



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 3WO4
Title : Crystal structure of the IL-18 signaling ternary complex
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Deposited on : 2013-12-19
Resolution : 3.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

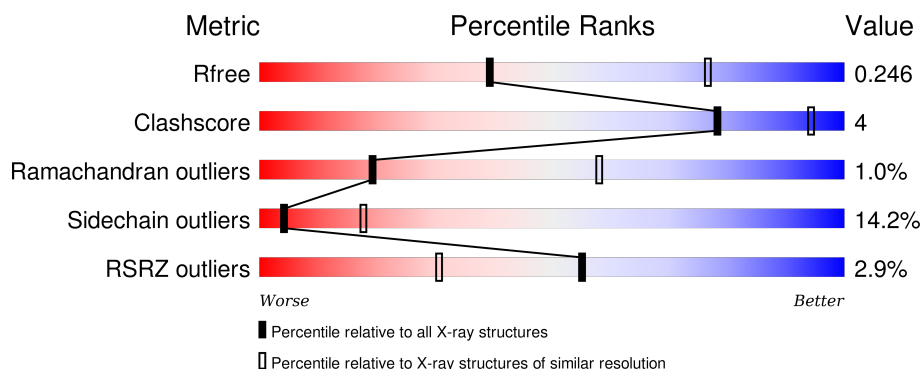
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	91344	1114 (3.14-3.06)
Clashscore	102246	1222 (3.14-3.06)
Ramachandran outliers	100387	1174 (3.14-3.06)
Sidechain outliers	100360	1174 (3.14-3.06)
RSRZ outliers	91569	1119 (3.14-3.06)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	157	<div> <div>75%</div> <div>23%</div> <div>.</div> </div>
2	B	312	<div> <div>%</div> <div>77%</div> <div>16%</div> <div>.</div> <div>.</div> </div>
3	C	344	<div> <div>6%</div> <div>64%</div> <div>13%</div> <div>.</div> <div>22%</div> </div>

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
10	NAG	C	902	-	-	-	X
11	CL	C	908	-	-	-	X
8	NAG	B	910	-	-	-	X

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 6030 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-18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	157	Total	C	N	O	S	0	0	0
			1266	796	209	251	10			

- Molecule 2 is a protein called Interleukin-18 receptor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	301	Total	C	N	O	S	0	1	0
			2375	1499	406	456	14			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	GLY	-	EXPRESSION TAG	UNP Q13478
B	-1	PRO	-	EXPRESSION TAG	UNP Q13478

- Molecule 3 is a protein called Interleukin-18 receptor accessory protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	270	Total	C	N	O	S	0	0	0
			2022	1263	347	402	10			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	GLY	-	EXPRESSION TAG	UNP O95256
C	-1	PRO	-	EXPRESSION TAG	UNP O95256

- Molecule 4 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 5 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	3	Total	C	N	O	0	0
			38	22	2	14		

- Molecule 6 is a polymer of unknown type called SUGAR (5-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 7 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 8 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	B	2	Total	C	N	O	0	0
			28	16	2	10		
8	C	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 9 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	B	4	Total	C	N	O	0	0
			49	28	2	19		

- Molecule 10 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	C	4	Total	C	N	O	0	0
			50	28	2	20		

- Molecule 11 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	C	1	Total	Cl	0	0
			1	1		

- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	14	Total	O	0	0
			14	14		
12	B	7	Total	O	0	0
			7	7		
12	C	10	Total	O	0	0
			10	10		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.56Å 111.56Å 134.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.00 – 3.10 49.34 – 3.09	Depositor EDS
% Data completeness (in resolution range)	85.0 (42.00-3.10) 84.8 (49.34-3.09)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.39 (at 3.07Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.188 , 0.232 0.198 , 0.246	Depositor DCC
R_{free} test set	881 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	58.9	Xtriage
Anisotropy	0.580	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 91.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 17449 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6030	wwPDB-VP
Average B, all atoms (Å ²)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.76% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: FUC, MAN, BMA, NAG, CL

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	0.49	0/1287	0.71	0/1726
2	B	0.45	0/2433	0.68	0/3310
3	C	0.45	0/2057	0.72	0/2800
All	All	0.46	0/5777	0.70	0/7836

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	1266	0	1237	13	0
2	B	2375	0	2231	17	0
3	C	2022	0	1857	15	0
4	B	28	0	26	0	0
4	C	14	0	13	0	0
5	B	38	0	34	0	0
6	B	61	0	52	0	0
7	B	39	0	34	0	0
8	B	28	0	25	0	0
8	C	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	B	49	0	43	0	0
10	C	50	0	43	0	0
11	C	1	0	0	0	0
12	A	14	0	0	1	0
12	B	7	0	0	0	0
12	C	10	0	0	0	0
All	All	6030	0	5620	42	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 4.

