



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:34 AM UTC

PDB ID : 3COR / pdb\_00003cor  
Title : Crystal structure of the complex of peptidoglycan recognition protein (PGRP-S) with N-acetylgalactosamine at 3.1 Å resolution  
Authors : Sharma, P.; Vikram, G.; Singh, N.; Sharma, S.; Kaur, P.; Singh, T.P.  
Deposited on : 2008-03-29  
Resolution : 3.10 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](mailto: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>.

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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

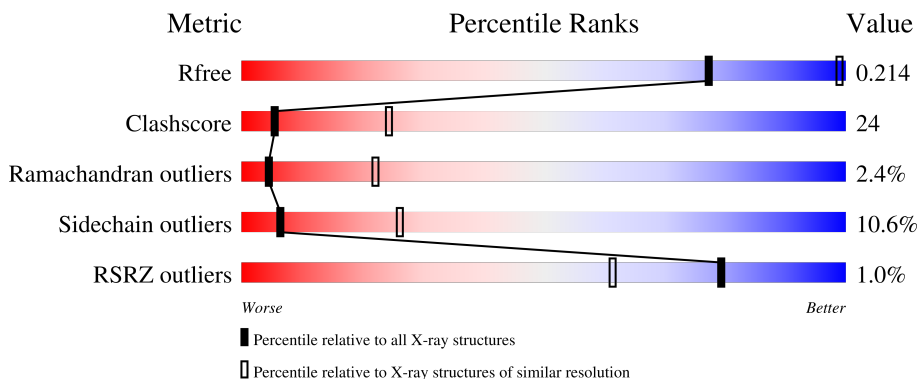
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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  $\geq 3$ , 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	171	<div style="display: flex; align-items: center;"> <div style="width: 2%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 59%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 29%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 9%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: red;"></div> </div> <p style="margin-top: 5px;">2% 59% 29% 9% .</p>
1	B	171	<div style="display: flex; align-items: center;"> <div style="width: 0%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 54%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 32%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 13%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: red;"></div> </div> <p style="margin-top: 5px;">% 54% 32% 13% .</p>
1	C	171	<div style="display: flex; align-items: center;"> <div style="width: 0%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 51%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 40%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 8%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: red;"></div> </div> <p style="margin-top: 5px;">% 51% 40% 8% .</p>
1	D	171	<div style="display: flex; align-items: center;"> <div style="width: 0%; height: 10px; background-color: red; margin-right: 5px;"></div> <div style="width: 47%; height: 10px; background-color: green; margin-right: 5px;"></div> <div style="width: 43%; height: 10px; background-color: yellow; margin-right: 5px;"></div> <div style="width: 9%; height: 10px; background-color: orange; margin-right: 5px;"></div> <div style="width: 2%; height: 10px; background-color: red;"></div> </div> <p style="margin-top: 5px;">47% 43% 9% .</p>

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
2	NGA	A	172	-	-	X	-
2	NGA	B	172	-	-	X	-
3	TLA	C	172	-	-	-	X

## 2 Entry composition [i](#)

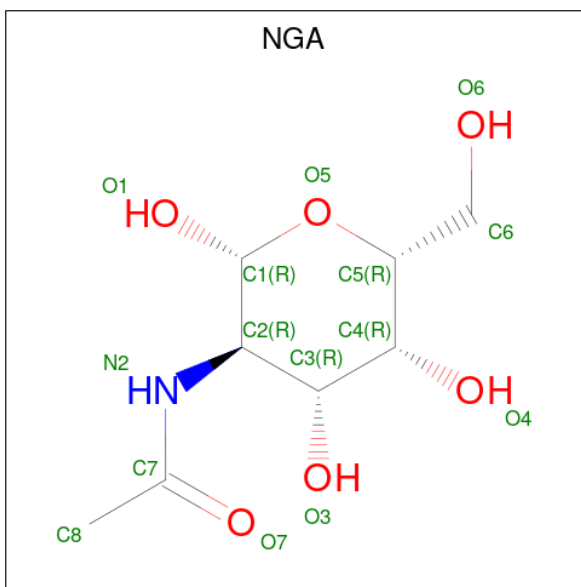
There are 3 unique types of molecules in this entry. The entry contains 5384 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Peptidoglycan recognition protein.

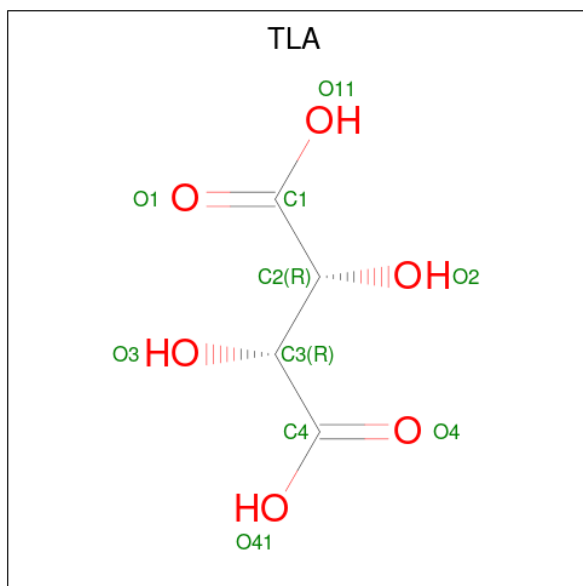
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	171	Total 1336	C 834	N 254	O 240	S 8	0	0	0
1	B	171	Total 1336	C 834	N 254	O 240	S 8	0	0	0
1	C	171	Total 1336	C 834	N 254	O 240	S 8	0	0	0
1	D	171	Total 1336	C 834	N 254	O 240	S 8	0	0	0

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-galactopyranose (CCD ID: NGA) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	Total 15	C 8	N 1	O 6	0	0
2	B	1	Total 15	C 8	N 1	O 6	0	0

- Molecule 3 is L(+)-TARTARIC ACID (CCD ID: TLA) (formula: C<sub>4</sub>H<sub>6</sub>O<sub>6</sub>).

