1.91	0.74
2:B:164:GLU:OE1	4:B:201:HOH:O	2.03	0.74
2:B:68:ARG:CG	4:B:208:HOH:O	2.34	0.74
1:E:114:LYS:CE	4:E:614:HOH:O	2.36	0.74
1:C:305:LYS:HD3	2:D:62:GLN:HB2	1.70	0.73
2:B:119:TYR:OH	4:B:205:HOH:O	2.08	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:150:GLU:N	4:D:202:HOH:O	2.23	0.72
1:E:237:ASN:OD1	4:E:606:HOH:O	2.07	0.71
2:F:94:TYR:OH	4:F:203:HOH:O	2.09	0.71
2:D:146:ASN:O	4:D:202:HOH:O	2.07	0.71
2:B:58:LYS:HE3	2:D:97:GLU:HB3	1.71	0.70
1:A:1:SER:HA	2:B:143:ARG:HH12	1.55	0.70
1:A:116:GLN:OE1	4:A:612:HOH:O	2.10	0.69
1:A:170:GLN:HB2	4:A:617:HOH:O	1.84	0.69
1:E:38:HIS:HB3	1:E:295:ILE:HD13	1.75	0.69
1:C:20:ILE:HD12	2:B:54:SER:HB2	1.74	0.69
1:E:307:VAL:HG13	1:E:309:SER:H	1.57	0.69
2:F:94:TYR:CE1	4:F:203:HOH:O	2.45	0.68
1:C:38:HIS:HB3	1:C:295:ILE:HD13	1.74	0.68
1:A:307:VAL:HG13	1:A:309:SER:H	1.59	0.68
1:C:307:VAL:HG13	1:C:309:SER:H	1.59	0.68
2:D:68:ARG:HH22	2:F:83:LYS:HD2	1.58	0.68
1:E:26:THR:OG1	4:E:602:HOH:O	2.13	0.66
1:C:88:ASN:HD22	1:C:88:ASN:N	1.93	0.66
1:C:282:PRO:HA	4:C:607:HOH:O	1.94	0.66
1:E:6:ILE:HD11	2:F:122:VAL:HG21	1.78	0.65
1:A:38:HIS:HB3	1:A:295:ILE:HD13	1.77	0.65
3:E:502:NAG:O4	4:E:607:HOH:O	2.15	0.64
1:A:190:ARG:CD	4:A:616:HOH:O	2.10	0.64
1:A:156:ASN:O	1:A:193:GLN:HG3	1.98	0.63
1:E:114:LYS:NZ	4:E:614:HOH:O	2.09	0.63
1:E:278:LYS:N	4:E:611:HOH:O	1.80	0.62
2:B:2:LEU:HD12	4:F:202:HOH:O	2.00	0.61
1:E:75:PRO:O	4:E:601:HOH:O	2.15	0.61
2:D:62:GLN:HG2	2:D:92:TRP:CD2	2.36	0.61
1:E:75:PRO:HD2	4:E:615:HOH:O	2.01	0.60
1:E:153:LYS:HD2	1:E:193:GLN:HG2	1.84	0.60
1:E:155:ASN:OD1	3:E:503:NAG:C7	2.49	0.60
1:A:119:PRO:HG3	4:A:612:HOH:O	2.02	0.59
1:C:314:LEU:HD13	2:D:100:VAL:HG22	1.83	0.59
1:E:156:ASN:O	1:E:193:GLN:HG3	2.03	0.59
1:A:160:THR:CG2	4:A:613:HOH:O	2.35	0.59
2:B:62:GLN:HG2	2:B:92:TRP:CD2	2.38	0.59
1:A:153:LYS:HD2	1:A:193:GLN:HG2	1.84	0.58
1:A:124:SER:N	4:A:606:HOH:O	2.36	0.58
2:B:2:LEU:HA	4:F:202:HOH:O	2.03	0.58
2:F:62:GLN:HG2	2:F:92:TRP:CD2	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:71:PHE:C	4:C:606:HOH:O	2.29	0.57
2:D:65:ALA:CA	4:D:203:HOH:O	2.10	0.57
1:E:277:THR:OG1	4:E:611:HOH:O	2.18	0.57
1:C:195:PRO:HG2	4:C:611:HOH:O	2.04	0.57
1:A:48:VAL:HG22	1:A:78:SER:HB3	1.85	0.57
2:F:94:TYR:CZ	4:F:203:HOH:O	2.55	0.56
1:C:48:VAL:HG22	1:C:78:SER:HB3	1.86	0.56
1:E:74:VAL:HG13	4:E:601:HOH:O	2.05	0.56
1:C:67:MET:HB3	1:C:88:ASN:OD1	2.05	0.56
2:B:159:TYR:O	2:B:161:GLN:N	2.39	0.56
1:C:298:LEU:HA	2:D:65:ALA:HB1	1.87	0.55
2:F:159:TYR:O	2:F:161:GLN:N	2.39	0.55
1:C:153:LYS:HD2	1:C:193:GLN:HG2	1.87	0.55
1:C:156:ASN:O	1:C:193:GLN:HG3	2.06	0.55
1:C:196:THR:CA	4:C:611:HOH:O	2.17	0.55
1:C:50:PRO:HG2	1:C:52:ILE:HD11	1.88	0.55
1:A:256:LYS:HB2	4:A:620:HOH:O	2.06	0.54
1:E:50:PRO:HG2	1:E:52:ILE:HD11	1.90	0.53
1:A:307:VAL:HG22	2:B:93:THR:HA	1.89	0.53
1:C:305:LYS:HB3	2:D:62:GLN:NE2	2.22	0.53
2:D:159:TYR:O	2:D:161:GLN:N	2.40	0.53
1:A:315:ALA:N	4:A:607:HOH:O	2.40	0.53
1:A:113:GLU:N	4:A:620:HOH:O	2.38	0.53
1:A:305:LYS:HD3	2:B:62:GLN:HB2	1.92	0.52
3:A:502:NAG:H61	4:A:615:HOH:O	2.10	0.52
1:A:34:LEU:HB2	1:A:312:LEU:HB2	1.91	0.52
1:E:48:VAL:HG22	1:E:78:SER:HB3	1.90	0.51
2:B:68:ARG:HH22	2:D:83:LYS:HD2	1.75	0.51
1:E:34:LEU:HB2	1:E:312:LEU:HB2	1.92	0.51
1:C:307:VAL:HG22	2:D:93:THR:HA	1.93	0.50
4:C:605:HOH:O	2:D:28:ASN:HB2	2.10	0.50
