



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:18 AM UTC

PDB ID : 4NW2 / pdb_00004nw2
Title : Tandem chromodomains of human CHD1 in complex with Influenza virus NS1 C-terminal tail trimethylated at K229
Authors : Qin, S.; Tempel, W.; Xu, C.; El Bakkouri, M.; Bountra, C.; Arrowsmith, C.H.; Edwards, A.M.; Min, J.; Structural Genomics Consortium (SGC)
Deposited on : 2013-12-05
Resolution : 1.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The 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

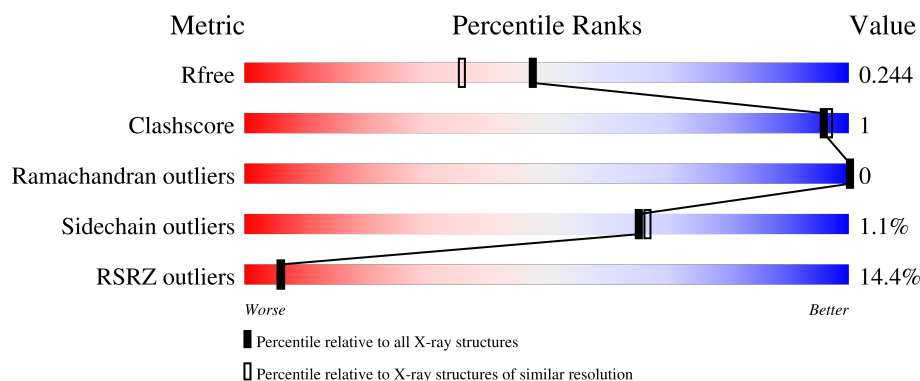
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	194	10% 87% 11%
1	C	194	10% 86% 11%
2	B	15	40% 80% 20%
2	D	15	47% 80% 7% 13%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3149 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 Chromodomain-helicase-DNA-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	173	Total	C	N	O	S	0	7	0
			1387	887	233	260	7			
1	C	173	Total	C	N	O	S	0	2	0
			1365	874	226	258	7			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	250	MET	-	expression tag	UNP O14646
A	251	HIS	-	expression tag	UNP O14646
A	252	HIS	-	expression tag	UNP O14646
A	253	HIS	-	expression tag	UNP O14646
A	254	HIS	-	expression tag	UNP O14646
A	255	HIS	-	expression tag	UNP O14646
A	256	HIS	-	expression tag	UNP O14646
A	257	SER	-	expression tag	UNP O14646
A	258	SER	-	expression tag	UNP O14646
A	259	GLY	-	expression tag	UNP O14646
A	260	ARG	-	expression tag	UNP O14646
A	261	GLU	-	expression tag	UNP O14646
A	262	ASN	-	expression tag	UNP O14646
A	263	LEU	-	expression tag	UNP O14646
A	264	TYR	-	expression tag	UNP O14646
A	265	PHE	-	expression tag	UNP O14646
A	266	GLN	-	expression tag	UNP O14646
A	267	GLY	-	expression tag	UNP O14646
C	250	MET	-	expression tag	UNP O14646
C	251	HIS	-	expression tag	UNP O14646
C	252	HIS	-	expression tag	UNP O14646
C	253	HIS	-	expression tag	UNP O14646
C	254	HIS	-	expression tag	UNP O14646
C	255	HIS	-	expression tag	UNP O14646
C	256	HIS	-	expression tag	UNP O14646

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Chain	Residue	Modelled	Actual	Comment	Reference
C	257	SER	-	expression tag	UNP O14646
C	258	SER	-	expression tag	UNP O14646
C	259	GLY	-	expression tag	UNP O14646
C	260	ARG	-	expression tag	UNP O14646
C	261	GLU	-	expression tag	UNP O14646
C	262	ASN	-	expression tag	UNP O14646
C	263	LEU	-	expression tag	UNP O14646
C	264	TYR	-	expression tag	UNP O14646
C	265	PHE	-	expression tag	UNP O14646
C	266	GLN	-	expression tag	UNP O14646
C	267	GLY	-	expression tag	UNP O14646