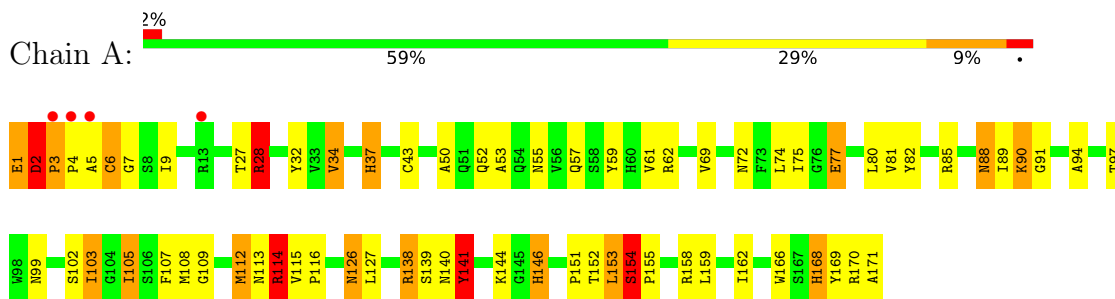


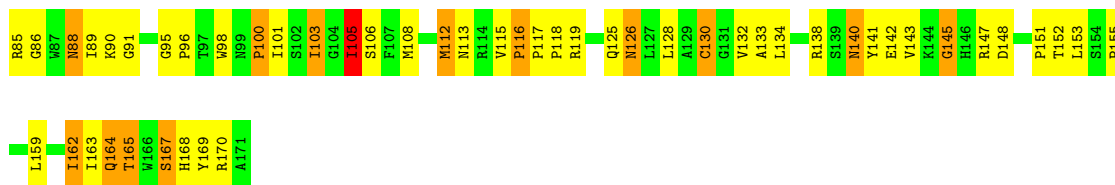
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
3	C	1	Total	C	O	0	0
			10	4	6		

### 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: Peptidoglycan recognition protein





## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	89.21Å 102.44Å 163.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.10 20.00 – 3.10	Depositor EDS
% Data completeness (in resolution range)	89.3 (20.00-3.10) 93.6 (20.00-3.10)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.12	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.44 (at 3.08Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.203 , 0.214 0.212 , 0.214	Depositor DCC
$R_{free}$ test set	669 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	58.3	Xtrriage
Anisotropy	0.215	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 52.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	5384	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.16% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: TLA, NGA

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	0.89	2/1373 (0.1%)	1.52	29/1871 (1.5%)
1	B	0.99	2/1373 (0.1%)	1.56	31/1871 (1.7%)
1	C	0.85	1/1373 (0.1%)	1.36	13/1871 (0.7%)
1	D	0.83	2/1373 (0.1%)	1.38	19/1871 (1.0%)
All	All	0.89	7/5492 (0.1%)	1.46	92/7484 (1.2%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	3	PRO	CA-C	9.64	1.61	1.52
1	A	3	PRO	CA-C	7.09	1.58	1.52
1	D	105	ILE	CA-CB	6.22	1.61	1.54
1	B	132	VAL	CA-CB	6.03	1.61	1.54
1	C	121	LEU	CA-C	-5.50	1.45	1.52
1	D	3	PRO	CA-C	5.49	1.57	1.52
1	A	69	VAL	CA-CB	5.18	1.61	1.54