2:D:149:MET:HB2	4:D:202:HOH:O	2.10	0.50
3:C:502:NAG:O4	4:C:613:HOH:O	2.19	0.50
1:A:190:ARG:CZ	4:A:603:HOH:O	2.55	0.50
1:C:34:LEU:HB2	1:C:312:LEU:HB2	1.92	0.50
1:C:8:TYR:CZ	2:D:6:ILE:HG23	2.47	0.50
1:A:298:LEU:HA	2:B:65:ALA:HB1	1.95	0.48
1:E:153:LYS:HE2	1:E:190:ARG:O	2.13	0.48
1:E:161:ILE:O	1:E:243:GLU:HA	2.14	0.48
1:A:20:ILE:HD11	2:F:51:LYS:HG3	1.96	0.48
1:A:50:PRO:HG2	1:A:52:ILE:HD11	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:94:TYR:OH	4:D:207:HOH:O	2.06	0.48
1:E:307:VAL:HG22	2:F:93:THR:HA	1.96	0.48
1:C:161:ILE:O	1:C:243:GLU:HA	2.14	0.47
1:E:67:MET:HB3	1:E:88:ASN:OD1	2.14	0.47
1:E:9:HIS:HB2	2:F:20:GLY:O	2.15	0.47
2:B:83:LYS:HD2	2:F:68:ARG:HH22	1.79	0.46
1:A:6:ILE:HD11	2:B:122:VAL:HG21	1.96	0.46
1:A:117:ILE:HG12	1:A:118:ILE:HG13	1.97	0.46
2:B:162:TYR:HE1	4:B:206:HOH:O	1.98	0.46
1:C:94:GLY:HA3	1:C:227:MET:O	2.15	0.45
1:E:92:TYR:CD2	1:E:227:MET:HG2	2.51	0.45
1:C:88:ASN:N	1:C:88:ASN:ND2	2.64	0.45
1:E:298:LEU:HA	2:F:65:ALA:HB1	1.98	0.45
1:C:20:ILE:HD11	2:B:51:LYS:HG3	1.98	0.45
1:C:155:ASN:N	4:C:604:HOH:O	2.49	0.45
1:C:24:ASN:CA	4:C:609:HOH:O	2.05	0.45
1:E:117:ILE:HG12	1:E:118:ILE:HG13	1.98	0.45
2:B:64:GLU:HB2	2:D:83:LYS:NZ	2.32	0.45
1:E:23:LYS:N	4:E:603:HOH:O	2.03	0.44
1:E:3:GLN:HA	2:F:140:PHE:HD1	1.81	0.44
1:A:84:ILE:HG12	1:A:269:GLU:OE2	2.18	0.44
2:B:83:LYS:NZ	2:F:64:GLU:HB2	2.33	0.44
1:E:208:GLN:HG3	1:E:210:LEU:HD13	1.99	0.44
1:E:237:ASN:HA	4:E:606:HOH:O	2.18	0.44
1:A:92:TYR:CD2	1:A:227:MET:HG2	2.53	0.43
2:B:62:GLN:HE21	2:B:62:GLN:HB3	1.65	0.43
2:B:105:GLU:HG2	2:F:106:ARG:HH22	1.83	0.43
1:A:161:ILE:O	1:A:243:GLU:HA	2.19	0.43
1:C:117:ILE:HG12	1:C:118:ILE:HG13	1.99	0.43
1:A:238:ASP:HA	3:A:502:NAG:H82	2.01	0.43
1:C:305:LYS:CD	2:D:62:GLN:HB2	2.45	0.43
1:C:35:GLU:O	4:C:616:HOH:O	2.21	0.42
1:C:266:MET:CB	4:C:607:HOH:O	2.51	0.42
1:C:318:LEU:H	1:C:318:LEU:HG	1.68	0.42
1:E:19:THR:HB	2:F:105:GLU:HB2	2.01	0.42
1:E:305:LYS:HD3	2:F:62:GLN:HB2	2.01	0.42
1:A:256:LYS:CB	4:A:620:HOH:O	2.57	0.42
1:E:88:ASN:N	1:E:88:ASN:HD22	2.17	0.42
1:C:295:ILE:N	4:C:608:HOH:O	2.31	0.42
1:E:6:ILE:HG23	2:F:118:LEU:HD23	2.01	0.42
1:C:308:LYS:CD	4:D:201:HOH:O	2.30	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:62:GLN:HE21	2:D:62:GLN:HB3	1.66	0.42
1:A:191:LEU:HD12	1:A:191:LEU:HA	1.89	0.42
1:C:213:LYS:O	1:C:217:ARG:NH2	2.52	0.42
2:B:59:MET:HG2	2:D:94:TYR:CE1	2.55	0.41
1:E:72:LEU:HD12	1:E:72:LEU:HA	1.84	0.41
1:C:92:TYR:CD2	1:C:227:MET:HG2	2.56	0.41
2:F:62:GLN:HE21	2:F:62:GLN:HB3	1.65	0.41
2:F:142:HIS:CA	4:F:204:HOH:O	2.61	0.41
1:C:72:LEU:HD12	1:C:72:LEU:HA	1.85	0.41
1:A:208:GLN:HG3	1:A:210:LEU:HD13	2.01	0.41
1:C:176:LEU:HD23	1:C:231:TRP:HB3	2.03	0.41
1:C:191:LEU:HD12	1:C:191:LEU:HA	1.92	0.41
1:A:211:VAL:HA	1:A:212:PRO:HD3	1.95	0.41
2:D:17:MET:SD	2:D:23:GLY:HA3	2.61	0.41
1:E:202:GLY:HA2	1:E:206:LEU:O	2.21	0.41
1:C:305:LYS:HD3	2:D:62:GLN:CB	2.47	0.40
1:E:114:LYS:HE3	4:E:614:HOH:O	2.11	0.40
2:F:17:MET:SD	2:F:23:GLY:HA3	2.61	0.40
1:A:153:LYS:HE2	1:A:190:ARG:O	2.21	0.40
1:E:213:LYS:O	1:E:217:ARG:NH2	2.54	0.40
1:A:171:GLU:HG2	1:A:258:VAL:HG12	2.03	0.40
1:A:213:LYS:O	1:A:217:ARG:NH2	2.55	0.40
1:E:174:LEU:HB3	1:E:255:TYR:HB2	2.04	0.40
1:E:125:ASP:N	4:E:604:HOH:O	2.36	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:258:VAL:O	1:E:141:ARG:NH2[1_655]	2.15	0.05

