



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:56 PM UTC

PDB ID : 5FUC / pdb_00005fuc
Title : Biophysical and cellular characterisation of a junctional epitope antibody that locks IL-6 and gp80 together in a stable complex: implications for new therapeutic strategies
Authors : Adams, R.; Griffin, R.; Doyle, C.; Ettorre, A.
Deposited on : 2016-01-25
Resolution : 2.70 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

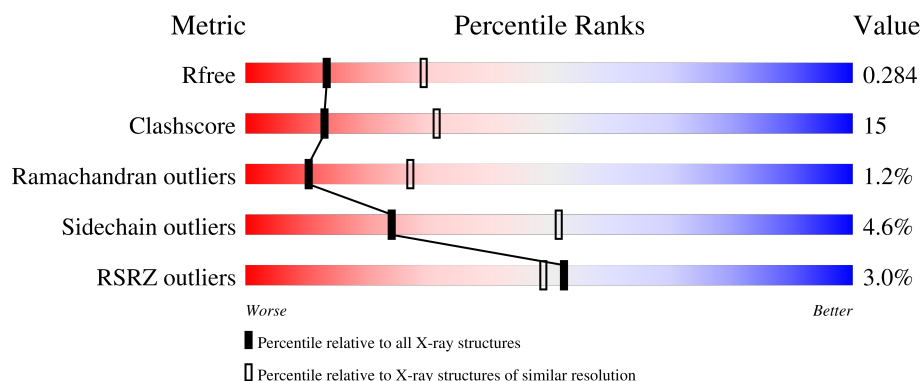
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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.



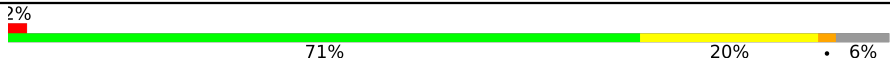
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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 $\leq 5\%$. 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	166	
1	B	166	
2	C	231	
2	D	231	
3	E	132	

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Mol	Chain	Length	Quality of chain
3	V	132	 A horizontal bar chart showing the quality of chain V. The bar is divided into four segments: a small red segment at the beginning labeled '2%', a large green segment labeled '71%', a yellow segment labeled '20%', and a small grey segment at the end labeled '6%'.

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7672 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 INTERLEUKIN-6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	152	Total	C	N	O	S	0	0	0
			1197	748	208	232	9			
1	B	160	Total	C	N	O	S	0	0	0
			1287	805	222	251	9			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	19	GLY	-	expression tag	UNP P05231
A	20	SER	-	expression tag	UNP P05231
B	19	GLY	-	expression tag	UNP P05231
B	20	SER	-	expression tag	UNP P05231

- Molecule 2 is a protein called INTERLEUKIN-6 RECEPTOR SUBUNIT ALPHA, INTERLEUKIN-6 RECEPTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	199	Total	C	N	O	S	0	0	0
			1598	1013	281	296	8			
2	D	198	Total	C	N	O	S	0	0	0
			1595	1012	279	296	8			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	73	GLY	-	expression tag	UNP D6R9R8
C	88	ALA	-	linker	UNP D6R9R8
C	89	GLY	-	linker	UNP D6R9R8
C	90	ALA	-	linker	UNP D6R9R8
C	91	GLY	-	linker	UNP D6R9R8
C	192	ALA	CYS	engineered mutation	UNP P08887
C	258	ALA	CYS	engineered mutation	UNP P08887

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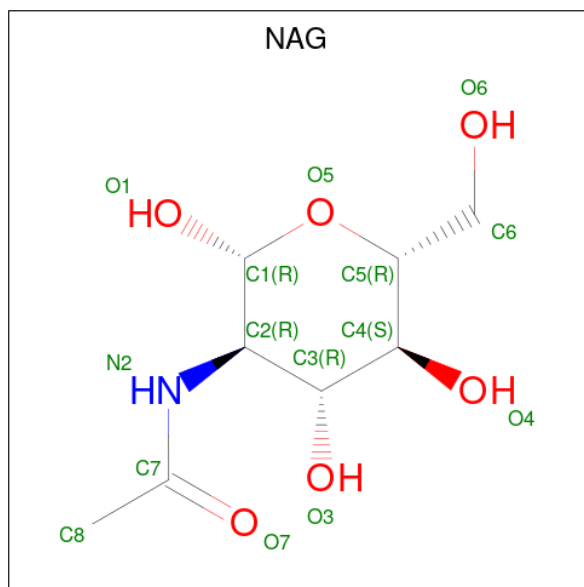
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Chain	Residue	Modelled	Actual	Comment	Reference
D	73	GLY	-	expression tag	UNP D6R9R8
D	88	ALA	-	linker	UNP D6R9R8
D	89	GLY	-	linker	UNP D6R9R8
D	90	ALA	-	linker	UNP D6R9R8
D	91	GLY	-	linker	UNP D6R9R8
D	192	ALA	CYS	engineered mutation	UNP P08887
D	258	ALA	CYS	engineered mutation	UNP P08887

- Molecule 3 is a protein called VHH6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	110	Total	C	N	O	S	4	0	0
			871	545	151	169	6			
3	V	124	Total	C	N	O	S	0	0	0
			957	596	167	188	6			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