All (92) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2	ASP	CA-C-N	13.23	134.01	120.38
1	B	2	ASP	C-N-CA	13.23	134.01	120.38
1	B	157	ASP	CA-CB-CG	12.29	124.89	112.60
1	A	154	SER	CA-C-N	-11.25	107.27	119.19
1	A	154	SER	C-N-CA	-11.25	107.27	119.19
1	D	126	ASN	CA-CB-CG	10.90	123.50	112.60
1	A	154	SER	N-CA-C	9.75	131.35	109.81
1	A	88	ASN	N-CA-C	8.98	124.43	113.38
1	C	3	PRO	CA-C-N	8.67	130.67	119.84
1	C	3	PRO	C-N-CA	8.67	130.67	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2	ASP	N-CA-C	8.46	128.51	109.81
1	B	78	ASP	N-CA-C	-8.18	103.30	113.20
1	D	167	SER	N-CA-C	-8.18	98.38	110.48
1	B	162	ILE	N-CA-C	8.17	118.75	110.82
1	B	160	TYR	N-CA-C	-8.08	102.87	112.89
1	B	155	PRO	CA-C-N	-7.87	105.99	121.41
1	B	155	PRO	C-N-CA	-7.87	105.99	121.41
1	A	28	ARG	CD-NE-CZ	7.81	135.34	124.40
1	B	3	PRO	CA-C-N	7.78	129.57	119.84
1	B	3	PRO	C-N-CA	7.78	129.57	119.84
1	A	3	PRO	N-CA-C	7.73	120.14	110.70
1	C	8	SER	N-CA-C	-7.67	100.97	111.56
1	C	88	ASN	N-CA-C	7.57	122.59	113.12
1	D	132	VAL	N-CA-C	-7.49	103.64	111.58
1	D	164	GLN	N-CA-C	-7.40	103.72	112.89
1	A	112	MET	N-CA-C	-7.37	103.18	111.14
1	C	18	LEU	N-CA-C	-7.32	100.86	110.53
1	A	99	ASN	CA-C-N	-7.13	112.26	120.89
1	A	99	ASN	C-N-CA	-7.13	112.26	120.89
1	A	50	ALA	N-CA-C	-7.04	103.65	111.82
1	C	2	ASP	CA-CB-CG	7.04	119.64	112.60
1	A	116	PRO	CA-C-N	7.01	124.78	119.66
1	A	116	PRO	C-N-CA	7.01	124.78	119.66
1	D	26	LEU	N-CA-C	-6.97	101.14	110.55
1	B	53	ALA	N-CA-C	-6.90	103.69	111.14
1	A	115	VAL	CA-C-N	-6.85	113.32	120.38
1	A	115	VAL	C-N-CA	-6.85	113.32	120.38
1	B	143	VAL	N-CA-C	6.84	116.57	106.85
1	A	59	TYR	N-CA-C	-6.62	104.14	111.82
1	B	157	ASP	CA-C-N	6.56	131.10	120.60
1	B	157	ASP	C-N-CA	6.56	131.10	120.60
1	A	169	TYR	N-CA-C	6.35	118.51	108.67
1	D	86	GLY	N-CA-C	6.34	124.05	112.37
1	B	166	TRP	N-CA-C	6.13	119.10	109.96
1	B	121	LEU	N-CA-C	-6.12	103.94	112.45
1	D	116	PRO	CA-C-N	6.12	126.68	120.38
1	D	116	PRO	C-N-CA	6.12	126.68	120.38
1	B	7	GLY	N-CA-C	6.10	127.65	113.18
1	C	156	GLY	N-CA-C	-6.07	103.77	111.72
1	C	31	ARG	N-CA-C	6.07	120.85	112.90
1	D	84	GLY	N-CA-C	-6.04	98.85	113.18
1	A	94	ALA	N-CA-C	5.86	119.71	112.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	63	ASN	N-CA-C	5.85	118.79	111.24
1	B	155	PRO	O-C-N	5.76	132.04	121.10
1	A	162	ILE	CB-CA-C	-5.71	104.55	112.02
1	A	77	GLU	N-CA-C	-5.70	106.28	113.18
1	A	146	HIS	N-CA-C	-5.68	105.16	111.36
1	B	169	TYR	N-CA-C	5.65	117.28	109.15
1	B	152	THR	N-CA-C	5.62	117.93	109.23
1	A	6	CYS	N-CA-C	5.60	122.72	110.80
1	D	145	GLY	N-CA-C	-5.59	105.11	112.82
1	D	88	ASN	N-CA-C	5.58	121.11	113.97
1	B	4	PRO	N-CA-C	5.58	123.96	112.47
1	B	168	HIS	N-CA-C	5.57	119.81	113.19
1	B	88	ASN	N-CA-C	5.53	120.90	114.04
1	A	126	ASN	N-CA-C	-5.51	105.28	111.28
1	D	6	CYS	N-CA-C	5.49	117.17	110.41
1	B	3	PRO	CB-CA-C	5.44	117.56	110.92
1	C	3	PRO	N-CA-C	5.36	117.24	110.70
1	B	148	ASP	CA-C-N	-5.34	115.30	122.72
1	B	148	ASP	C-N-CA	-5.34	115.30	122.72
1	A	166	TRP	N-CA-C	5.32	117.75	110.24
1	B	2	ASP	C-N-CD	-5.28	103.34	125.00
1	B	50	ALA	N-CA-C	-5.28	105.70	111.82
1	D	2	ASP	CA-C-N	-5.24	114.98	120.38
1	D	2	ASP	C-N-CA	-5.24	114.98	120.38
1	A	90	LYS	N-CA-C	-5.23	102.64	110.23
1	C	146	HIS	N-CA-C	-5.23	105.47	111.07
1	B	147	ARG	N-CA-C	-5.16	104.72	111.02
1	D	16	ARG	N-CA-C	5.15	118.69	111.74
1	C	54	GLN	N-CA-C	-5.14	105.76	111.36
1	D	50	ALA	N-CA-C	-5.14	105.86	111.82
1	D	162	ILE	CB-CA-C	-5.13	105.22	112.14
1	A	114	ARG	N-CA-C	5.12	121.71	110.80
1	A	168	HIS	N-CA-C	5.10	119.19	112.92
1	D	32	TYR	N-CA-C	5.10	118.05	109.95
1	B	6	CYS	CA-CB-SG	-5.07	102.74	114.40
1	C	112	MET	N-CA-C	-5.06	105.41	111.03
1	D	101	ILE	CB-CA-C	-5.06	105.73	112.46
1	A	141	TYR	N-CA-C	5.03	121.51	110.80
1	C	82	TYR	N-CA-C	5.03	116.92	108.73
1	A	80	LEU	N-CA-C	5.01	117.92	109.95

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	1336	0	1288	50	0
1	B	1336	0	1288	73	0
1	C	1336	0	1288	71	0
1	D	1336	0	1288	65	0
2	A	15	0	15	8	0
2	B	15	0	15	9	0
3	C	10	0	4	3	0
All	All	5384	0	5186	252	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 24.

