



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 30, 2026 – 08:03 AM UTC

PDB ID : 6YFG / pdb_00006yfg
Title : Virus-like particle of Beihai levi-like virus 32
Authors : Rumnieks, J.; Kalnins, G.; Sisovs, M.; Lieknina, I.; Tars, K.
Deposited on : 2020-03-26
Resolution : 3.90 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

<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	:	FAILED
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

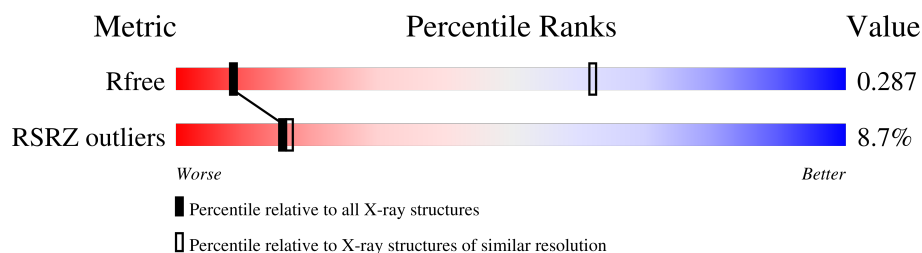
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.90 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	1270 (4.10-3.70)
RSRZ outliers	180081	1269 (4.10-3.70)

MolProbity failed to run properly - the sequence quality summary graphics cannot be shown.

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 363000 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 coat protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AA	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AB	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AC	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AD	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AE	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AF	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AG	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AH	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AI	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AJ	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AK	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AL	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AM	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AN	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AO	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AP	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AQ	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AR	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AS	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AT	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AU	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AV	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AW	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AX	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AY	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	AZ	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BA	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BB	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BC	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BD	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BE	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BF	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BG	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BH	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BI	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BJ	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BK	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	BL	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BM	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BN	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BO	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BP	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BQ	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BR	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BS	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BT	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BU	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BV	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BW	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BX	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BY	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	BZ	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CA	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CB	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CC	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CD	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CE	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CF	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	CG	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CH	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CI	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CJ	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CK	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CL	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CM	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CN	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CO	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CP	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CQ	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CR	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CS	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CT	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CU	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CV	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CW	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CX	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CY	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	CZ	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	DA	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	DB	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DC	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DD	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DE	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DF	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DG	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DH	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DI	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DJ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DK	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DL	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DM	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DN	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DO	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DP	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DQ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DR	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DS	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DT	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DU	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DV	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	DW	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DX	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DY	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	DZ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	EA	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	EB	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	EC	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	ED	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	EE	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	EF	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	EG	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	EH	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	EI	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	EJ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	EK	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	EL	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	EM	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	EN	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	EO	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	EP	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	EQ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	ER	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	ES	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	ET	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	EU	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	EV	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	EW	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	EX	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	EY	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	EZ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FA	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FB	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FC	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FD	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FE	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FF	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FG	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FH	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FI	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FJ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FK	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FL	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	FM	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FN	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FO	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FP	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FQ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FR	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FS	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FT	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FU	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FV	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FW	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FX	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FY	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	FZ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	GA	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	GB	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	GC	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	GD	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	GE	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	GF	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	GG	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	GH	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	GI	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	GJ	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	GK	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	GL	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	GM	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	GN	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	GO	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	GP	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	GQ	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	GR	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	GS	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	GT	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	GU	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	GV	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	GW	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	GX	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	GY	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	GZ	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	HA	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	HB	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	HC	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	HD	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	HE	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	HF	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	HG	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	HH	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	HI	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	HJ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	HK	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	HL	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	HM	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	HN	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	HO	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	HP	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	HQ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	HR	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	HS	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	HT	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	HU	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	HV	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	HW	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	HX	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	HY	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	HZ	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	IA	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	IB	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	IC	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	ID	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	IE	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	IF	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	IG	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	IH	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	II	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	IJ	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	IK	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	IL	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	IM	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	IN	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	IO	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	IP	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	IQ	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	IR	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	IS	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	IT	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	IU	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	IV	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	IW	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	IX	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	IY	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	IZ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JA	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JB	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JC	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JD	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JE	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JF	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JG	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JH	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JI	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JJ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JK	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JL	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JM	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	JN	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JO	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JP	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JQ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JR	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JS	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JT	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JU	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JV	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JW	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JX	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JY	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	JZ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KA	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KB	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KC	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KD	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KE	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KF	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KG	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KH	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	KI	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KJ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KK	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KL	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KM	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KN	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KO	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KP	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KQ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KR	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KS	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KT	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KU	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KV	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KW	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KX	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KY	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	KZ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	LA	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	LB	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	LC	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	LD	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	LE	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	LF	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	LG	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	LH	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	LI	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	LJ	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	LK	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	LL	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	LM	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	LN	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	LO	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	LP	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	LQ	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	LR	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	LS	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	LT	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	LU	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	LV	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	LW	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	LX	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	LY	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	LZ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MA	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MB	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MC	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MD	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	ME	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MF	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MG	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MH	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MI	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MJ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MK	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	ML	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MM	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MN	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MO	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MP	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MQ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MR	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MS	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	MT	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MU	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MV	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MW	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MX	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MY	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	MZ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	NA	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	NB	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	NC	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	ND	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	NE	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	NF	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	NG	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	NH	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	NI	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	NJ	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	NK	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	NL	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	NM	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0
1	NN	130	Total 1008	C 641	N 169	O 196	S 2	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	NO	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	NP	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	NQ	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	NR	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	NS	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	NT	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	NU	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			
1	NV	130	Total	C	N	O	S	0	0	0
			1008	641	169	196	2			