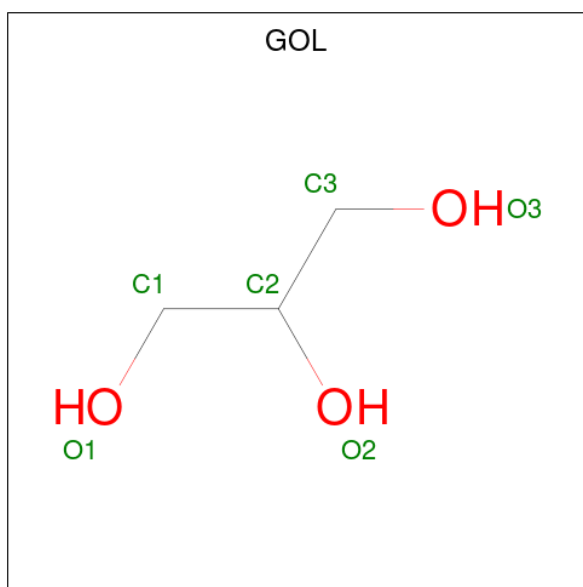
- Molecule 2 is a protein called Nonstructural protein 1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	12	Total	C	N	O	0	0	0
			92	56	22	14			
2	D	13	Total	C	N	O	0	1	0
			101	61	23	17			

- Molecule 3 is UNKNOWN ATOM OR ION (CCD ID: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	18	Total	X	0	0
			18	18		
3	C	12	Total	X	0	0
			12	12		
3	D	1	Total	X	0	0
			1	1		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

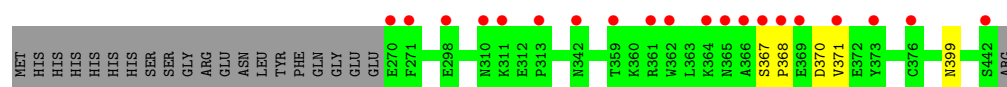
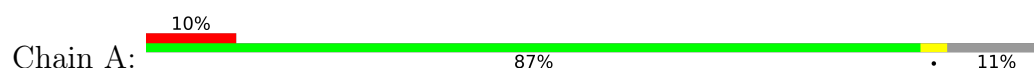
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	73	Total	O	0	0
			73	73		
5	B	4	Total	O	0	0
			4	4		
5	C	80	Total	O	0	0
			80	80		
5	D	4	Total	O	0	0
			4	4		

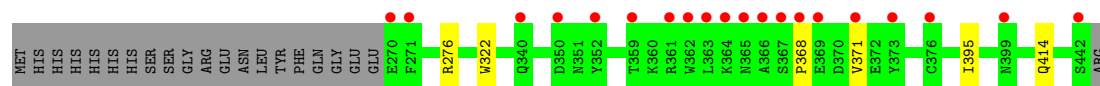
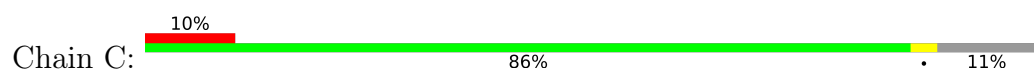
3 Residue-property plots [i](#)

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.

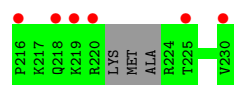
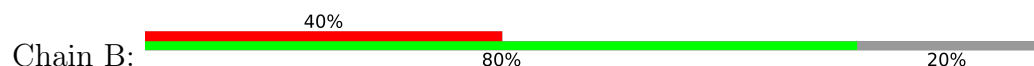
- Molecule 1: Chromodomain-helicase-DNA-binding protein 1



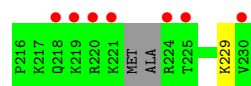
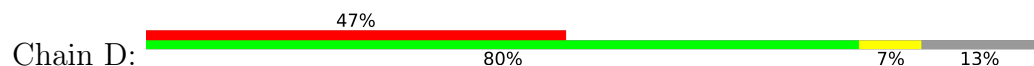
- Molecule 1: Chromodomain-helicase-DNA-binding protein 1



- Molecule 2: Nonstructural protein 1



- Molecule 2: Nonstructural protein 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	48.56Å 92.25Å 110.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.97 – 1.90 42.97 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.9 (42.97-1.90) 99.9 (42.97-1.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.32 (at 1.90Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.199 , 0.242 0.202 , 0.244	Depositor DCC
R_{free} test set	2444 reflections (2.98%)	wwPDB-VP
Wilson B-factor (Å ²)	29.1	Xtriage
Anisotropy	0.575	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 54.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3149	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 43.93 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.6425e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: M3L, UNX, GOL