All (252) 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:B:112:MET:HE3	1:B:153:LEU:HG	1.38	1.04
1:D:74:LEU:HD22	1:D:108:MET:HE3	1.36	1.03
1:B:60:HIS:HD2	1:B:70:GLY:H	0.98	0.94
1:B:60:HIS:CD2	1:B:70:GLY:H	1.86	0.93
1:B:37:HIS:HD2	1:B:154:SER:HB2	1.35	0.92
1:A:6:CYS:SG	1:A:7:GLY:N	2.44	0.91
1:B:35:VAL:HG22	1:B:105:ILE:HD11	1.49	0.91
1:C:39:ALA:HB2	3:C:172:TLA:O2	1.71	0.91
1:C:112:MET:HE2	1:C:156:GLY:HA2	1.55	0.88
1:B:112:MET:CE	1:B:153:LEU:HG	2.03	0.88
1:D:6:CYS:SG	1:D:134:LEU:HD11	2.16	0.84
1:B:37:HIS:CD2	1:B:154:SER:HB2	2.13	0.82
1:D:43:CYS:O	1:D:77:GLU:HB2	1.79	0.82
1:C:157:ASP:HB3	1:C:158:ARG:HH11	1.45	0.80
1:B:158:ARG:HG3	1:B:158:ARG:HH11	1.47	0.80
1:C:140:ASN:H	1:C:140:ASN:HD22	1.28	0.79
1:B:3:PRO:HB2	1:B:134:LEU:CD2	2.13	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:SER:N	2:A:172:NGA:H62	2.01	0.76
1:B:154:SER:CB	2:B:172:NGA:H62	2.16	0.76
1:B:72:ASN:CG	1:B:103:ILE:HD13	2.10	0.76
1:D:116:PRO:HG2	1:D:159:LEU:HD13	1.66	0.76
1:D:74:LEU:HD22	1:D:108:MET:CE	2.15	0.75
1:C:162:ILE:O	1:C:165:THR:HB	1.87	0.75
1:C:43:CYS:O	1:C:77:GLU:HB2	1.88	0.74
1:B:69:VAL:HG21	1:B:74:LEU:HD11	1.71	0.72
1:A:2:ASP:O	1:A:4:PRO:HD3	1.87	0.72
1:D:53:ALA:HA	1:D:108:MET:HE1	1.69	0.72
1:B:3:PRO:HG3	1:D:138:ARG:HH21	1.54	0.72
1:C:73:PHE:C	1:C:74:LEU:HD12	2.14	0.72
1:C:157:ASP:HB3	1:C:158:ARG:NH1	2.05	0.72
1:B:154:SER:HB3	2:B:172:NGA:H62	1.72	0.71
1:D:167:SER:O	1:D:168:HIS:HB2	1.90	0.70
1:C:7:GLY:HA2	1:C:9:ILE:CD1	2.22	0.70
1:D:57:GLN:O	1:D:61:VAL:HG12	1.92	0.70
1:C:52:GLN:HB3	1:C:108:MET:CE	2.22	0.70
1:B:98:TRP:CE3	1:B:101:ILE:HD11	2.28	0.69
1:C:1:GLU:O	1:C:2:ASP:HB3	1.90	0.69
1:A:153:LEU:HB2	2:A:172:NGA:H61	1.74	0.69
1:B:112:MET:HE2	1:B:156:GLY:HA2	1.75	0.68
1:B:60:HIS:HD2	1:B:70:GLY:N	1.82	0.68
1:A:72:ASN:CG	1:A:103:ILE:HD13	2.18	0.68
1:B:90:LYS:HE3	1:B:99:ASN:HB3	1.73	0.68
1:A:52:GLN:HA	1:A:55:ASN:HD22	1.57	0.68
1:D:128:LEU:HD13	1:D:141:TYR:OH	1.93	0.67
1:C:75:ILE:HD13	1:C:105:ILE:HD13	1.76	0.67
1:D:85:ARG:HD2	1:D:91:GLY:HA2	1.75	0.67
1:A:112:MET:HE1	1:A:153:LEU:CB	2.24	0.67
1:C:140:ASN:HD22	1:C:140:ASN:N	1.94	0.65
1:B:142:GLU:OE1	1:B:170:ARG:HG3	1.97	0.65
1:C:37:HIS:CD2	1:C:154:SER:HA	2.31	0.64
1:B:31:ARG:HG2	1:B:32:TYR:CD1	2.32	0.64
1:B:163:ILE:HD12	1:B:164:GLN:N	2.12	0.64
1:C:126:ASN:O	1:C:129:ALA:HB3	1.98	0.63
1:B:3:PRO:HB2	1:B:134:LEU:HD22	1.79	0.63
1:D:53:ALA:CA	1:D:108:MET:HE1	2.29	0.62
1:B:159:LEU:O	1:B:163:ILE:HG13	2.00	0.62
1:B:144:LYS:NZ	1:B:171:ALA:C	2.58	0.62
1:C:85:ARG:HD2	1:C:91:GLY:HA2	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:7:GLY:HA2	1:C:9:ILE:HD12	1.80	0.62
1:B:6:CYS:HA	1:B:130:CYS:HB2	1.81	0.61
1:D:58:SER:O	1:D:62:ARG:HG2	2.01	0.61
1:D:155:PRO:HB2	1:D:159:LEU:HD23	1.82	0.61
1:B:159:LEU:O	1:B:159:LEU:HD12	2.00	0.61
1:B:98:TRP:HE3	1:B:101:ILE:HD11	1.64	0.61
1:A:112:MET:HE1	1:A:153:LEU:HB3	1.82	0.61
1:B:158:ARG:HG3	1:B:158:ARG:NH1	2.11	0.60
1:D:142:GLU:CD	1:D:170:ARG:HD3	2.26	0.60
1:D:143:VAL:N	1:D:168:HIS:O	2.29	0.60
1:C:2:ASP:O	1:C:3:PRO:C	2.42	0.60
1:B:3:PRO:HB2	1:B:134:LEU:HD21	1.84	0.59
1:D:162:ILE:O	1:D:165:THR:HB	2.03	0.59
1:B:112:MET:HE3	1:B:153:LEU:CG	2.24	0.59
1:D:1:GLU:HG2	1:D:2:ASP:H	1.68	0.58
1:D:159:LEU:O	1:D:163:ILE:HG23	2.03	0.58
1:D:89:ILE:HD12	1:D:89:ILE:N	2.18	0.58
1:C:96:PRO:HG3	1:D:96:PRO:HG3	1.86	0.58
1:D:71:TYR:CD2	1:D:106:SER:HB2	2.39	0.58
1:A:138:ARG:HE	1:A:140:ASN:HD22	1.52	0.58
1:B:3:PRO:HG3	1:D:138:ARG:NH2	2.19	0.57
1:D:116:PRO:CG	1:D:159:LEU:HD13	2.33	0.57
1:B:160:TYR:CD1	1:B:163:ILE:HD11	2.39	0.57
1:C:119:ARG:HA	1:C:122:ARG:NH1	2.20	0.57
1:A:32:TYR:O	1:A:102:SER:HA	2.05	0.57
1:C:132:VAL:HG13	1:C:139:SER:HA	1.85	0.56
1:A:153:LEU:HB2	2:A:172:NGA:C6	2.35	0.56