The worst 5 of 42 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)
2:B:295:LEU:HD12	2:B:312:ILE:HD11	1.64	0.80
2:B:180:GLN:HG3	2:B:205:THR:HA	1.77	0.67
2:B:301:ALA:HA	2:B:306:THR:HG22	1.79	0.64
3:C:216:GLN:HG3	3:C:241:ARG:HA	1.84	0.59
2:B:54:LYS:HB3	2:B:98:PHE:HE1	1.68	0.58

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	155/157 (99%)	142 (92%)	12 (8%)	1 (1%)	30	68
2	B	300/312 (96%)	278 (93%)	18 (6%)	4 (1%)	15	50
3	C	264/344 (77%)	237 (90%)	25 (10%)	2 (1%)	24	63
All	All	719/813 (88%)	657 (91%)	55 (8%)	7 (1%)	19	58

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	116	PRO
2	B	72	SER
2	B	80	ASP
2	B	166	ASN
2	B	209	ASP

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	145/148 (98%)	124 (86%)	21 (14%)	4	16
2	B	263/288 (91%)	227 (86%)	36 (14%)	4	19
3	C	212/321 (66%)	181 (85%)	31 (15%)	4	16
All	All	620/757 (82%)	532 (86%)	88 (14%)	4	18

5 of 88 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	198	ILE
2	B	255	ASN
3	C	336	VAL
2	B	199	THR
2	B	218	LEU

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

Mol	Chain	Res	Type
1	A	111	ASN
1	A	114	GLN
2	B	192	ASN
2	B	212	ASN
3	C	340	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

23 carbohydrates 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	$\# Z > 2$
5	NAG	B	903	2,5	14,14,15	0.28	0	15,19,21	0.56	0
5	NAG	B	904	5	14,14,15	0.27	0	15,19,21	0.56	0
6	NAG	B	905	2,6	14,14,15	0.26	0	15,19,21	0.63	1 (6%)
6	NAG	B	906	6	14,14,15	0.33	0	15,19,21	1.59	3 (20%)
7	NAG	B	907	2,7	14,14,15	0.28	0	15,19,21	0.72	1 (6%)
7	NAG	B	908	7	14,14,15	0.35	0	15,19,21	1.67	3 (20%)
8	NAG	B	909	8,2	14,14,15	0.29	0	15,19,21	0.73	0
8	NAG	B	910	8	14,14,15	0.31	0	15,19,21	0.34	0
9	NAG	B	911	9,2	14,14,15	0.28	0	15,19,21	0.69	0
9	NAG	B	912	9	14,14,15	0.30	0	15,19,21	0.39	0
6	BMA	B	951	6	11,11,12	0.32	0	14,15,17	0.97	1 (7%)
6	MAN	B	952	6	11,11,12	0.38	0	14,15,17	1.11	1 (7%)
6	MAN	B	953	6	11,11,12	0.50	0	14,15,17	1.69	2 (14%)
7	BMA	B	955	7	11,11,12	0.36	0	14,15,17	0.91	1 (7%)
9	BMA	B	958	9	11,11,12	0.34	0	14,15,17	0.67	0
5	FUC	B	998	5	10,10,11	0.43	0	14,14,16	1.22	1 (7%)
9	FUC	B	999	9	10,10,11	0.56	0	14,14,16	1.37	2 (14%)
10	NAG	C	902	10,3	14,14,15	0.30	0	15,19,21	0.65	1 (6%)
10	NAG	C	903	10	14,14,15	0.30	0	15,19,21	0.61	0
8	NAG	C	904	8,3	14,14,15	0.29	0	15,19,21	0.35	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	NAG	C	905	8	14,14,15	0.27	0	15,19,21	0.51	0
10	BMA	C	951	10	11,11,12	0.30	0	14,15,17	0.55	0
10	MAN	C	952	10	11,11,12	0.40	0	14,15,17	0.90	2 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	B	903	2,5	-	0/6/23/26	0/1/1/1
5	NAG	B	904	5	-	0/6/23/26	0/1/1/1
6	NAG	B	905	2,6	-	0/6/23/26	0/1/1/1
6	NAG	B	906	6	-	0/6/23/26	0/1/1/1
7	NAG	B	907	2,7	-	0/6/23/26	0/1/1/1
7	NAG	B	908	7	-	0/6/23/26	0/1/1/1
8	NAG	B	909	8,2	-	0/6/23/26	0/1/1/1
8	NAG	B	910	8	-	0/6/23/26	0/1/1/1
9	NAG	B	911	9,2	-	0/6/23/26	0/1/1/1
9	NAG	B	912	9	-	0/6/23/26	0/1/1/1
6	BMA	B	951	6	-	0/2/19/22	0/1/1/1
6	MAN	B	952	6	-	0/2/19/22	0/1/1/1
6	MAN	B	953	6	-	0/2/19/22	0/1/1/1
7	BMA	B	955	7	-	0/2/19/22	0/1/1/1
9	BMA	B	958	9	-	0/2/19/22	0/1/1/1
5	FUC	B	998	5	-	0/0/17/20	0/1/1/1
9	FUC	B	999	9	-	0/0/17/20	0/1/1/1
10	NAG	C	902	10,3	-	0/6/23/26	0/1/1/1
10	NAG	C	903	10	-	0/6/23/26	0/1/1/1
8	NAG	C	904	8,3	-	0/6/23/26	0/1/1/1
8	NAG	C	905	8	-	0/6/23/26	0/1/1/1
10	BMA	C	951	10	-	0/2/19/22	0/1/1/1
10	MAN	C	952	10	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	907	NAG	C1-O5-C5	2.03	114.83	112.25
10	C	952	MAN	C1-C2-C3	2.14	112.08	109.54
6	B	905	NAG	C1-O5-C5	2.20	115.04	112.25
7	B	908	NAG	O4-C4-C3	2.21	115.31	110.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	C	902	NAG	C1-O5-C5	2.23	115.07	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 for Mogul analysis.