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

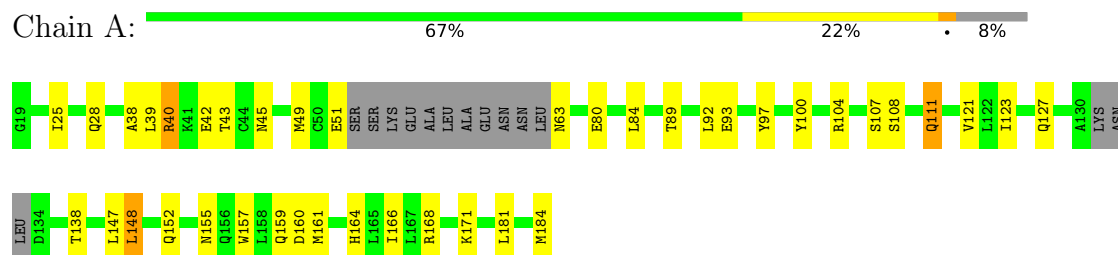
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	14	Total	O	0	0
			14	14		
5	B	24	Total	O	0	0
			24	24		
5	C	34	Total	O	0	0
			34	34		
5	D	23	Total	O	0	0
			23	23		
5	E	8	Total	O	0	0
			8	8		
5	V	8	Total	O	0	0
			8	8		

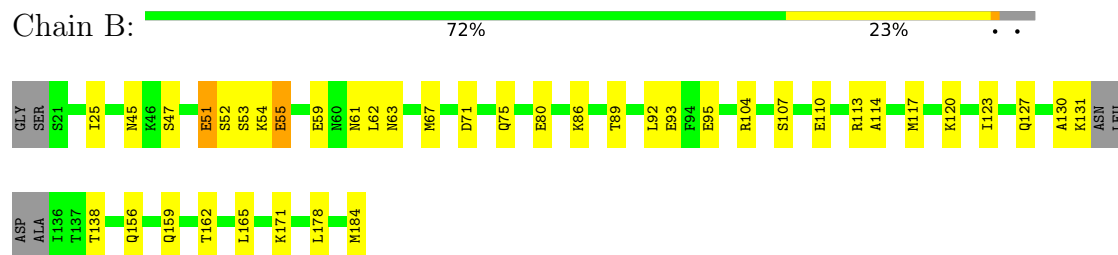
3 Residue-property plots [i](#)

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.