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	0.41	0/1456	0.67	0/1974
1	C	0.44	0/1407	0.68	0/1910
2	B	0.29	0/79	0.58	0/101
2	D	0.28	0/90	0.57	0/115
All	All	0.42	0/3032	0.67	0/4100

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	1387	0	1251	4	0
1	C	1365	0	1229	4	0
2	B	92	0	93	0	0
2	D	101	0	103	1	0
3	A	18	0	0	0	0
3	C	12	0	0	0	0
3	D	1	0	0	0	0
4	B	6	0	8	0	0
4	C	6	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	73	0	0	0	0
5	B	4	0	0	0	0
5	C	80	0	0	0	0
5	D	4	0	0	0	0
All	All	3149	0	2692	6	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 1.

All (6) 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:370:ASP:HA	1:C:276:ARG:HH22	1.62	0.63
1:A:370:ASP:HA	1:C:276:ARG:NH2	2.27	0.48
1:C:368:PRO:HA	1:C:371[A]:VAL:HG22	1.97	0.46
1:C:322:TRP:CG	2:D:229:M3L:HM22	2.51	0.46
1:A:367:SER:O	1:A:370:ASP:N	2.44	0.45
1:A:368:PRO:HA	1:A:371:VAL:HB	2.04	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	178/194 (92%)	177 (99%)	1 (1%)	0	100	100
1	C	173/194 (89%)	173 (100%)	0	0	100	100
2	B	7/15 (47%)	7 (100%)	0	0	100	100
2	D	9/15 (60%)	8 (89%)	1 (11%)	0	100	100
All	All	367/418 (88%)	365 (100%)	2 (0%)	0	100	100

There are no Ramachandran outliers to report.

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	134/170 (79%)	133 (99%)	1 (1%)	76	78
1	C	128/170 (75%)	126 (98%)	2 (2%)	55	54
2	B	6/12 (50%)	6 (100%)	0	100	100
2	D	8/12 (67%)	8 (100%)	0	100	100
All	All	276/364 (76%)	273 (99%)	3 (1%)	65	67

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	399	ASN
1	C	395	ILE
1	C	414	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	434	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	M3L	B	229	2	10,11,12	0.51	0	9,14,16	0.55	0
2	M3L	D	229	2	10,11,12	0.51	0	9,14,16	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
2	M3L	B	229	2	-	5/9/10/12	-
2	M3L	D	229	2	-	1/9/10/12	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	229	M3L	CA-CB-CG-CD
2	B	229	M3L	CE-CD-CG-CB
2	B	229	M3L	CD-CE-NZ-CM1
2	B	229	M3L	CD-CE-NZ-CM3
2	B	229	M3L	CD-CE-NZ-CM2
2	D	229	M3L	CD-CE-NZ-CM2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	229	M3L	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 33 ligands modelled in this entry, 31 are unknown - leaving 2 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	GOL	C	513	-	5,5,5	0.28	0	5,5,5	0.72	0
4	GOL	B	301	-	5,5,5	0.38	0	5,5,5	0.65	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	GOL	C	513	-	-	0/4/4/4	-
4	GOL	B	301	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

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 ⓘ

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	173/194 (89%)	0.61	20 (11%) 9 10	18, 34, 78, 101	7 (4%)
1	C	173/194 (89%)	0.59	20 (11%) 9 10	20, 33, 77, 96	2 (1%)
2	B	11/15 (73%)	2.33	6 (54%) 0 0	42, 62, 81, 83	0
2	D	12/15 (80%)	2.35	7 (58%) 0 0	28, 63, 89, 97	1 (8%)
All	All	369/418 (88%)	0.71	53 (14%) 6 6	18, 34, 81, 101	10 (2%)