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	AB	1	Total	Ca	0	0
			1	1		
2	AH	1	Total	Ca	0	0
			1	1		
2	AJ	1	Total	Ca	0	0
			1	1		
2	AK	1	Total	Ca	0	0
			1	1		
2	AN	1	Total	Ca	0	0
			1	1		
2	AQ	1	Total	Ca	0	0
			1	1		
2	AT	1	Total	Ca	0	0
			1	1		
2	AW	1	Total	Ca	0	0
			1	1		
2	AZ	1	Total	Ca	0	0
			1	1		
2	BB	1	Total	Ca	0	0
			1	1		
2	BC	1	Total	Ca	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	BF	1	Total 1	Ca 1	0	0
2	BI	1	Total 1	Ca 1	0	0
2	BL	1	Total 1	Ca 1	0	0
2	BO	1	Total 1	Ca 1	0	0
2	BU	1	Total 1	Ca 1	0	0
2	BX	1	Total 1	Ca 1	0	0
2	CA	1	Total 1	Ca 1	0	0
2	CD	1	Total 1	Ca 1	0	0
2	CG	1	Total 1	Ca 1	0	0
2	CJ	1	Total 1	Ca 1	0	0
2	CM	1	Total 1	Ca 1	0	0
2	CO	1	Total 1	Ca 1	0	0
2	CP	1	Total 1	Ca 1	0	0
2	CS	1	Total 1	Ca 1	0	0
2	CV	1	Total 1	Ca 1	0	0
2	CY	1	Total 1	Ca 1	0	0
2	DB	1	Total 1	Ca 1	0	0
2	DE	1	Total 1	Ca 1	0	0
2	DH	1	Total 1	Ca 1	0	0
2	DQ	1	Total 1	Ca 1	0	0
2	DT	1	Total 1	Ca 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	DW	1	Total 1	Ca 1	0	0
2	DZ	1	Total 1	Ca 1	0	0
2	EB	1	Total 1	Ca 1	0	0
2	EC	1	Total 1	Ca 1	0	0
2	EF	1	Total 1	Ca 1	0	0
2	EI	1	Total 1	Ca 1	0	0
2	EL	1	Total 1	Ca 1	0	0
2	EO	1	Total 1	Ca 1	0	0
2	ER	1	Total 1	Ca 1	0	0
2	EU	1	Total 1	Ca 1	0	0
2	EX	1	Total 1	Ca 1	0	0
2	FA	1	Total 1	Ca 1	0	0
2	FD	1	Total 1	Ca 1	0	0
2	FG	1	Total 1	Ca 1	0	0
2	FJ	1	Total 1	Ca 1	0	0
2	FM	1	Total 1	Ca 1	0	0
2	FS	1	Total 1	Ca 1	0	0
2	FV	1	Total 1	Ca 1	0	0
2	FY	1	Total 1	Ca 1	0	0
2	GB	1	Total 1	Ca 1	0	0
2	GE	1	Total 1	Ca 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	GH	1	Total 1	Ca 1	0	0
2	GK	1	Total 1	Ca 1	0	0
2	GN	1	Total 1	Ca 1	0	0
2	GQ	1	Total 1	Ca 1	0	0
2	GS	1	Total 1	Ca 1	0	0
2	GT	1	Total 1	Ca 1	0	0
2	GW	1	Total 1	Ca 1	0	0
2	GZ	1	Total 1	Ca 1	0	0
2	HC	1	Total 1	Ca 1	0	0
2	HF	1	Total 1	Ca 1	0	0
2	HI	1	Total 1	Ca 1	0	0
2	HL	1	Total 1	Ca 1	0	0
2	HO	1	Total 1	Ca 1	0	0
2	HR	1	Total 1	Ca 1	0	0
2	HU	1	Total 1	Ca 1	0	0
2	HX	1	Total 1	Ca 1	0	0
2	IA	1	Total 1	Ca 1	0	0
2	ID	1	Total 1	Ca 1	0	0
2	IG	1	Total 1	Ca 1	0	0
2	IJ	1	Total 1	Ca 1	0	0
2	IM	1	Total 1	Ca 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	IS	1	Total 1	Ca 1	0	0
2	IV	1	Total 1	Ca 1	0	0
2	IY	1	Total 1	Ca 1	0	0
2	JB	1	Total 1	Ca 1	0	0
2	JD	1	Total 1	Ca 1	0	0
2	JE	1	Total 1	Ca 1	0	0
2	JH	1	Total 1	Ca 1	0	0
2	JN	1	Total 1	Ca 1	0	0
2	JQ	1	Total 1	Ca 1	0	0
2	JT	1	Total 1	Ca 1	0	0
2	JW	1	Total 1	Ca 1	0	0
2	JZ	1	Total 1	Ca 1	0	0
2	KC	1	Total 1	Ca 1	0	0
2	KF	1	Total 1	Ca 1	0	0
2	KI	1	Total 1	Ca 1	0	0
2	KL	1	Total 1	Ca 1	0	0
2	KO	1	Total 1	Ca 1	0	0
2	KR	1	Total 1	Ca 1	0	0
2	KU	1	Total 1	Ca 1	0	0
2	KX	1	Total 1	Ca 1	0	0
2	KZ	1	Total 1	Ca 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	LA	1	Total 1	Ca 1	0	0
2	LD	1	Total 1	Ca 1	0	0
2	LG	1	Total 1	Ca 1	0	0
2	LJ	1	Total 1	Ca 1	0	0
2	LM	1	Total 1	Ca 1	0	0
2	LP	1	Total 1	Ca 1	0	0
2	LS	1	Total 1	Ca 1	0	0
2	LV	1	Total 1	Ca 1	0	0
2	LY	1	Total 1	Ca 1	0	0
2	MB	1	Total 1	Ca 1	0	0
2	ME	1	Total 1	Ca 1	0	0
2	MH	1	Total 1	Ca 1	0	0
2	MK	1	Total 1	Ca 1	0	0
2	MN	1	Total 1	Ca 1	0	0
2	MQ	1	Total 1	Ca 1	0	0
2	MT	1	Total 1	Ca 1	0	0
2	MW	1	Total 1	Ca 1	0	0
2	MZ	1	Total 1	Ca 1	0	0
2	NC	1	Total 1	Ca 1	0	0
2	NF	1	Total 1	Ca 1	0	0
2	NI	1	Total 1	Ca 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	NL	1	Total 1	Ca 1	0	0
2	NO	1	Total 1	Ca 1	0	0
2	NR	1	Total 1	Ca 1	0	0
2	NU	1	Total 1	Ca 1	0	0