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	319/321 (99%)	304 (95%)	15 (5%)	0	100	100
1	C	319/321 (99%)	308 (97%)	11 (3%)	0	100	100
1	E	319/321 (99%)	305 (96%)	14 (4%)	0	100	100
2	B	162/164 (99%)	150 (93%)	9 (6%)	3 (2%)	8	15
2	D	162/164 (99%)	150 (93%)	9 (6%)	3 (2%)	8	15
2	F	162/164 (99%)	150 (93%)	9 (6%)	3 (2%)	8	15
All	All	1443/1455 (99%)	1367 (95%)	67 (5%)	9 (1%)	25	47

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	66	VAL
2	D	66	VAL
2	F	66	VAL
2	B	127	ARG
2	B	160	PRO
2	D	127	ARG
2	D	160	PRO
2	F	127	ARG
2	F	160	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	290/290 (100%)	259 (89%)	31 (11%)	6	12
1	C	290/290 (100%)	261 (90%)	29 (10%)	7	14
1	E	290/290 (100%)	257 (89%)	33 (11%)	5	10
2	B	140/140 (100%)	129 (92%)	11 (8%)	12	24
2	D	140/140 (100%)	129 (92%)	11 (8%)	12	24
2	F	140/140 (100%)	129 (92%)	11 (8%)	12	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1290/1290 (100%)	1164 (90%)	126 (10%)	8 15