1:C:151:PRO:HA	1:D:59:TYR:OH	2.05	0.56
1:A:89:ILE:N	1:A:89:ILE:HD12	2.21	0.56
1:B:158:ARG:HH12	1:B:161:GLU:CD	2.12	0.56
1:D:145:GLY:O	1:D:148:ASP:HB2	2.05	0.56
1:B:105:ILE:HD13	1:B:105:ILE:H	1.69	0.56
1:D:2:ASP:H	1:D:3:PRO:HD3	1.70	0.56
1:D:164:GLN:HG2	1:D:169:TYR:CZ	2.41	0.55
1:C:60:HIS:O	1:C:66:TRP:HB2	2.07	0.55
1:B:92:ALA:HA	1:B:99:ASN:ND2	2.21	0.55
1:C:39:ALA:CB	3:C:172:TLA:O2	2.51	0.55
1:C:128:LEU:HD13	1:C:141:TYR:CE1	2.41	0.55
1:A:146:HIS:HB3	1:A:154:SER:HB3	1.89	0.54
1:D:60:HIS:O	1:D:66:TRP:HB2	2.07	0.54
1:D:67:CYS:O	1:D:68:ASP:HB2	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:ASN:OD1	1:B:7:GLY:HA2	2.08	0.54
1:A:85:ARG:HD2	1:A:91:GLY:HA3	1.90	0.53
1:D:167:SER:O	1:D:168:HIS:CB	2.56	0.53
1:B:59:TYR:HD1	1:B:63:ASN:HD22	1.57	0.53
1:A:52:GLN:C	1:A:108:MET:HE1	2.34	0.53
1:B:72:ASN:CB	1:B:103:ILE:HD13	2.38	0.53
1:A:37:HIS:HB2	1:A:109:GLY:O	2.08	0.53
1:A:170:ARG:O	1:A:171:ALA:C	2.51	0.53
1:A:43:CYS:O	1:A:77:GLU:HB2	2.09	0.53
1:C:81:VAL:HG11	1:C:127:LEU:HD13	1.90	0.53
1:A:113:ASN:O	1:A:158:ARG:HB2	2.09	0.52
1:A:141:TYR:O	1:A:168:HIS:HD2	1.91	0.52
1:B:75:ILE:HD11	1:B:105:ILE:HB	1.92	0.52
1:A:9:ILE:HD12	1:A:9:ILE:N	2.25	0.52
1:D:116:PRO:HG2	1:D:159:LEU:CD1	2.38	0.52
1:D:2:ASP:H	1:D:3:PRO:CD	2.23	0.52
1:C:32:TYR:CE1	1:C:101:ILE:HD12	2.45	0.51
1:C:115:VAL:HG12	1:C:162:ILE:HD11	1.91	0.51
1:C:68:ASP:O	1:C:69:VAL:C	2.54	0.51
1:A:72:ASN:CB	1:A:103:ILE:HD13	2.41	0.51
1:B:12:ARG:NH1	1:B:84:GLY:O	2.44	0.51
1:C:138:ARG:O	1:C:139:SER:C	2.53	0.51
1:C:112:MET:HE2	1:C:156:GLY:CA	2.34	0.51
1:B:6:CYS:HA	1:B:130:CYS:CB	2.41	0.50
1:D:118:PRO:O	1:D:119:ARG:C	2.54	0.50
1:B:75:ILE:N	1:B:75:ILE:HD12	2.27	0.50
1:B:154:SER:N	2:B:172:NGA:C6	2.74	0.50
1:C:96:PRO:HG3	1:D:96:PRO:CG	2.42	0.50
1:C:9:ILE:HG23	1:C:81:VAL:HG12	1.92	0.50
1:C:143:VAL:HG12	1:C:144:LYS:N	2.26	0.50
1:C:52:GLN:CB	1:C:108:MET:CE	2.89	0.50
1:A:146:HIS:H	1:A:155:PRO:HG3	1.77	0.50
1:A:155:PRO:O	1:A:159:LEU:HD23	2.11	0.50
1:A:89:ILE:HG22	1:A:90:LYS:O	2.12	0.49
1:B:38:THR:C	1:B:40:GLY:H	2.20	0.49
1:B:12:ARG:HH22	1:B:68:ASP:CG	2.21	0.49
1:D:55:ASN:O	1:D:56:VAL:C	2.51	0.49
1:C:37:HIS:NE2	1:C:154:SER:HA	2.27	0.49
1:D:105:ILE:C	1:D:105:ILE:HD12	2.36	0.49
1:A:154:SER:N	2:A:172:NGA:C6	2.75	0.49
1:B:115:VAL:HG13	1:B:158:ARG:HG2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:88:ASN:HB2	1:D:89:ILE:HD12	1.94	0.49
1:C:33:VAL:HG21	1:C:128:LEU:HD22	1.95	0.49
1:C:76:GLY:C	1:C:78:ASP:H	2.20	0.49
1:D:3:PRO:O	1:D:4:PRO:C	2.55	0.49
1:D:77:GLU:OE2	1:D:117:PRO:HD3	2.13	0.48
1:C:59:TYR:OH	1:D:151:PRO:HA	2.13	0.48
1:C:75:ILE:HD12	1:C:75:ILE:N	2.28	0.48
1:D:6:CYS:SG	1:D:134:LEU:CD1	2.96	0.48
1:C:12:ARG:NH1	1:C:84:GLY:O	2.47	0.48
1:C:105:ILE:C	1:C:105:ILE:HD12	2.38	0.48
1:A:105:ILE:C	1:A:105:ILE:HD12	2.39	0.48
1:C:69:VAL:O	1:C:85:ARG:NE	2.45	0.48
1:B:31:ARG:NH2	1:B:142:GLU:OE2	2.47	0.48
1:C:9:ILE:HD12	1:C:9:ILE:H	1.78	0.48
1:D:1:GLU:HG2	1:D:2:ASP:N	2.29	0.48
1:D:142:GLU:OE1	1:D:170:ARG:HD3	2.14	0.48
1:A:77:GLU:OE2	1:A:114:ARG:NH2	2.48	0.47
1:D:164:GLN:HG2	1:D:169:TYR:CE2	2.50	0.47
1:B:154:SER:CA	2:B:172:NGA:H62	2.44	0.47
1:B:38:THR:C	1:B:40:GLY:N	2.71	0.47
1:B:39:ALA:HB2	2:B:172:NGA:H5	1.97	0.47
1:B:143:VAL:O	1:B:169:TYR:CD1	2.67	0.47
1:D:112:MET:CE	1:D:153:LEU:HB3	2.43	0.47
1:A:152:THR:OG1	2:A:172:NGA:H4	2.15	0.47
1:B:30:VAL:CG1	1:B:102:SER:HA	2.45	0.47
1:C:128:LEU:HD13	1:C:141:TYR:HE1	1.79	0.47
1:A:153:LEU:CB	2:A:172:NGA:H61	2.45	0.46
1:C:75:ILE:CD1	1:C:105:ILE:HD13	2.45	0.46
1:A:74:LEU:HB2	1:A:82:TYR:HB2	1.97	0.46
1:B:154:SER:H	2:B:172:NGA:C6	2.28	0.46
1:B:150:GLN:O	1:B:152:THR:N	2.48	0.46
1:C:132:VAL:CG1	1:C:139:SER:HA	2.46	0.46