MolProbity failed to run properly - this section is therefore empty.

3 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	291.94Å 292.53Å 469.20Å 75.79° 77.92° 69.51°	Depositor
Resolution (Å)	49.83 – 3.90 49.83 – 3.90	Depositor EDS
% Data completeness (in resolution range)	95.4 (49.83-3.90) 96.2 (49.83-3.90)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.02 (at 3.88Å)	Xtriage
Refinement program	PHENIX 1.14 _3260	Depositor
R, R_{free}	0.282 , 0.285 0.283 , 0.287	Depositor DCC
R_{free} test set	20043 reflections (1.63%)	wwPDB-VP
Wilson B-factor (Å ²)	146.8	Xtriage
Anisotropy	0.146	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 145.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	0.087 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	363000	wwPDB-VP
Average B, all atoms (Å ²)	170.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.26% 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.

4 Model quality [i](#)

4.1 Standard geometry [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.2 Too-close contacts [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3 Torsion angles [i](#)

4.3.1 Protein backbone [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.2 Protein sidechains [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.3.3 RNA [i](#)

MolProbity failed to run properly - this section is therefore empty.

4.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

Of 120 ligands modelled in this entry, 120 are monoatomic - leaving 0 for Mogul analysis.

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.

4.7 Other polymers [i](#)

There are no such residues in this entry.