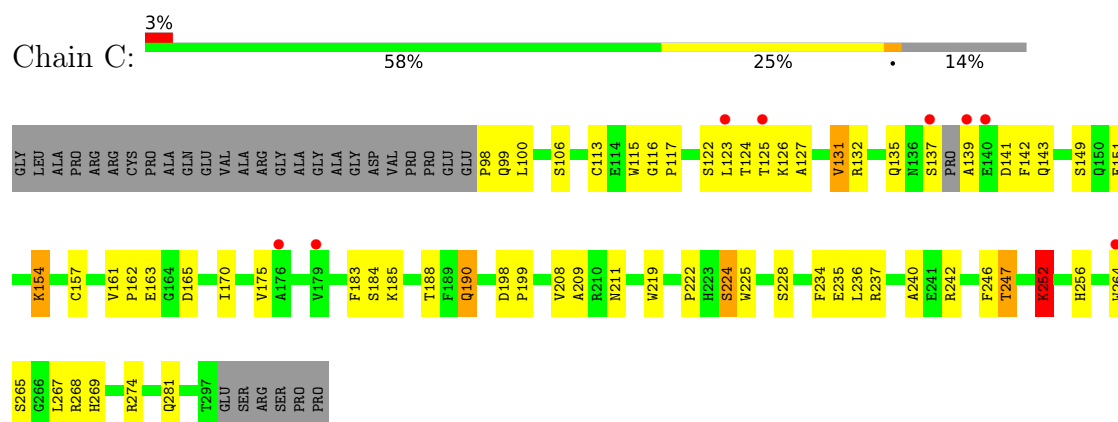
- Molecule 1: INTERLEUKIN-6



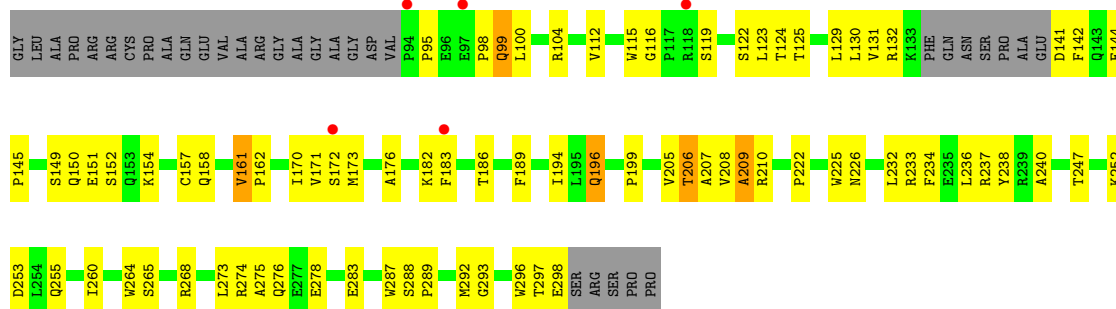
- Molecule 1: INTERLEUKIN-6



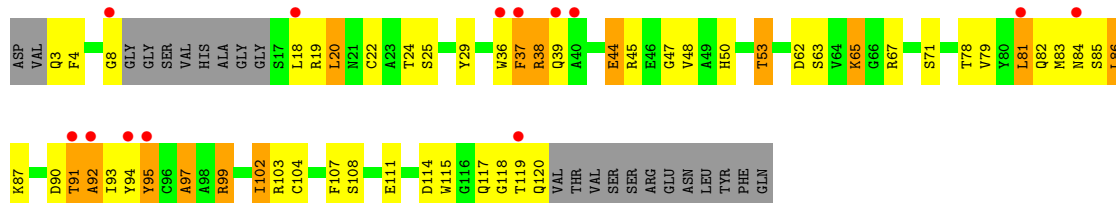
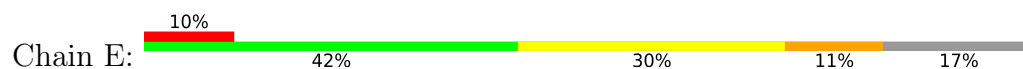
- Molecule 2: INTERLEUKIN-6 RECEPTOR SUBUNIT ALPHA, INTERLEUKIN-6 RECEPTOR



- Molecule 2: INTERLEUKIN-6 RECEPTOR SUBUNIT ALPHA, INTERLEUKIN-6 RECEPTOR



• Molecule 3: VHH6



• Molecule 3: VHH6



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	249.03Å 67.80Å 78.16Å 90.00° 104.53° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70 20.00 – 2.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (20.00-2.70) 99.7 (20.00-2.70)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.98 (at 2.69Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.231 , 0.287 0.232 , 0.284	Depositor DCC
R_{free} test set	3472 reflections (9.93%)	wwPDB-VP
Wilson B-factor (Å ²)	58.4	Xtriage
Anisotropy	0.137	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 30.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7672	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.56% 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

5.1 Standard geometry

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	0.50	0/1210	0.84	0/1622
1	B	0.48	0/1301	0.89	2/1743 (0.1%)
2	C	0.49	0/1647	1.05	12/2241 (0.5%)
2	D	0.44	0/1645	0.98	9/2239 (0.4%)
3	E	0.46	0/891	0.90	2/1203 (0.2%)
3	V	0.47	0/979	0.93	2/1325 (0.2%)
All	All	0.48	0/7673	0.95	27/10373 (0.3%)

There are no bond length outliers.

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	278	GLU	N-CA-C	7.22	120.07	111.33
2	D	265	SER	N-CA-C	7.16	120.37	110.35
2	C	161	VAL	CA-C-N	6.84	126.82	119.78
2	C	161	VAL	C-N-CA	6.84	126.82	119.78
2	C	234	PHE	N-CA-C	6.43	119.66	109.50
3	V	53	THR	N-CA-C	6.34	119.00	111.71
2	C	240	ALA	N-CA-C	-6.29	100.97	110.28
2	D	240	ALA	N-CA-C	-6.28	100.99	110.28
2	D	161	VAL	CA-C-N	6.27	127.67	119.84
2	D	161	VAL	C-N-CA	6.27	127.67	119.84
2	C	228	SER	N-CA-C	-6.26	105.96	113.97
3	E	97	ALA	N-CA-C	5.94	116.39	108.38
1	B	107	SER	N-CA-C	-5.94	107.27	114.75
2	D	234	PHE	N-CA-C	5.81	118.23	109.23
3	E	53	THR	N-CA-C	5.65	118.17	111.33
2	C	247	THR	N-CA-C	-5.62	100.23	109.40
2	D	150	GLN	N-CA-C	-5.62	106.35	113.43
2	C	116	GLY	CA-C-N	5.46	125.44	120.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	116	GLY	C-N-CA	5.46	125.44	120.03
1	B	47	SER	N-CA-C	-5.46	101.40	109.86
2	C	265	SER	N-CA-C	5.36	118.25	110.42
3	V	97	ALA	N-CA-C	5.36	117.12	109.14
2	C	131	VAL	N-CA-C	5.21	116.09	108.53
2	D	247	THR	N-CA-C	-5.13	100.05	108.41
2	D	206	THR	N-CA-C	5.09	117.71	109.06
2	C	211	ASN	CA-C-N	5.08	126.18	119.84
2	C	211	ASN	C-N-CA	5.08	126.18	119.84

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	1197	0	1190	33	0
1	B	1287	0	1303	29	0
2	C	1598	0	1516	50	0
2	D	1595	0	1520	52	0
3	E	871	0	816	49	0
3	V	957	0	901	22	0
4	C	28	0	26	0	0
4	D	28	0	26	2	0
5	A	14	0	0	1	0
5	B	24	0	0	4	0
5	C	34	0	0	0	0
5	D	23	0	0	0	0
5	E	8	0	0	1	0
5	V	8	0	0	0	0
All	All	7672	0	7298	222	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 15.