All (126) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	ILE
1	A	48	VAL
1	A	53	LEU
1	A	72	LEU
1	A	96	PHE
1	A	105	LEU
1	A	106	LEU
1	A	117	ILE
1	A	146	ARG
1	A	163	ARG
1	A	173	LEU
1	A	183	ASN
1	A	191	LEU
1	A	192	TYR
1	A	204	SER
1	A	205	THR
1	A	208	GLN
1	A	210	LEU
1	A	211	VAL
1	A	218	SER
1	A	234	LEU
1	A	252	GLU
1	A	260	LYS
1	A	271	GLU
1	A	289	SER
1	A	298	LEU
1	A	299	THR
1	A	307	VAL
1	A	314	LEU
1	A	318	LEU
1	A	321	SER
1	C	20	ILE
1	C	48	VAL
1	C	53	LEU
1	C	72	LEU
1	C	88	ASN
1	C	96	PHE

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Mol	Chain	Res	Type
1	C	105	LEU
1	C	106	LEU
1	C	117	ILE
1	C	146	ARG
1	C	163	ARG
1	C	173	LEU
1	C	183	ASN
1	C	191	LEU
1	C	192	TYR
1	C	204	SER
1	C	205	THR
1	C	210	LEU
1	C	218	SER
1	C	234	LEU
1	C	252	GLU
1	C	260	LYS
1	C	271	GLU
1	C	289	SER
1	C	298	LEU
1	C	299	THR
1	C	307	VAL
1	C	314	LEU
1	C	321	SER
1	E	20	ILE
1	E	48	VAL
1	E	53	LEU
1	E	72	LEU
1	E	96	PHE
1	E	105	LEU
1	E	106	LEU
1	E	117	ILE
1	E	141	ARG
1	E	146	ARG
1	E	155	ASN
1	E	163	ARG
1	E	173	LEU
1	E	183	ASN
1	E	191	LEU
1	E	192	TYR
1	E	204	SER
1	E	205	THR
1	E	208	GLN