4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

5 Fit of model and data ⓘ

5.1 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	AA	130/130 (100%)	0.56	10 (7%) 19 18	111, 164, 226, 246	0
1	AB	130/130 (100%)	0.44	7 (5%) 31 25	110, 166, 236, 289	0
1	AC	130/130 (100%)	0.63	8 (6%) 26 23	110, 168, 223, 278	0
1	AD	130/130 (100%)	0.57	9 (6%) 23 20	111, 164, 226, 246	0
1	AE	130/130 (100%)	0.84	15 (11%) 9 12	110, 166, 236, 289	0
1	AF	130/130 (100%)	0.64	14 (10%) 11 14	110, 168, 223, 278	0
1	AG	130/130 (100%)	0.70	9 (6%) 23 20	111, 164, 226, 246	0
1	AH	130/130 (100%)	0.73	14 (10%) 11 14	110, 166, 236, 289	0
1	AI	130/130 (100%)	0.61	14 (10%) 11 14	110, 168, 223, 278	0
1	AJ	130/130 (100%)	0.54	10 (7%) 19 18	111, 164, 226, 246	0
1	AK	130/130 (100%)	0.71	10 (7%) 19 18	110, 166, 236, 289	0
1	AL	130/130 (100%)	0.68	9 (6%) 23 20	110, 168, 223, 278	0
1	AM	130/130 (100%)	0.62	14 (10%) 11 14	111, 164, 226, 246	0
1	AN	130/130 (100%)	0.70	9 (6%) 23 20	110, 166, 236, 289	0
1	AO	130/130 (100%)	0.52	9 (6%) 23 20	110, 168, 223, 278	0
1	AP	130/130 (100%)	0.42	4 (3%) 51 36	111, 164, 226, 246	0
1	AQ	130/130 (100%)	0.42	7 (5%) 31 25	110, 166, 236, 289	0
1	AR	130/130 (100%)	0.61	13 (10%) 12 15	110, 168, 223, 278	0
1	AS	130/130 (100%)	0.57	13 (10%) 12 15	111, 164, 226, 246	0
1	AT	130/130 (100%)	0.61	10 (7%) 19 18	110, 166, 236, 289	0
1	AU	130/130 (100%)	0.83	18 (13%) 6 10	110, 168, 223, 278	0
1	AV	130/130 (100%)	0.58	10 (7%) 19 18	111, 164, 226, 246	0
1	AW	130/130 (100%)	0.75	8 (6%) 26 23	110, 166, 236, 289	0
1	AX	130/130 (100%)	0.70	15 (11%) 9 12	110, 168, 223, 278	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	AY	130/130 (100%)	0.73	12 (9%) 14 16	111, 164, 226, 246	0
1	AZ	130/130 (100%)	0.78	14 (10%) 11 14	110, 166, 236, 289	0
1	BA	130/130 (100%)	0.75	15 (11%) 9 12	110, 168, 223, 278	0
1	BB	130/130 (100%)	0.60	7 (5%) 31 25	111, 164, 226, 246	0
1	BC	130/130 (100%)	0.74	12 (9%) 14 16	110, 166, 236, 289	0
1	BD	130/130 (100%)	0.55	10 (7%) 19 18	110, 168, 223, 278	0
1	BE	130/130 (100%)	0.65	13 (10%) 12 15	111, 164, 226, 246	0
1	BF	130/130 (100%)	0.63	13 (10%) 12 15	110, 166, 236, 289	0
1	BG	130/130 (100%)	0.63	8 (6%) 26 23	110, 168, 223, 278	0
1	BH	130/130 (100%)	0.34	7 (5%) 31 25	111, 164, 226, 246	0
1	BI	130/130 (100%)	0.69	14 (10%) 11 14	110, 166, 236, 289	0
1	BJ	130/130 (100%)	0.63	12 (9%) 14 16	110, 168, 223, 278	0
1	BK	130/130 (100%)	0.45	7 (5%) 31 25	111, 164, 226, 246	0
1	BL	130/130 (100%)	0.65	15 (11%) 9 12	110, 166, 236, 289	0
1	BM	130/130 (100%)	0.70	13 (10%) 12 15	110, 168, 223, 278	0
1	BN	130/130 (100%)	0.57	13 (10%) 12 15	111, 164, 226, 246	0
1	BO	130/130 (100%)	0.57	8 (6%) 26 23	110, 166, 236, 289	0
1	BP	130/130 (100%)	0.48	8 (6%) 26 23	110, 168, 223, 278	0
1	BQ	130/130 (100%)	0.43	9 (6%) 23 20	111, 164, 226, 246	0
1	BR	130/130 (100%)	0.77	14 (10%) 11 14	110, 166, 236, 289	0
1	BS	130/130 (100%)	0.64	8 (6%) 26 23	110, 168, 223, 278	0
1	BT	130/130 (100%)	0.57	14 (10%) 11 14	111, 164, 226, 246	0
1	BU	130/130 (100%)	0.59	9 (6%) 23 20	110, 166, 236, 289	0
1	BV	130/130 (100%)	0.66	9 (6%) 23 20	110, 168, 223, 278	0
1	BW	130/130 (100%)	0.56	8 (6%) 26 23	111, 164, 226, 246	0
1	BX	130/130 (100%)	0.57	10 (7%) 19 18	110, 166, 236, 289	0
1	BY	130/130 (100%)	0.56	9 (6%) 23 20	110, 168, 223, 278	0
1	BZ	130/130 (100%)	0.65	12 (9%) 14 16	111, 164, 226, 246	0
1	CA	130/130 (100%)	0.53	6 (4%) 37 28	110, 166, 236, 289	0
1	CB	130/130 (100%)	0.69	15 (11%) 9 12	110, 168, 223, 278	0
1	CC	130/130 (100%)	0.82	18 (13%) 6 10	111, 164, 226, 246	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	CD	130/130 (100%)	0.61	10 (7%) 19 18	110, 166, 236, 289	0