All (222) 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:40:ARG:HH11	1:A:40:ARG:HB2	1.27	1.00
3:E:39:GLN:O	3:E:92:ALA:HB1	1.66	0.95
2:D:196:GLN:HG2	2:D:283:GLU:HB2	1.49	0.94
1:B:45:ASN:HB3	2:D:264:TRP:CH2	2.03	0.94
2:D:255:GLN:HE22	3:V:26:GLY:HA3	1.34	0.89
1:A:108:SER:HB2	1:A:111:GLN:HB2	1.55	0.88
1:B:75:GLN:HB3	2:C:163:GLU:OE2	1.76	0.86
3:V:20:LEU:HG	3:V:83:MET:HE2	1.60	0.83
2:C:242:ARG:HH21	2:C:267:LEU:HD11	1.42	0.83
1:A:45:ASN:HB3	2:C:264:TRP:CH2	2.14	0.82
1:B:89:THR:O	1:B:93:GLU:HG3	1.82	0.80
3:V:103:ARG:HG2	3:V:103:ARG:HH11	1.48	0.78
3:V:28:ILE:HG22	3:V:34:MET:HE1	1.64	0.77
1:B:92:LEU:HD13	1:B:138:THR:HG22	1.68	0.74
1:B:45:ASN:HB3	2:D:264:TRP:CZ2	2.24	0.73
2:D:99:GLN:H	2:D:115:TRP:CD1	2.07	0.71
1:A:40:ARG:HB2	1:A:40:ARG:NH1	2.06	0.69
2:D:122:SER:OG	2:D:125:THR:HG23	1.92	0.69
1:A:89:THR:O	1:A:93:GLU:HG3	1.93	0.68
1:B:75:GLN:HB3	2:C:163:GLU:CD	2.19	0.68
1:A:28:GLN:NE2	1:A:121:VAL:HB	2.09	0.68
1:A:148:LEU:O	1:A:152:GLN:HG2	1.94	0.67
2:C:98:PRO:O	2:C:184:SER:HB2	1.95	0.66
3:E:38:ARG:HD2	3:E:38:ARG:C	2.21	0.66
3:E:38:ARG:HG2	3:E:38:ARG:HH11	1.61	0.66
1:B:54:LYS:HD2	2:C:170:ILE:HD11	1.78	0.66
1:B:51:GLU:O	1:B:52:SER:HB3	1.95	0.65
2:D:255:GLN:HE22	3:V:26:GLY:CA	2.07	0.65
1:A:40:ARG:NH2	1:A:168:ARG:HA	2.11	0.65
3:V:103:ARG:HG2	3:V:103:ARG:NH1	2.12	0.64
1:A:38:ALA:HB3	1:A:111:GLN:HG2	1.80	0.64
3:E:93:ILE:HG12	3:E:120:GLN:HB2	1.80	0.64
2:C:115:TRP:CH2	2:C:117:PRO:HB3	2.33	0.63
3:E:37:PHE:CE1	3:E:95:TYR:HB2	2.32	0.63
1:A:49:MET:HB3	1:A:164:HIS:CD2	2.34	0.62
2:D:232:LEU:HD22	2:D:275:ALA:HB1	1.81	0.62
2:D:132:ARG:HB3	2:D:170:ILE:HB	1.80	0.62
1:B:165:LEU:O	1:B:165:LEU:HD12	2.00	0.61
1:A:148:LEU:HD22	1:A:152:GLN:HE21	1.65	0.60
3:V:91:THR:HG23	3:V:122:THR:HA	1.82	0.60
2:D:226:ASN:ND2	4:D:1300:NAG:H82	2.17	0.59
1:B:95:GLU:OE2	1:B:120:LYS:HD3	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:19:ARG:HG2	3:E:20:LEU:N	2.17	0.59
1:A:45:ASN:CB	2:C:264:TRP:CH2	2.85	0.59
2:C:242:ARG:HH21	2:C:267:LEU:CD1	2.14	0.59
2:D:151:GLU:CD	2:D:151:GLU:H	2.11	0.59
3:E:90:ASP:O	3:E:91:THR:C	2.47	0.58
3:E:38:ARG:HG3	3:E:48:VAL:CG2	2.32	0.58
2:C:149:SER:C	2:C:151:GLU:H	2.11	0.58
3:V:28:ILE:HG22	3:V:34:MET:CE	2.32	0.58
2:D:98:PRO:HA	2:D:115:TRP:CE2	2.39	0.58
3:E:20:LEU:HD23	3:E:36:TRP:CZ3	2.39	0.57
3:E:97:ALA:HB2	3:E:115:TRP:HB3	1.85	0.57
1:A:111:GLN:HA	1:A:111:GLN:OE1	2.04	0.57
2:D:129:LEU:HD11	2:D:171:VAL:HB	1.86	0.56
3:E:37:PHE:HE2	3:E:45:ARG:HH11	1.53	0.56
1:A:49:MET:HE1	1:A:160:ASP:HB3	1.87	0.56