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Mol	Chain	Res	Type
1	E	210	LEU
1	E	211	VAL
1	E	218	SER
1	E	234	LEU
1	E	252	GLU
1	E	260	LYS
1	E	271	GLU
1	E	289	SER
1	E	298	LEU
1	E	299	THR
1	E	307	VAL
1	E	314	LEU
1	E	318	LEU
1	E	321	SER
2	B	11	GLU
2	B	19	ASP
2	B	26	HIS
2	B	27	SER
2	B	62	GLN
2	B	84	MET
2	B	124	LEU
2	B	127	ARG
2	B	133	LEU
2	B	163	SER
2	B	164	GLU
2	D	11	GLU
2	D	19	ASP
2	D	26	HIS
2	D	27	SER
2	D	62	GLN
2	D	84	MET
2	D	124	LEU
2	D	127	ARG
2	D	133	LEU
2	D	163	SER
2	D	164	GLU
2	F	11	GLU
2	F	19	ASP
2	F	26	HIS
2	F	27	SER
2	F	62	GLN
2	F	84	MET

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Mol	Chain	Res	Type
2	F	124	LEU
2	F	127	ARG
2	F	133	LEU
2	F	163	SER
2	F	164	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	88	ASN
1	E	88	ASN
2	B	62	GLN
2	D	62	GLN
2	F	62	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)

7 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	NAG	A	502	1	14,14,15	0.47	0	17,19,21	1.27	1 (5%)
3	NAG	E	503	1	14,14,15	0.29	0	17,19,21	0.61	0
3	NAG	C	502	1	14,14,15	0.40	0	17,19,21	1.44	4 (23%)
3	NAG	E	502	1	14,14,15	0.53	0	17,19,21	1.02	2 (11%)
3	NAG	C	501	1	14,14,15	0.67	0	17,19,21	1.25	3 (17%)
3	NAG	E	501	1	14,14,15	0.59	0	17,19,21	0.95	1 (5%)
3	NAG	A	501	1	14,14,15	0.48	0	17,19,21	1.05	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	A	502	1	-	4/6/23/26	0/1/1/1
3	NAG	E	503	1	-	4/6/23/26	0/1/1/1
3	NAG	C	502	1	-	2/6/23/26	0/1/1/1
3	NAG	E	502	1	-	4/6/23/26	0/1/1/1
3	NAG	C	501	1	-	0/6/23/26	0/1/1/1
3	NAG	E	501	1	-	0/6/23/26	0/1/1/1
3	NAG	A	501	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	502	NAG	O5-C5-C6	3.51	112.71	107.20
3	C	502	NAG	C1-O5-C5	3.07	116.35	112.19
3	C	501	NAG	C4-C3-C2	2.96	115.35	111.02
3	C	501	NAG	O5-C5-C6	2.77	111.54	107.20
3	A	501	NAG	O5-C5-C6	2.76	111.53	107.20
3	C	502	NAG	O5-C5-C6	2.62	111.31	107.20
3	E	501	NAG	O5-C5-C6	2.51	111.14	107.20
3	E	502	NAG	C2-N2-C7	-2.31	119.61	122.90
3	C	502	NAG	C4-C3-C2	-2.25	107.72	111.02
3	C	501	NAG	O5-C1-C2	2.14	114.67	111.29
3	C	502	NAG	C2-N2-C7	-2.09	119.92	122.90
3	E	502	NAG	C1-O5-C5	2.08	115.00	112.19

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	503	NAG	O5-C5-C6-O6
3	E	502	NAG	O5-C5-C6-O6
3	C	502	NAG	O5-C5-C6-O6
3	E	503	NAG	C4-C5-C6-O6
3	A	502	NAG	C8-C7-N2-C2
3	A	501	NAG	O5-C5-C6-O6
3	E	502	NAG	C4-C5-C6-O6
3	A	502	NAG	O7-C7-N2-C2
3	C	502	NAG	C4-C5-C6-O6
3	A	501	NAG	C4-C5-C6-O6
3	A	502	NAG	C4-C5-C6-O6
3	E	502	NAG	C8-C7-N2-C2
3	E	503	NAG	C8-C7-N2-C2
3	A	502	NAG	O5-C5-C6-O6
3	E	502	NAG	O7-C7-N2-C2
3	E	503	NAG	O7-C7-N2-C2