1	CE	130/130 (100%)	0.61	9 (6%) 23 20	110, 168, 223, 278	0
1	CF	130/130 (100%)	0.57	7 (5%) 31 25	111, 164, 226, 246	0
1	CG	130/130 (100%)	0.56	13 (10%) 12 15	110, 166, 236, 289	0
1	CH	130/130 (100%)	0.80	19 (14%) 6 9	110, 168, 223, 278	0
1	CI	130/130 (100%)	0.55	10 (7%) 19 18	111, 164, 226, 246	0
1	CJ	130/130 (100%)	0.78	11 (8%) 16 17	110, 166, 236, 289	0
1	CK	130/130 (100%)	0.65	13 (10%) 12 15	110, 168, 223, 278	0
1	CL	130/130 (100%)	0.56	9 (6%) 23 20	111, 164, 226, 246	0
1	CM	130/130 (100%)	0.65	12 (9%) 14 16	110, 166, 236, 289	0
1	CN	130/130 (100%)	0.73	9 (6%) 23 20	110, 168, 223, 278	0
1	CO	130/130 (100%)	0.43	3 (2%) 61 43	111, 164, 226, 246	0
1	CP	130/130 (100%)	0.72	15 (11%) 9 12	110, 166, 236, 289	0
1	CQ	130/130 (100%)	0.57	8 (6%) 26 23	110, 168, 223, 278	0
1	CR	130/130 (100%)	0.83	14 (10%) 11 14	111, 164, 226, 246	0
1	CS	130/130 (100%)	0.70	12 (9%) 14 16	110, 166, 236, 289	0
1	CT	130/130 (100%)	0.61	8 (6%) 26 23	110, 168, 223, 278	0
1	CU	130/130 (100%)	0.61	13 (10%) 12 15	111, 164, 226, 246	0
1	CV	130/130 (100%)	0.63	12 (9%) 14 16	110, 166, 236, 289	0
1	CW	130/130 (100%)	0.65	11 (8%) 16 17	110, 168, 223, 278	0
1	CX	130/130 (100%)	0.57	9 (6%) 23 20	111, 164, 226, 246	0
1	CY	130/130 (100%)	0.69	13 (10%) 12 15	110, 166, 236, 289	0
1	CZ	130/130 (100%)	0.58	8 (6%) 26 23	110, 168, 223, 278	0
1	DA	130/130 (100%)	0.60	15 (11%) 9 12	111, 164, 226, 246	0
1	DB	130/130 (100%)	0.56	9 (6%) 23 20	110, 166, 236, 289	0
1	DC	130/130 (100%)	0.67	16 (12%) 8 11	110, 168, 223, 278	0
1	DD	130/130 (100%)	0.62	10 (7%) 19 18	111, 164, 226, 246	0
1	DE	130/130 (100%)	0.62	10 (7%) 19 18	110, 166, 236, 289	0
1	DF	130/130 (100%)	0.61	13 (10%) 12 15	110, 168, 223, 278	0
1	DG	130/130 (100%)	0.47	8 (6%) 26 23	111, 164, 226, 246	0
1	DH	130/130 (100%)	0.73	11 (8%) 16 17	110, 166, 236, 289	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	DI	130/130 (100%)	0.63	9 (6%)	23	20	110, 168, 223, 278	0
1	DJ	130/130 (100%)	0.60	13 (10%)	12	15	111, 164, 226, 246	0
1	DK	130/130 (100%)	0.65	13 (10%)	12	15	110, 166, 236, 289	0
1	DL	130/130 (100%)	0.56	11 (8%)	16	17	110, 168, 223, 278	0
1	DM	130/130 (100%)	0.59	10 (7%)	19	18	111, 164, 226, 246	0
1	DN	130/130 (100%)	0.61	10 (7%)	19	18	110, 166, 236, 289	0
1	DO	130/130 (100%)	0.66	10 (7%)	19	18	110, 168, 223, 278	0
1	DP	130/130 (100%)	0.49	10 (7%)	19	18	111, 164, 226, 246	0
1	DQ	130/130 (100%)	0.58	11 (8%)	16	17	110, 166, 236, 289	0
1	DR	130/130 (100%)	0.50	9 (6%)	23	20	110, 168, 223, 278	0
1	DS	130/130 (100%)	0.74	16 (12%)	8	11	111, 164, 226, 246	0
1	DT	130/130 (100%)	0.83	18 (13%)	6	10	110, 166, 236, 289	0
1	DU	130/130 (100%)	0.60	10 (7%)	19	18	110, 168, 223, 278	0
1	DV	130/130 (100%)	0.66	14 (10%)	11	14	111, 164, 226, 246	0
1	DW	130/130 (100%)	0.61	14 (10%)	11	14	110, 166, 236, 289	0
1	DX	130/130 (100%)	0.67	8 (6%)	26	23	110, 168, 223, 278	0
1	DY	130/130 (100%)	0.42	7 (5%)	31	25	111, 164, 226, 246	0
1	DZ	130/130 (100%)	0.62	13 (10%)	12	15	110, 166, 236, 289	0
1	EA	130/130 (100%)	0.73	15 (11%)	9	12	110, 168, 223, 278	0
1	EB	130/130 (100%)	0.54	12 (9%)	14	16	111, 164, 226, 246	0
1	EC	130/130 (100%)	0.68	11 (8%)	16	17	110, 166, 236, 289	0
1	ED	130/130 (100%)	0.67	14 (10%)	11	14	110, 168, 223, 278	0
1	EE	130/130 (100%)	0.69	12 (9%)	14	16	111, 164, 226, 246	0
1	EF	130/130 (100%)	0.73	13 (10%)	12	15	110, 166, 236, 289	0
1	EG	130/130 (100%)	0.54	10 (7%)	19	18	110, 168, 223, 278	0
1	EH	130/130 (100%)	0.56	11 (8%)	16	17	111, 164, 226, 246	0
1	EI	130/130 (100%)	0.70	15 (11%)	9	12	110, 166, 236, 289	0