3:E:95:TYR:CD1	3:E:95:TYR:N	2.73	0.56
3:V:29:TYR:CE1	3:V:53:THR:HG21	2.40	0.56
3:E:4:PHE:HE1	3:E:114:ASP:OD2	1.88	0.56
3:E:102:ILE:HG13	3:E:102:ILE:O	2.05	0.56
3:E:38:ARG:HD2	3:E:38:ARG:O	2.05	0.56
1:B:59:GLU:HG3	5:B:2011:HOH:O	2.07	0.55
2:C:98:PRO:HB2	2:C:184:SER:HB3	1.89	0.55
2:C:236:LEU:HD23	2:C:237:ARG:N	2.22	0.55
3:E:93:ILE:HB	3:E:95:TYR:CE1	2.42	0.55
3:V:91:THR:O	3:V:92:ALA:HB2	2.06	0.55
2:D:205:VAL:CG1	2:D:293:GLY:HA3	2.37	0.55
2:C:131:VAL:O	2:C:141:ASP:HB2	2.07	0.54
2:D:112:VAL:HG22	2:D:158:GLN:OE1	2.08	0.54
3:E:117:GLN:OE1	3:E:117:GLN:HA	2.06	0.54
1:B:104:ARG:HH21	1:B:159:GLN:NE2	2.06	0.54
2:C:115:TRP:CZ2	2:C:117:PRO:HB3	2.43	0.54
1:B:171:LYS:HE2	5:B:2006:HOH:O	2.07	0.53
2:C:236:LEU:HD23	2:C:236:LEU:C	2.33	0.53
3:V:20:LEU:HB3	3:V:36:TRP:CH2	2.43	0.53
1:A:80:GLU:HG3	1:A:184:MET:HG2	1.90	0.53
3:E:18:LEU:HD12	3:E:83:MET:HE3	1.91	0.53
1:A:100:TYR:O	1:A:104:ARG:HD2	2.07	0.53
2:D:268:ARG:NH1	2:D:268:ARG:HG3	2.24	0.53
2:D:199:PRO:O	2:D:222:PRO:HB3	2.09	0.53
3:V:57:ARG:NH1	3:V:59:TYR:OH	2.40	0.53
2:C:100:LEU:HD11	2:C:113:CYS:HB3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:268:ARG:HG3	2:D:268:ARG:HH11	1.74	0.52
3:E:19:ARG:HA	3:E:82:GLN:HA	1.91	0.52
2:D:226:ASN:HD22	4:D:1300:NAG:H82	1.73	0.52
2:C:198:ASP:OD2	2:C:224:SER:HB2	2.10	0.52
1:A:157:TRP:CZ2	1:A:161:MET:HE3	2.45	0.52
1:A:45:ASN:HD22	2:C:264:TRP:HH2	1.57	0.52
2:D:205:VAL:HG11	2:D:293:GLY:HA3	1.92	0.52
3:E:8:GLY:N	3:E:119:THR:HG21	2.25	0.52
1:A:45:ASN:HB3	2:C:264:TRP:CZ3	2.45	0.52
3:E:84:ASN:HB3	5:E:2007:HOH:O	2.10	0.52
1:A:39:LEU:O	1:A:43:THR:HG23	2.09	0.51
2:D:210:ARG:HA	2:D:296:TRP:CE3	2.45	0.51
3:E:22:CYS:C	3:E:78:THR:HG23	2.35	0.51
2:C:237:ARG:HA	2:C:247:THR:O	2.10	0.51
3:E:37:PHE:O	3:E:37:PHE:CG	2.63	0.51
2:D:95:PRO:HB2	2:D:182:LYS:HB2	1.93	0.51
1:A:42:GLU:OE1	1:A:107:SER:HB3	2.11	0.51
1:B:67:MET:HG2	5:B:2013:HOH:O	2.11	0.50
2:C:264:TRP:H	2:C:269:HIS:CE1	2.29	0.50
1:B:25:ILE:HB	5:B:2002:HOH:O	2.11	0.50
2:D:189:PHE:CG	2:D:194:ILE:HD12	2.46	0.50
2:C:132:ARG:HB3	2:C:170:ILE:HB	1.93	0.50
3:E:38:ARG:HG3	3:E:48:VAL:HG21	1.92	0.50
3:E:50:HIS:CE1	3:E:99:ARG:HD2	2.47	0.50
2:C:122:SER:C	2:C:124:THR:H	2.20	0.49
3:E:111:GLU:OE1	3:E:111:GLU:HA	2.12	0.49
1:B:156:GLN:O	1:B:159:GLN:HB2	2.12	0.49
2:C:252:LYS:NZ	2:C:252:LYS:HB3	2.26	0.49
2:C:268:ARG:HG3	2:C:268:ARG:HH11	1.76	0.49
1:B:178:LEU:C	1:B:178:LEU:HD23	2.38	0.49
3:V:20:LEU:HB2	3:V:81:LEU:HB3	1.94	0.49
3:V:28:ILE:HG23	3:V:32:TYR:HD2	1.78	0.48