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	B	901	2	14,14,15	0.27	0	15,19,21	0.63	1 (6%)
4	NAG	B	902	2	14,14,15	0.30	0	15,19,21	0.64	1 (6%)
4	NAG	C	901	3	14,14,15	0.28	0	15,19,21	0.55	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	B	901	2	-	0/6/23/26	0/1/1/1
4	NAG	B	902	2	-	0/6/23/26	0/1/1/1
4	NAG	C	901	3	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	902	NAG	C1-O5-C5	2.14	114.96	112.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	901	NAG	C1-O5-C5	2.17	115.01	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	157/157 (100%)	-0.32	0 100 100	30, 48, 80, 109	0
2	B	301/312 (96%)	0.03	2 (0%) 89 78	36, 74, 118, 151	0
3	C	270/344 (78%)	0.28	19 (7%) 19 7	38, 80, 145, 164	0
All	All	728/813 (89%)	0.05	21 (2%) 55 31	30, 68, 136, 164	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	72	SER	4.9
3	C	120	ASN	4.7
2	B	68	LEU	3.9
3	C	45	PHE	3.5
3	C	109	CYS	3.4

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](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	LLDF	B-factors(Å ²)	Q<0.9
8	NAG	B	910	14/15	0.74	0.45	3.74	118,126,130,131	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
10	NAG	C	902	14/15	0.73	0.33	2.60	162,167,170,171	0
7	NAG	B	907	14/15	0.91	0.17	-0.40	97,101,107,116	0
8	NAG	C	904	14/15	0.90	0.16	-0.68	94,98,103,109	0
6	NAG	B	905	14/15	0.94	0.20	-0.84	113,120,126,129	0
9	NAG	B	911	14/15	0.93	0.16	-0.94	82,88,93,101	0
8	NAG	B	909	14/15	0.92	0.17	-1.26	107,112,115,118	0
9	BMA	B	958	11/12	0.75	0.36	-	132,138,143,144	0
6	MAN	B	952	11/12	0.79	0.25	-	175,179,184,185	0
5	FUC	B	998	10/11	0.91	0.25	-	140,141,144,145	0
5	NAG	B	904	14/15	0.84	0.29	-	150,155,162,162	0
10	BMA	C	951	11/12	0.65	0.29	-	174,177,182,183	0
10	NAG	C	903	14/15	0.73	0.42	-	162,171,174,175	0
9	FUC	B	999	10/11	0.88	0.25	-	90,93,95,95	0
7	BMA	B	955	11/12	0.76	0.24	-	143,146,148,149	0
6	NAG	B	906	14/15	0.92	0.21	-	132,139,148,153	0
6	MAN	B	953	11/12	0.59	0.24	-	171,175,182,184	0
8	NAG	C	905	14/15	0.85	0.23	-	114,116,119,121	0
6	BMA	B	951	11/12	0.69	0.20	-	158,168,174,179	0
5	NAG	B	903	14/15	0.83	0.23	-	129,136,143,147	0
9	NAG	B	912	14/15	0.90	0.24	-	106,112,120,125	0
10	MAN	C	952	11/12	0.58	0.45	-	180,184,187,188	0
7	NAG	B	908	14/15	0.86	0.28	-	118,129,138,142	0

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	LLDF	B-factors(\AA^2)	Q<0.9
11	CL	C	908	1/1	0.98	0.28	2.68	55,55,55,55	0
4	NAG	B	901	14/15	0.73	0.56	-	146,149,153,156	0
4	NAG	B	902	14/15	0.84	0.36	-	124,132,140,143	0
4	NAG	C	901	14/15	0.70	0.55	-	180,182,186,188	0

6.5 Other polymers ⓘ

There are no such residues in this entry.