1	EJ	130/130 (100%)	0.64	13 (10%)	12	15	110, 168, 223, 278	0
1	EK	130/130 (100%)	0.69	10 (7%)	19	18	111, 164, 226, 246	0
1	EL	130/130 (100%)	0.41	8 (6%)	26	23	110, 166, 236, 289	0
1	EM	130/130 (100%)	0.76	11 (8%)	16	17	110, 168, 223, 278	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	EN	130/130 (100%)	0.58	8 (6%) 26 23	111, 164, 226, 246	0
1	EO	130/130 (100%)	0.65	13 (10%) 12 15	110, 166, 236, 289	0
1	EP	130/130 (100%)	0.70	13 (10%) 12 15	110, 168, 223, 278	0
1	EQ	130/130 (100%)	0.64	11 (8%) 16 17	111, 164, 226, 246	0
1	ER	130/130 (100%)	0.59	11 (8%) 16 17	110, 166, 236, 289	0
1	ES	130/130 (100%)	0.68	13 (10%) 12 15	110, 168, 223, 278	0
1	ET	130/130 (100%)	0.60	11 (8%) 16 17	111, 164, 226, 246	0
1	EU	130/130 (100%)	0.60	9 (6%) 23 20	110, 166, 236, 289	0
1	EV	130/130 (100%)	0.51	9 (6%) 23 20	110, 168, 223, 278	0
1	EW	130/130 (100%)	0.56	7 (5%) 31 25	111, 164, 226, 246	0
1	EX	130/130 (100%)	0.77	15 (11%) 9 12	110, 166, 236, 289	0
1	EY	130/130 (100%)	0.63	7 (5%) 31 25	110, 168, 223, 278	0
1	EZ	130/130 (100%)	0.59	10 (7%) 19 18	111, 164, 226, 246	0
1	FA	130/130 (100%)	0.65	12 (9%) 14 16	110, 166, 236, 289	0
1	FB	130/130 (100%)	0.58	11 (8%) 16 17	110, 168, 223, 278	0
1	FC	130/130 (100%)	0.62	11 (8%) 16 17	111, 164, 226, 246	0
1	FD	130/130 (100%)	0.53	10 (7%) 19 18	110, 166, 236, 289	0
1	FE	130/130 (100%)	0.54	9 (6%) 23 20	110, 168, 223, 278	0
1	FF	130/130 (100%)	0.69	10 (7%) 19 18	111, 164, 226, 246	0
1	FG	130/130 (100%)	0.50	7 (5%) 31 25	110, 166, 236, 289	0
1	FH	130/130 (100%)	0.53	9 (6%) 23 20	110, 168, 223, 278	0
1	FI	130/130 (100%)	0.76	12 (9%) 14 16	111, 164, 226, 246	0
1	FJ	130/130 (100%)	0.56	6 (4%) 37 28	110, 166, 236, 289	0
1	FK	130/130 (100%)	0.72	11 (8%) 16 17	110, 168, 223, 278	0
1	FL	130/130 (100%)	0.61	11 (8%) 16 17	111, 164, 226, 246	0
1	FM	130/130 (100%)	0.65	7 (5%) 31 25	110, 166, 236, 289	0
1	FN	130/130 (100%)	0.73	15 (11%) 9 12	110, 168, 223, 278	0
1	FO	130/130 (100%)	0.69	12 (9%) 14 16	111, 164, 226, 246	0
1	FP	130/130 (100%)	0.59	9 (6%) 23 20	110, 166, 236, 289	0
1	FQ	130/130 (100%)	0.82	20 (15%) 5 8	110, 168, 223, 278	0
1	FR	130/130 (100%)	0.60	9 (6%) 23 20	111, 164, 226, 246	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	FS	130/130 (100%)	0.62	14 (10%) 11 14	110, 166, 236, 289	0
1	FT	130/130 (100%)	0.85	12 (9%) 14 16	110, 168, 223, 278	0
1	FU	130/130 (100%)	0.74	12 (9%) 14 16	111, 164, 226, 246	0
1	FV	130/130 (100%)	0.59	11 (8%) 16 17	110, 166, 236, 289	0
1	FW	130/130 (100%)	0.52	9 (6%) 23 20	110, 168, 223, 278	0
1	FX	130/130 (100%)	0.60	8 (6%) 26 23	111, 164, 226, 246	0
1	FY	130/130 (100%)	0.59	11 (8%) 16 17	110, 166, 236, 289	0
1	FZ	130/130 (100%)	0.64	12 (9%) 14 16	110, 168, 223, 278	0
1	GA	130/130 (100%)	0.71	13 (10%) 12 15	111, 164, 226, 246	0
1	GB	130/130 (100%)	0.54	8 (6%) 26 23	110, 166, 236, 289	0
1	GC	130/130 (100%)	0.70	15 (11%) 9 12	110, 168, 223, 278	0
1	GD	130/130 (100%)	0.69	14 (10%) 11 14	111, 164, 226, 246	0
1	GE	130/130 (100%)	0.50	6 (4%) 37 28	110, 166, 236, 289	0
1	GF	130/130 (100%)	0.65	12 (9%) 14 16	110, 168, 223, 278	0
1	GG	130/130 (100%)	0.54	10 (7%) 19 18	111, 164, 226, 246	0
1	GH	130/130 (100%)	0.64	12 (9%) 14 16	110, 166, 236, 289	0
1	GI	130/130 (100%)	0.75	13 (10%) 12 15	110, 168, 223, 278	0
1	GJ	130/130 (100%)	0.58	9 (6%) 23 20	111, 164, 226, 246	0
1	GK	130/130 (100%)	0.67	12 (9%) 14 16	110, 166, 236, 289	0
1	GL	130/130 (100%)	0.53	11 (8%) 16 17	110, 168, 223, 278	0
1	GM	130/130 (100%)	0.82	17 (13%) 7 10	111, 164, 226, 246	0
1	GN	130/130 (100%)	0.73	13 (10%) 12 15	110, 166, 236, 289	0