1:B:61:ASN:O	1:B:63:ASN:N	2.44	0.48
3:E:62:ASP:OD1	3:E:65:LYS:HE2	2.14	0.48
2:C:267:LEU:O	2:C:269:HIS:HD2	1.96	0.48
3:V:3:GLN:OE1	3:V:28:ILE:HD11	2.14	0.48
2:C:122:SER:O	2:C:123:LEU:HB3	2.13	0.48
2:C:99:GLN:H	2:C:115:TRP:CD1	2.32	0.48
3:E:38:ARG:HG2	3:E:38:ARG:NH1	2.26	0.48
3:E:20:LEU:HD13	3:E:83:MET:CE	2.44	0.47
2:C:199:PRO:O	2:C:222:PRO:HB3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:123:ILE:O	1:A:127:GLN:HG3	2.15	0.47
1:B:75:GLN:HB3	2:C:163:GLU:OE1	2.14	0.47
3:V:29:TYR:CZ	3:V:53:THR:HG21	2.50	0.47
1:A:148:LEU:CD2	1:A:152:GLN:HE21	2.27	0.47
2:D:149:SER:HB3	2:D:152:SER:OG	2.14	0.47
2:D:100:LEU:HD13	2:D:173:MET:HB2	1.96	0.47
1:B:62:LEU:HD11	1:B:162:THR:HG23	1.97	0.47
3:E:99:ARG:NH2	3:E:111:GLU:HB2	2.30	0.46
3:V:2:VAL:HG23	3:V:3:GLN:HE21	1.80	0.46
1:A:97:TYR:HB3	1:A:166:ILE:HD13	1.98	0.46
1:B:130:ALA:O	1:B:131:LYS:HD3	2.15	0.46
2:D:268:ARG:HG2	2:D:292:MET:HE3	1.97	0.46
3:E:37:PHE:CD2	3:E:45:ARG:HD2	2.51	0.46
3:E:47:GLY:HA3	3:E:107:PHE:HD1	1.80	0.46
2:D:255:GLN:NE2	3:V:26:GLY:HA3	2.15	0.46
3:E:36:TRP:CD1	3:E:81:LEU:HD22	2.50	0.46
2:D:151:GLU:CD	2:D:151:GLU:N	2.74	0.46
2:D:172:SER:OG	2:D:186:THR:HA	2.16	0.46
1:A:104:ARG:NH2	1:A:159:GLN:HB3	2.31	0.46
2:C:137:SER:HA	2:C:139:ALA:N	2.31	0.46
2:D:123:LEU:N	2:D:123:LEU:HD12	2.31	0.45
2:D:206:THR:HG22	2:D:207:ALA:O	2.16	0.45
2:D:210:ARG:HA	2:D:296:TRP:CZ3	2.51	0.45
2:C:125:THR:O	2:C:126:LYS:HD2	2.16	0.45
1:A:39:LEU:HD21	1:A:111:GLN:HB3	1.98	0.45
2:C:235:GLU:OE1	2:C:274:ARG:NE	2.49	0.45
2:D:122:SER:C	2:D:124:THR:H	2.25	0.45
2:C:264:TRP:H	2:C:269:HIS:HE1	1.64	0.45
2:D:189:PHE:CD2	2:D:194:ILE:HD12	2.52	0.45
3:V:6:GLU:O	3:V:7:SER:HB3	2.16	0.44
2:C:142:PHE:CD1	2:C:142:PHE:N	2.84	0.44
1:A:97:TYR:OH	1:A:147:LEU:HD21	2.17	0.44
2:C:222:PRO:HG2	2:C:225:TRP:HB2	1.99	0.44
1:A:28:GLN:HE22	1:A:121:VAL:HB	1.80	0.44
1:B:114:ALA:HA	1:B:117:MET:HE3	2.00	0.44
2:D:131:VAL:O	2:D:141:ASP:HA	2.18	0.44
2:D:208:VAL:O	2:D:209:ALA:C	2.60	0.44
2:D:274:ARG:HD3	2:D:287:TRP:CE2	2.52	0.44
2:C:124:THR:O	2:C:126:LYS:N	2.43	0.44
3:E:93:ILE:HB	3:E:95:TYR:CZ	2.53	0.44
3:E:20:LEU:HD13	3:E:83:MET:HE1	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:44:GLU:OE1	3:E:45:ARG:HG2	2.18	0.44
2:D:125:THR:HA	2:D:176:ALA:O	2.17	0.43
1:B:62:LEU:HD12	1:B:165:LEU:HD23	2.01	0.43
1:A:84:LEU:HD12	1:A:84:LEU:O	2.19	0.43
1:B:53:SER:HB2	1:B:55:GLU:OE2	2.19	0.43
2:C:142:PHE:HB2	2:C:143:GLN:H	1.67	0.43
2:D:225:TRP:CD1	2:D:225:TRP:O	2.71	0.43
3:V:28:ILE:HG23	3:V:32:TYR:CD2	2.53	0.43