1:A:112:MET:HE1	1:A:153:LEU:HB2	1.98	0.46
1:A:34:VAL:HG23	1:A:102:SER:HB2	1.97	0.46
1:C:9:ILE:HD12	1:C:9:ILE:N	2.32	0.46
1:B:154:SER:HB3	2:B:172:NGA:C6	2.45	0.45
1:C:4:PRO:O	1:C:5:ALA:HB3	2.15	0.45
1:B:154:SER:H	2:B:172:NGA:H61	1.80	0.45
1:B:52:GLN:HB3	1:B:108:MET:HE3	1.98	0.45
1:B:132:VAL:O	1:B:133:ALA:C	2.59	0.45
1:C:141:TYR:O	1:C:168:HIS:CD2	2.69	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:52:GLN:HE21	1:D:55:ASN:HD22	1.65	0.45
1:B:158:ARG:NH1	1:B:161:GLU:OE2	2.50	0.45
1:C:12:ARG:HG3	1:C:83:GLU:OE1	2.17	0.45
1:B:154:SER:N	2:B:172:NGA:H62	2.32	0.45
1:D:52:GLN:NE2	1:D:55:ASN:HD22	2.15	0.45
1:A:52:GLN:HB3	1:A:108:MET:HE2	1.98	0.44
1:B:89:ILE:HD12	1:B:89:ILE:N	2.32	0.44
1:C:140:ASN:N	1:C:140:ASN:ND2	2.64	0.44
1:D:57:GLN:HG3	1:D:69:VAL:HB	1.98	0.44
1:D:112:MET:HE1	1:D:153:LEU:HB3	1.99	0.44
1:C:52:GLN:HB3	1:C:108:MET:HE3	1.99	0.44
1:D:33:VAL:HG22	1:D:103:ILE:HG22	1.99	0.44
1:A:85:ARG:HD2	1:A:91:GLY:CA	2.46	0.44
1:C:160:TYR:O	1:C:164:GLN:HG3	2.16	0.44
1:D:71:TYR:CE2	1:D:106:SER:HB2	2.52	0.44
1:D:147:ARG:HA	1:D:152:THR:HG22	2.00	0.44
1:C:52:GLN:HB3	1:C:108:MET:HE2	2.00	0.44
1:D:98:TRP:C	1:D:100:PRO:HD2	2.42	0.44
1:D:75:ILE:CD1	1:D:81:VAL:HG22	2.48	0.44
1:A:52:GLN:HB3	1:A:108:MET:CE	2.48	0.44
1:A:75:ILE:HB	1:A:107:PHE:HA	2.00	0.44
1:D:2:ASP:N	1:D:3:PRO:CD	2.80	0.44
1:D:52:GLN:HE21	1:D:52:GLN:HA	1.83	0.44
1:B:2:ASP:HA	1:B:3:PRO:HD2	1.68	0.43
1:B:52:GLN:O	1:B:56:VAL:HG23	2.18	0.43
1:C:55:ASN:O	1:C:56:VAL:C	2.60	0.43
1:C:127:LEU:O	1:C:130:CYS:HB3	2.19	0.43
1:C:80:LEU:HA	1:C:80:LEU:HD23	1.77	0.43
1:D:46:PRO:HA	1:D:78:ASP:OD1	2.18	0.43
1:D:90:LYS:HD2	1:D:100:PRO:HB3	2.00	0.43
1:A:141:TYR:O	1:A:168:HIS:CD2	2.71	0.43
1:B:68:ASP:O	1:B:69:VAL:C	2.61	0.43
1:B:101:ILE:HD12	1:B:102:SER:N	2.34	0.43
1:D:130:CYS:O	1:D:133:ALA:HB3	2.19	0.43
1:B:78:ASP:C	1:B:78:ASP:OD2	2.61	0.43
1:C:112:MET:HE3	1:C:153:LEU:HB3	2.01	0.43
1:C:114:ARG:HE	1:C:114:ARG:HB3	1.73	0.43
1:A:138:ARG:HD3	1:A:140:ASN:HB2	2.01	0.42
1:A:146:HIS:ND1	1:A:154:SER:CB	2.82	0.42
1:D:58:SER:HA	1:D:61:VAL:HG12	2.00	0.42
1:A:53:ALA:N	1:A:108:MET:HE1	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:69:VAL:HG13	1:B:69:VAL:O	2.19	0.42
1:D:140:ASN:C	1:D:140:ASN:HD22	2.27	0.42
1:B:31:ARG:HB2	1:B:138:ARG:HH11	1.85	0.42
1:B:35:VAL:HG11	1:B:163:ILE:HG21	2.01	0.42
1:B:68:ASP:OD1	1:B:69:VAL:HG12	2.19	0.42
1:B:138:ARG:O	1:B:141:TYR:N	2.52	0.42
1:D:63:ASN:HD22	1:D:63:ASN:HA	1.62	0.42
1:C:111:TYR:CE2	1:C:116:PRO:HB3	2.55	0.42
1:C:39:ALA:HB2	3:C:172:TLA:HA	1.78	0.42
1:D:12:ARG:HG3	1:D:83:GLU:OE1	2.20	0.42
1:A:37:HIS:CE1	2:A:172:NGA:O6	2.73	0.42
1:C:140:ASN:O	1:C:140:ASN:CG	2.61	0.41
1:C:74:LEU:HD12	1:C:74:LEU:N	2.35	0.41
1:A:103:ILE:O	1:A:103:ILE:HG22	2.20	0.41
1:C:145:GLY:O	1:C:148:ASP:HB2	2.19	0.41
1:A:154:SER:H	2:A:172:NGA:H62	1.81	0.41
1:C:153:LEU:O	1:C:154:SER:C	2.63	0.41
1:D:53:ALA:HA	1:D:108:MET:CE	2.45	0.41
1:A:1:GLU:C	1:A:3:PRO:HD3	2.45	0.41
1:A:32:TYR:O	1:A:102:SER:CA	2.69	0.41
1:C:140:ASN:H	1:C:140:ASN:ND2	2.06	0.41
1:A:57:GLN:O	1:A:61:VAL:HG23	2.21	0.41
1:B:35:VAL:O	1:B:155:PRO:HG3	2.21	0.41
1:C:37:HIS:CD2	1:C:155:PRO:HA	2.56	0.41
1:C:33:VAL:HG21	1:C:128:LEU:CD2	2.51	0.41
1:A:81:VAL:HG11	1:A:127:LEU:HD13	2.02	0.40
1:C:143:VAL:CG1	1:C:144:LYS:N	2.84	0.40
1:A:28:ARG:NH1	1:A:88:ASN:OD1	2.53	0.40
1:B:143:VAL:O	1:B:169:TYR:HD1	2.04	0.40
1:C:158:ARG:O	1:C:161:GLU:HB2	2.21	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	169/171 (99%)	150 (89%)	13 (8%)	6 (4%)	2	16
1	B	169/171 (99%)	151 (89%)	12 (7%)	6 (4%)	2	16
1	C	169/171 (99%)	152 (90%)	16 (10%)	1 (1%)	21	52
1	D	169/171 (99%)	150 (89%)	16 (10%)	3 (2%)	6	28
All	All	676/684 (99%)	603 (89%)	57 (8%)	16 (2%)	4	22