1	GO	130/130 (100%)	0.80	15 (11%) 9 12	110, 168, 223, 278	0
1	GP	130/130 (100%)	0.65	13 (10%) 12 15	111, 164, 226, 246	0
1	GQ	130/130 (100%)	0.52	8 (6%) 26 23	110, 166, 236, 289	0
1	GR	130/130 (100%)	0.66	13 (10%) 12 15	110, 168, 223, 278	0
1	GS	130/130 (100%)	0.67	14 (10%) 11 14	111, 164, 226, 246	0
1	GT	130/130 (100%)	0.63	14 (10%) 11 14	110, 166, 236, 289	0
1	GU	130/130 (100%)	0.59	13 (10%) 12 15	110, 168, 223, 278	0
1	GV	130/130 (100%)	0.53	7 (5%) 31 25	111, 164, 226, 246	0
1	GW	130/130 (100%)	0.55	9 (6%) 23 20	110, 166, 236, 289	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	GX	130/130 (100%)	0.65	14 (10%) 11 14	110, 168, 223, 278	0
1	GY	130/130 (100%)	0.60	11 (8%) 16 17	111, 164, 226, 246	0
1	GZ	130/130 (100%)	0.63	8 (6%) 26 23	110, 166, 236, 289	0
1	HA	130/130 (100%)	0.73	14 (10%) 11 14	110, 168, 223, 278	0
1	HB	130/130 (100%)	0.42	8 (6%) 26 23	111, 164, 226, 246	0
1	HC	130/130 (100%)	0.59	9 (6%) 23 20	110, 166, 236, 289	0
1	HD	130/130 (100%)	0.61	8 (6%) 26 23	110, 168, 223, 278	0
1	HE	130/130 (100%)	0.63	13 (10%) 12 15	111, 164, 226, 246	0
1	HF	130/130 (100%)	0.63	10 (7%) 19 18	110, 166, 236, 289	0
1	HG	130/130 (100%)	0.50	6 (4%) 37 28	110, 168, 223, 278	0
1	HH	130/130 (100%)	0.50	8 (6%) 26 23	111, 164, 226, 246	0
1	HI	130/130 (100%)	0.55	4 (3%) 51 36	110, 166, 236, 289	0
1	HJ	130/130 (100%)	0.60	10 (7%) 19 18	110, 168, 223, 278	0
1	HK	130/130 (100%)	0.45	5 (3%) 44 32	111, 164, 226, 246	0
1	HL	130/130 (100%)	0.63	6 (4%) 37 28	110, 166, 236, 289	0
1	HM	130/130 (100%)	0.49	6 (4%) 37 28	110, 168, 223, 278	0
1	HN	130/130 (100%)	0.72	13 (10%) 12 15	111, 164, 226, 246	0
1	HO	130/130 (100%)	0.37	7 (5%) 31 25	110, 166, 236, 289	0
1	HP	130/130 (100%)	0.53	8 (6%) 26 23	110, 168, 223, 278	0
1	HQ	130/130 (100%)	0.64	9 (6%) 23 20	111, 164, 226, 246	0
1	HR	130/130 (100%)	0.73	15 (11%) 9 12	110, 166, 236, 289	0
1	HS	130/130 (100%)	0.68	11 (8%) 16 17	110, 168, 223, 278	0
1	HT	130/130 (100%)	0.58	5 (3%) 44 32	111, 164, 226, 246	0
1	HU	130/130 (100%)	0.54	6 (4%) 37 28	110, 166, 236, 289	0
1	HV	130/130 (100%)	0.64	10 (7%) 19 18	110, 168, 223, 278	0
1	HW	130/130 (100%)	0.60	8 (6%) 26 23	111, 164, 226, 246	0
1	HX	130/130 (100%)	0.67	11 (8%) 16 17	110, 166, 236, 289	0
1	HY	130/130 (100%)	0.64	11 (8%) 16 17	110, 168, 223, 278	0
1	HZ	130/130 (100%)	0.50	8 (6%) 26 23	111, 164, 226, 246	0
1	IA	130/130 (100%)	0.36	7 (5%) 31 25	110, 166, 236, 289	0
1	IB	130/130 (100%)	0.69	13 (10%) 12 15	110, 168, 223, 278	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	IC	130/130 (100%)	0.72	14 (10%) 11 14	111, 164, 226, 246	0
1	ID	130/130 (100%)	0.56	11 (8%) 16 17	110, 166, 236, 289	0
1	IE	130/130 (100%)	0.57	10 (7%) 19 18	110, 168, 223, 278	0
1	IF	130/130 (100%)	0.50	7 (5%) 31 25	111, 164, 226, 246	0
1	IG	130/130 (100%)	0.65	13 (10%) 12 15	110, 166, 236, 289	0
1	IH	130/130 (100%)	0.70	13 (10%) 12 15	110, 168, 223, 278	0
1	II	130/130 (100%)	0.96	22 (16%) 4 7	111, 164, 226, 246	0
1	IJ	130/130 (100%)	0.63	7 (5%) 31 25	110, 166, 236, 289	0
1	IK	130/130 (100%)	0.81	16 (12%) 8 11	110, 168, 223, 278	0
1	IL	130/130 (100%)	0.63	11 (8%) 16 17	111, 164, 226, 246	0
1	IM	130/130 (100%)	0.73	13 (10%) 12 15	110, 166, 236, 289	0
1	IN	130/130 (100%)	0.60	10 (7%) 19 18	110, 168, 223, 278	0
1	IO	130/130 (100%)	0.53	8 (6%) 26 23	111, 164, 226, 246	0
1	IP	130/130 (100%)	0.74	15 (11%) 9 12	110, 166, 236, 289	0
1	IQ	130/130 (100%)	0.61	13 (10%) 12 15	110, 168, 223, 278	0
1	IR	130/130 (100%)	0.61	13 (10%) 12 15	111, 164, 226, 246	0
1	IS	130/130 (100%)	0.70	9 (6%) 23 20	110, 166, 236, 289	0
1	IT	130/130 (100%)	0.57	10 (7%) 19 18	110, 168, 223, 278	0