2:D:238:TYR:CD2	2:D:260:ILE:HD13	2.54	0.43
1:B:54:LYS:O	1:B:54:LYS:HG2	2.19	0.43
2:D:144:GLU:OE1	2:D:145:PRO:HD2	2.19	0.43
2:D:297:THR:O	2:D:298:GLU:HB2	2.19	0.43
2:D:268:ARG:NH2	2:D:292:MET:HB2	2.33	0.43
1:B:123:ILE:O	1:B:127:GLN:HG3	2.19	0.42
3:E:67:ARG:HG2	3:E:85:SER:HB2	2.00	0.42
3:E:71:SER:O	3:E:79:VAL:HG13	2.19	0.42
1:B:80:GLU:O	1:B:184:MET:HE2	2.18	0.42
2:C:149:SER:OG	2:C:151:GLU:HB3	2.20	0.42
3:E:18:LEU:C	3:E:18:LEU:HD13	2.44	0.42
3:E:108:SER:OG	3:E:111:GLU:HG2	2.19	0.42
1:A:92:LEU:HD23	1:A:123:ILE:HD13	2.00	0.42
2:C:208:VAL:O	2:C:209:ALA:C	2.62	0.42
2:D:99:GLN:H	2:D:115:TRP:NE1	2.17	0.42
2:D:142:PHE:HD1	2:D:142:PHE:H	1.66	0.42
3:V:76:LYS:O	3:V:77:ASN:C	2.63	0.42
2:C:124:THR:C	2:C:126:LYS:H	2.27	0.42
3:E:102:ILE:O	3:E:103:ARG:HG2	2.20	0.42
3:V:70:ILE:HA	3:V:80:TYR:O	2.19	0.42
2:C:115:TRP:O	2:C:154:LYS:HB2	2.20	0.42
3:E:8:GLY:O	3:E:119:THR:HG22	2.19	0.42
3:E:107:PHE:O	3:E:108:SER:C	2.63	0.42
2:C:162:PRO:HG2	2:C:165:ASP:HB2	2.02	0.41
2:D:161:VAL:HA	2:D:162:PRO:HD2	1.81	0.41
1:B:110:GLU:OE1	1:B:113:ARG:NH2	2.48	0.41
2:C:219:TRP:CZ2	2:C:256:HIS:HA	2.56	0.41
2:D:233:ARG:NH2	2:D:276:GLN:OE1	2.47	0.41
3:E:86:LEU:C	3:E:87:LYS:HG3	2.45	0.41
2:D:288:SER:HB2	2:D:289:PRO:HD2	2.02	0.41
2:C:127:ALA:CB	2:C:175:VAL:HG22	2.50	0.41
2:C:281:GLN:HE21	2:C:281:GLN:HB2	1.67	0.41
2:D:130:LEU:O	2:D:171:VAL:HA	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:171:LYS:HE2	5:A:2013:HOH:O	2.20	0.41
1:A:25:ILE:HG21	1:A:181:LEU:HD13	2.03	0.41
2:D:236:LEU:HD23	2:D:237:ARG:N	2.36	0.41
3:E:18:LEU:O	3:E:83:MET:HE3	2.21	0.41
3:E:94:TYR:O	3:E:118:GLY:HA2	2.21	0.41
2:C:190:GLN:HE21	2:C:190:GLN:HB3	1.50	0.41
3:E:24:THR:OG1	3:E:25:SER:N	2.54	0.41
3:E:18:LEU:HD12	3:E:83:MET:CE	2.51	0.40
1:A:155:ASN:OD1	1:A:157:TRP:HB3	2.20	0.40
2:D:116:GLY:HA2	2:D:154:LYS:HB3	2.03	0.40
2:D:183:PHE:CD1	2:D:183:PHE:N	2.86	0.40
3:E:29:TYR:CZ	3:E:53:THR:HG21	2.55	0.40
1:B:71:ASP:OD1	1:B:86:LYS:HD3	2.21	0.40
2:C:183:PHE:CD1	2:C:183:PHE:N	2.88	0.40
2:C:237:ARG:HD2	2:C:246:PHE:CG	2.56	0.40
2:C:267:LEU:O	2:C:269:HIS:CD2	2.75	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	146/166 (88%)	141 (97%)	5 (3%)	0	100	100
1	B	156/166 (94%)	147 (94%)	8 (5%)	1 (1%)	21	44
2	C	195/231 (84%)	177 (91%)	17 (9%)	1 (0%)	24	48
2	D	194/231 (84%)	180 (93%)	12 (6%)	2 (1%)	12	32
3	E	106/132 (80%)	86 (81%)	14 (13%)	6 (6%)	1	2
3	V	122/132 (92%)	114 (93%)	7 (6%)	1 (1%)	16	37
All	All	919/1058 (87%)	845 (92%)	63 (7%)	11 (1%)	10	27