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	502	NAG	2	0
3	E	503	NAG	2	0
3	C	502	NAG	1	0
3	E	502	NAG	2	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	321/321 (100%)	-0.17	4 (1%)	79	76	33, 57, 94, 151	0
1	C	321/321 (100%)	-0.07	3 (0%)	84	82	29, 56, 93, 132	0
1	E	321/321 (100%)	0.14	12 (3%)	41	34	37, 64, 108, 172	0
2	B	164/164 (100%)	0.56	20 (12%)	4	2	35, 92, 136, 170	0
2	D	164/164 (100%)	0.28	3 (1%)	68	64	32, 87, 118, 158	0
2	F	164/164 (100%)	1.14	37 (22%)	0	0	26, 108, 185, 213	0
All	All	1455/1455 (100%)	0.20	79 (5%)	25	20	26, 67, 136, 213	0

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	7	GLY	10.4
2	F	35	ALA	9.2
2	F	33	GLY	8.9
2	F	143	ARG	8.0
1	E	6	ILE	7.9
2	F	144	CYS	7.8
2	F	34	TYR	7.8
2	F	138	PHE	6.2
2	F	25	HIS	6.0
2	F	24	TYR	5.6
1	E	4	ILE	5.4
2	F	141	TYR	5.2
2	F	20	GLY	5.1
2	F	29	GLU	4.9
2	F	140	PHE	4.6
2	B	162	TYR	4.6
1	E	3	GLN	4.3
2	B	27	SER	4.2
1	A	12	ASN	4.2

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Mol	Chain	Res	Type	RSRZ
2	F	153	ARG	4.1
1	E	5	CYS	3.8
2	F	145	ASP	3.8
2	F	32	SER	3.8
2	F	36	ALA	3.7
2	D	1	GLY	3.6
2	F	160	PRO	3.6
2	F	131	LYS	3.4
2	F	23	GLY	3.4
1	E	29	HIS	3.4
2	F	26	HIS	3.4
2	F	27	SER	3.3
2	F	148	CYS	3.3
2	D	64	GLU	3.3
1	E	12	ASN	3.2
2	F	16	GLY	3.2
2	F	156	THR	3.2
2	F	152	VAL	3.1
2	B	15	GLN	3.1
1	A	215	ALA	2.9
1	E	152	ILE	2.9
2	B	144	CYS	2.9
2	F	17	MET	2.9
2	B	25	HIS	2.6
2	B	126	LEU	2.6
1	A	2	ASP	2.6
2	B	29	GLU	2.6
2	F	142	HIS	2.6
2	F	14	TRP	2.5
2	F	22	TYR	2.5
2	B	117	ASN	2.5
2	F	19	ASP	2.5
2	B	31	GLY	2.5
1	E	318	LEU	2.5
2	F	139	GLU	2.5
2	F	15	GLN	2.5
2	B	106	ARG	2.5
2	B	3	PHE	2.5
2	F	130	ALA	2.4
2	B	158	ASP	2.4
1	E	39	ASN	2.3
2	B	4	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
2	B	32	SER	2.3
2	F	11	GLU	2.3
2	B	2	LEU	2.3
2	B	141	TYR	2.2
2	B	1	GLY	2.2
2	B	63	PHE	2.2
2	F	3	PHE	2.2
2	F	106	ARG	2.2
1	A	15	GLU	2.1
1	C	286	ILE	2.1
1	C	302	GLU	2.1
2	F	128	ASP	2.1
1	E	53	LEU	2.1
2	B	18	VAL	2.1
2	B	64	GLU	2.1
2	D	23	GLY	2.1
1	C	12	ASN	2.0
1	E	320	ASN	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 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	E	503	14/15	0.71	0.23	91,119,128,128	0
3	NAG	E	501	14/15	0.80	0.16	107,125,134,141	0
3	NAG	A	501	14/15	0.81	0.20	114,125,131,136	0
3	NAG	C	501	14/15	0.82	0.19	85,124,138,142	0
3	NAG	C	502	14/15	0.89	0.13	36,67,88,94	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	NAG	A	502	14/15	0.92	0.14	42,60,92,95	0
3	NAG	E	502	14/15	0.96	0.10	39,65,90,92	0

6.5 Other polymers (i)

There are no such residues in this entry.