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	114	ARG
1	B	3	PRO
1	B	4	PRO
1	B	7	GLY
1	C	3	PRO
1	A	5	ALA
1	A	141	TYR
1	D	2	ASP
1	A	154	SER
1	A	2	ASP
1	A	151	PRO
1	B	148	ASP
1	B	39	ALA
1	D	95	GLY
1	B	151	PRO
1	D	4	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	139/139 (100%)	126 (91%)	13 (9%)	8	31
1	B	139/139 (100%)	123 (88%)	16 (12%)	5	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	139/139 (100%)	125 (90%)	14 (10%)	7	28
1	D	139/139 (100%)	123 (88%)	16 (12%)	5	23
All	All	556/556 (100%)	497 (89%)	59 (11%)	6	26

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	GLU
1	A	27	THR
1	A	28	ARG
1	A	34	VAL
1	A	37	HIS
1	A	62	ARG
1	A	97	THR
1	A	103	ILE
1	A	105	ILE
1	A	138	ARG
1	A	139	SER
1	A	144	LYS
1	A	153	LEU
1	B	2	ASP
1	B	27	THR
1	B	33	VAL
1	B	62	ARG
1	B	69	VAL
1	B	74	LEU
1	B	103	ILE
1	B	105	ILE
1	B	113	ASN
1	B	115	VAL
1	B	130	CYS
1	B	154	SER
1	B	157	ASP
1	B	158	ARG
1	B	164	GLN
1	B	165	THR
1	C	4	PRO
1	C	28	ARG
1	C	105	ILE
1	C	114	ARG
1	C	115	VAL