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	51	GLU
2	D	209	ALA
3	E	65	LYS
3	E	81	LEU
3	V	92	ALA
2	C	252	LYS
3	E	91	THR
3	E	92	ALA
2	D	252	LYS
3	E	63	SER
3	E	102	ILE

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	133/150 (89%)	127 (96%)	6 (4%)	24	52
1	B	146/150 (97%)	145 (99%)	1 (1%)	76	90
2	C	176/200 (88%)	167 (95%)	9 (5%)	21	48
2	D	177/200 (88%)	170 (96%)	7 (4%)	28	56
3	E	91/108 (84%)	82 (90%)	9 (10%)	7	19
3	V	100/108 (93%)	94 (94%)	6 (6%)	17	41
All	All	823/916 (90%)	785 (95%)	38 (5%)	24	51

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	ARG
1	A	51	GLU
1	A	63	ASN
1	A	111	GLN
1	A	138	THR
1	A	148	LEU

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Mol	Chain	Res	Type
1	B	55	GLU
2	C	106	SER
2	C	135	GLN
2	C	154	LYS
2	C	157	CYS
2	C	185	LYS
2	C	188	THR
2	C	190	GLN
2	C	224	SER
2	C	252	LYS
2	D	99	GLN
2	D	104	ARG
2	D	119	SER
2	D	157	CYS
2	D	196	GLN
2	D	253	ASP
2	D	273	LEU
3	E	3	GLN
3	E	20	LEU
3	E	37	PHE
3	E	38	ARG
3	E	44	GLU
3	E	86	LEU
3	E	95	TYR
3	E	99	ARG
3	E	104	CYS
3	V	1	ASP
3	V	62	ASP
3	V	79	VAL
3	V	103	ARG
3	V	104	CYS
3	V	119	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	45	ASN
1	A	152	GLN
1	A	164	HIS
1	B	103	ASN
1	B	127	GLN
1	B	152	GLN

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Mol	Chain	Res	Type
1	B	154	GLN
1	B	159	GLN
2	C	153	GLN
2	C	190	GLN
2	C	255	GLN
2	C	269	HIS
2	D	190	GLN
2	D	211	ASN
2	D	255	GLN
3	E	72	GLN
3	E	120	GLN
3	V	3	GLN
3	V	77	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	C	1298	2	14,14,15	0.55	0	17,19,21	0.64	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	D	1300	2	14,14,15	0.80	1 (7%)	17,19,21	0.67	0
4	NAG	C	1299	2	14,14,15	0.81	1 (7%)	17,19,21	0.59	0
4	NAG	D	1299	2	14,14,15	0.60	0	17,19,21	0.66	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	C	1298	2	-	4/6/23/26	0/1/1/1
4	NAG	D	1300	2	-	3/6/23/26	0/1/1/1
4	NAG	C	1299	2	-	4/6/23/26	0/1/1/1
4	NAG	D	1299	2	-	4/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1300	NAG	C1-C2	2.33	1.55	1.52
4	C	1299	NAG	C1-C2	2.17	1.55	1.52

There are no bond angle outliers.

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	1299	NAG	C8-C7-N2-C2
4	C	1299	NAG	O7-C7-N2-C2
4	D	1300	NAG	C8-C7-N2-C2
4	D	1300	NAG	O7-C7-N2-C2
4	D	1299	NAG	O5-C5-C6-O6
4	D	1299	NAG	C4-C5-C6-O6
4	D	1299	NAG	C8-C7-N2-C2
4	C	1298	NAG	C4-C5-C6-O6
4	D	1299	NAG	O7-C7-N2-C2
4	C	1298	NAG	C8-C7-N2-C2
4	C	1298	NAG	O5-C5-C6-O6
4	C	1298	NAG	O7-C7-N2-C2
4	C	1299	NAG	C4-C5-C6-O6
4	C	1299	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
4	D	1300	NAG	C1-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	1300	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 ⓘ

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	152/166 (91%)	-0.10	0	100	100	33, 51, 77, 83	0
1	B	160/166 (96%)	-0.14	0	100	100	33, 51, 67, 75	0
2	C	199/231 (86%)	0.06	8 (4%)	42	38	29, 49, 83, 95	0
2	D	198/231 (85%)	0.18	5 (2%)	58	55	36, 60, 89, 97	0
3	E	110/132 (83%)	0.67	13 (11%)	9	7	38, 67, 92, 97	1 (0%)
3	V	124/132 (93%)	-0.14	2 (1%)	70	68	34, 52, 68, 82	0
All	All	943/1058 (89%)	0.07	28 (2%)	52	49	29, 54, 84, 97	1 (0%)

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	94	PRO	4.5
3	E	119	THR	3.9
2	C	125	THR	3.8
3	E	8	GLY	3.2
2	C	176	ALA	3.2
2	C	123	LEU	3.1
3	E	94	TYR	3.1
3	E	81	LEU	3.1
3	E	37	PHE	3.0
3	V	1	ASP	2.8
3	E	92	ALA	2.8
3	E	36	TRP	2.7
3	V	2	VAL	2.7
2	D	172	SER	2.7
2	C	139	ALA	2.7
3	E	95	TYR	2.5
2	C	140	GLU	2.5
2	C	264	TRP	2.4
3	E	40	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
3	E	18	LEU	2.4
2	D	183	PHE	2.4
2	C	137	SER	2.3
3	E	91	THR	2.3
2	C	179	VAL	2.2
2	D	97	GLU	2.2
2	D	118	ARG	2.1
3	E	84	ASN	2.0
3	E	39	GLN	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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
4	NAG	C	1299	14/15	0.56	0.15	70,75,77,78	0
4	NAG	C	1298	14/15	0.57	0.14	75,79,82,84	0
4	NAG	D	1300	14/15	0.60	0.15	83,87,89,89	0
4	NAG	D	1299	14/15	0.77	0.12	56,60,64,66	0

6.5 Other polymers [i](#)

There are no such residues in this entry.