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	230	VAL	5.3
1	A	373	TYR	4.9
1	C	368	PRO	4.3
2	B	225	THR	4.2
1	C	371[A]	VAL	4.2
2	D	221	LYS	4.2
1	A	368	PRO	4.1
1	A	271[A]	PHE	4.1
1	C	369	GLU	4.1
2	D	219	LYS	4.0
1	A	366	ALA	3.8
1	A	270	GLU	3.8
1	C	361	ARG	3.7
1	C	271	PHE	3.7
1	C	367	SER	3.7
1	A	367	SER	3.6
1	C	364	LYS	3.6
2	D	225	THR	3.5
1	C	373	TYR	3.5
1	A	310	ASN	3.5
1	A	369	GLU	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	362	TRP	3.4
1	C	270	GLU	3.2
2	B	219	LYS	3.1
1	A	442	SER	3.1
1	A	371	VAL	3.0
1	A	364	LYS	3.0
1	C	365	ASN	2.9
1	C	363	LEU	2.9
2	D	230	VAL	2.9
1	C	362	TRP	2.9
1	A	365	ASN	2.8
2	B	218	GLN	2.8
2	B	220	ARG	2.8
1	A	313	PRO	2.8
1	C	442	SER	2.7
1	C	340	GLN	2.7
2	D	218	GLN	2.6
2	D	220	ARG	2.6
1	C	366	ALA	2.6
2	D	224	ARG	2.5
1	C	350	ASP	2.5
1	A	298	GLU	2.4
1	C	359	THR	2.3
1	A	342	ASN	2.3
1	C	376	CYS	2.3
1	C	399	ASN	2.2
1	A	359	THR	2.2
1	C	352	TYR	2.2
1	A	361	ARG	2.1
2	B	216	PRO	2.1
1	A	376	CYS	2.0
1	A	311	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
2	M3L	D	229	12/13	0.91	0.11	34,39,48,49	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	M3L	B	229	12/13	0.92	0.13	35,41,48,49	0

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
3	UNX	A	505	1/1	0.78	0.17	43,43,43,43	0
3	UNX	C	506	1/1	0.79	0.31	54,54,54,54	0
3	UNX	C	501	1/1	0.83	0.34	57,57,57,57	0
3	UNX	A	502	1/1	0.85	0.25	50,50,50,50	0
3	UNX	A	513	1/1	0.85	0.13	26,26,26,26	0
3	UNX	A	508	1/1	0.86	0.22	47,47,47,47	0
3	UNX	A	516	1/1	0.87	0.12	43,43,43,43	0
3	UNX	D	301	1/1	0.87	0.30	42,42,42,42	0
3	UNX	C	504	1/1	0.88	0.12	38,38,38,38	0
3	UNX	C	507	1/1	0.89	0.13	25,25,25,25	0
3	UNX	C	510	1/1	0.89	0.11	30,30,30,30	0
3	UNX	C	505	1/1	0.89	0.21	41,41,41,41	0
3	UNX	A	515	1/1	0.90	0.36	57,57,57,57	0
3	UNX	A	509	1/1	0.90	0.21	44,44,44,44	0
3	UNX	A	506	1/1	0.90	0.20	39,39,39,39	0
3	UNX	A	517	1/1	0.91	0.12	30,30,30,30	0
3	UNX	A	518	1/1	0.91	0.12	38,38,38,38	0
3	UNX	A	510	1/1	0.91	0.13	49,49,49,49	0
3	UNX	A	512	1/1	0.92	0.19	26,26,26,26	0
3	UNX	C	502	1/1	0.92	0.14	24,24,24,24	0
3	UNX	A	504	1/1	0.92	0.12	41,41,41,41	0
3	UNX	C	511	1/1	0.92	0.07	30,30,30,30	0
3	UNX	A	511	1/1	0.92	0.08	33,33,33,33	0
3	UNX	A	514	1/1	0.93	0.29	44,44,44,44	0
3	UNX	A	507	1/1	0.93	0.12	45,45,45,45	0
4	GOL	C	513	6/6	0.93	0.10	23,31,35,37	0
3	UNX	A	503	1/1	0.94	0.08	18,18,18,18	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	UNX	C	509	1/1	0.94	0.15	40,40,40,40	0
4	GOL	B	301	6/6	0.95	0.09	22,29,30,31	0
3	UNX	C	503	1/1	0.95	0.07	17,17,17,17	0
3	UNX	C	512	1/1	0.97	0.08	44,44,44,44	0
3	UNX	C	508	1/1	0.98	0.07	19,19,19,19	0
3	UNX	A	501	1/1	0.98	0.04	16,16,16,16	0

6.5 Other polymers [i](#)

There are no such residues in this entry.