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Mol	Chain	Res	Type
1	C	117	PRO
1	C	122	ARG
1	C	125	GLN
1	C	140	ASN
1	C	144	LYS
1	C	153	LEU
1	C	157	ASP
1	C	158	ARG
1	C	167	SER
1	D	8	SER
1	D	21	GLU
1	D	24	GLU
1	D	36	SER
1	D	51	GLN
1	D	100	PRO
1	D	103	ILE
1	D	105	ILE
1	D	112	MET
1	D	113	ASN
1	D	115	VAL
1	D	125	GLN
1	D	126	ASN
1	D	130	CYS
1	D	140	ASN
1	D	165	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	HIS
1	A	54	GLN
1	A	55	ASN
1	A	93	HIS
1	A	125	GLN
1	A	140	ASN
1	A	168	HIS
1	B	54	GLN
1	B	60	HIS
1	B	63	ASN
1	B	93	HIS
1	B	113	ASN
1	B	164	GLN

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Mol	Chain	Res	Type
1	B	168	HIS
1	C	54	GLN
1	C	55	ASN
1	C	63	ASN
1	C	113	ASN
1	C	125	GLN
1	C	140	ASN
1	C	164	GLN
1	C	168	HIS
1	D	52	GLN
1	D	63	ASN
1	D	93	HIS
1	D	113	ASN
1	D	140	ASN
1	D	150	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 oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

3 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
2	NGA	B	172	-	15,15,15	0.50	0	21,21,21	1.16	2 (9%)
2	NGA	A	172	-	15,15,15	2.64	4 (26%)	21,21,21	1.88	4 (19%)
3	TLA	C	172	-	9,9,9	1.41	2 (22%)	12,12,12	1.44	3 (25%)

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
2	NGA	B	172	-	-	0/6/26/26	0/1/1/1
2	NGA	A	172	-	-	0/6/26/26	0/1/1/1
3	TLA	C	172	-	-	0/12/12/12	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	172	NGA	C8-C7	-7.59	1.34	1.50
2	A	172	NGA	C2-N2	-5.22	1.37	1.45
3	C	172	TLA	O11-C1	-3.20	1.20	1.30
3	C	172	TLA	O2-C2	-2.11	1.38	1.42
2	A	172	NGA	C7-N2	-2.10	1.27	1.34
2	A	172	NGA	C4-C5	2.04	1.57	1.53

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	172	NGA	C1-C2-N2	-5.21	104.70	110.73
2	A	172	NGA	C8-C7-N2	-3.64	110.08	116.12
2	A	172	NGA	O7-C7-N2	3.19	127.61	121.98
2	A	172	NGA	C4-C3-C2	-3.12	105.86	110.40
2	B	172	NGA	C1-O5-C5	-3.07	107.72	113.65
3	C	172	TLA	O4-C4-C3	-2.76	114.26	121.62
3	C	172	TLA	O1-C1-C2	-2.45	115.09	121.62
3	C	172	TLA	O41-C4-C3	2.38	119.93	113.31
2	B	172	NGA	C8-C7-N2	2.34	120.00	116.12

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	172	NGA	9	0
2	A	172	NGA	8	0
3	C	172	TLA	3	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	171/171 (100%)	-0.29	4 (2%) 61 39	30, 43, 58, 88	0
1	B	171/171 (100%)	-0.19	1 (0%) 85 70	31, 49, 66, 89	0
1	C	171/171 (100%)	-0.30	2 (1%) 76 58	29, 42, 60, 85	0
1	D	171/171 (100%)	-0.26	0 100 100	30, 46, 61, 91	0
All	All	684/684 (100%)	-0.26	7 (1%) 79 61	29, 45, 64, 91	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	4	PRO	3.7
1	C	158	ARG	3.3
1	A	3	PRO	3.2
1	A	5	ALA	3.1
1	B	3	PRO	2.5
1	A	13	ARG	2.5
1	C	76	GLY	2.3

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	NGA	A	172	15/15	0.60	0.31	20,20,20,20	0
2	NGA	B	172	15/15	0.60	0.31	20,20,20,20	0
3	TLA	C	172	10/10	0.64	0.41	20,20,20,20	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.