1	IU	130/130 (100%)	0.71	14 (10%) 11 14	111, 164, 226, 246	0
1	IV	130/130 (100%)	0.64	8 (6%) 26 23	110, 166, 236, 289	0
1	IW	130/130 (100%)	0.56	11 (8%) 16 17	110, 168, 223, 278	0
1	IX	130/130 (100%)	0.47	6 (4%) 37 28	111, 164, 226, 246	0
1	IY	130/130 (100%)	0.55	11 (8%) 16 17	110, 166, 236, 289	0
1	IZ	130/130 (100%)	0.75	7 (5%) 31 25	110, 168, 223, 278	0
1	JA	130/130 (100%)	0.62	10 (7%) 19 18	111, 164, 226, 246	0
1	JB	130/130 (100%)	0.79	14 (10%) 11 14	110, 166, 236, 289	0
1	JC	130/130 (100%)	0.72	18 (13%) 6 10	110, 168, 223, 278	0
1	JD	130/130 (100%)	0.67	14 (10%) 11 14	111, 164, 226, 246	0
1	JE	130/130 (100%)	0.70	15 (11%) 9 12	110, 166, 236, 289	0
1	JF	130/130 (100%)	0.76	14 (10%) 11 14	110, 168, 223, 278	0
1	JG	130/130 (100%)	0.61	12 (9%) 14 16	111, 164, 226, 246	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	JH	130/130 (100%)	0.53	9 (6%) 23 20	110, 166, 236, 289	0
1	JI	130/130 (100%)	0.63	11 (8%) 16 17	110, 168, 223, 278	0
1	JJ	130/130 (100%)	0.69	13 (10%) 12 15	111, 164, 226, 246	0
1	JK	130/130 (100%)	0.83	17 (13%) 7 10	110, 166, 236, 289	0
1	JL	130/130 (100%)	0.73	17 (13%) 7 10	110, 168, 223, 278	0
1	JM	130/130 (100%)	0.48	6 (4%) 37 28	111, 164, 226, 246	0
1	JN	130/130 (100%)	0.73	14 (10%) 11 14	110, 166, 236, 289	0
1	JO	130/130 (100%)	0.50	5 (3%) 44 32	110, 168, 223, 278	0
1	JP	130/130 (100%)	0.69	10 (7%) 19 18	111, 164, 226, 246	0
1	JQ	130/130 (100%)	0.70	12 (9%) 14 16	110, 166, 236, 289	0
1	JR	130/130 (100%)	0.54	10 (7%) 19 18	110, 168, 223, 278	0
1	JS	130/130 (100%)	0.87	16 (12%) 8 11	111, 164, 226, 246	0
1	JT	130/130 (100%)	0.73	15 (11%) 9 12	110, 166, 236, 289	0
1	JU	130/130 (100%)	0.79	12 (9%) 14 16	110, 168, 223, 278	0
1	JV	130/130 (100%)	0.63	14 (10%) 11 14	111, 164, 226, 246	0
1	JW	130/130 (100%)	0.76	17 (13%) 7 10	110, 166, 236, 289	0
1	JX	130/130 (100%)	0.78	16 (12%) 8 11	110, 168, 223, 278	0
1	JY	130/130 (100%)	0.58	11 (8%) 16 17	111, 164, 226, 246	0
1	JZ	130/130 (100%)	0.69	14 (10%) 11 14	110, 166, 236, 289	0
1	KA	130/130 (100%)	0.71	11 (8%) 16 17	110, 168, 223, 278	0
1	KB	130/130 (100%)	0.52	10 (7%) 19 18	111, 164, 226, 246	0
1	KC	130/130 (100%)	0.65	10 (7%) 19 18	110, 166, 236, 289	0
1	KD	130/130 (100%)	0.58	11 (8%) 16 17	110, 168, 223, 278	0
1	KE	130/130 (100%)	0.54	7 (5%) 31 25	111, 164, 226, 246	0
1	KF	130/130 (100%)	0.72	13 (10%) 12 15	110, 166, 236, 289	0
1	KG	130/130 (100%)	0.69	12 (9%) 14 16	110, 168, 223, 278	0
1	KH	130/130 (100%)	0.63	10 (7%) 19 18	111, 164, 226, 246	0
1	KI	130/130 (100%)	0.53	11 (8%) 16 17	110, 166, 236, 289	0
1	KJ	130/130 (100%)	0.64	12 (9%) 14 16	110, 168, 223, 278	0
1	KK	130/130 (100%)	0.57	4 (3%) 51 36	111, 164, 226, 246	0
1	KL	130/130 (100%)	0.85	17 (13%) 7 10	110, 166, 236, 289	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	KM	130/130 (100%)	0.83	15 (11%) 9 12	110, 168, 223, 278	0
1	KN	130/130 (100%)	0.45	7 (5%) 31 25	111, 164, 226, 246	0
1	KO	130/130 (100%)	0.67	16 (12%) 8 11	110, 166, 236, 289	0
1	KP	130/130 (100%)	0.65	11 (8%) 16 17	110, 168, 223, 278	0
1	KQ	130/130 (100%)	0.61	10 (7%) 19 18	111, 164, 226, 246	0
1	KR	130/130 (100%)	0.69	13 (10%) 12 15	110, 166, 236, 289	0
1	KS	130/130 (100%)	0.56	10 (7%) 19 18	110, 168, 223, 278	0
1	KT	130/130 (100%)	0.56	10 (7%) 19 18	111, 164, 226, 246	0
1	KU	130/130 (100%)	0.72	15 (11%) 9 12	110, 166, 236, 289	0
1	KV	130/130 (100%)	0.74	13 (10%) 12 15	110, 168, 223, 278	0
1	KW	130/130 (100%)	0.56	10 (7%) 19 18	111, 164, 226, 246	0
1	KX	130/130 (100%)	0.67	15 (11%) 9 12	110, 166, 236, 289	0
1	KY	130/130 (100%)	0.59	16 (12%) 8 11	110, 168, 223, 278	0
1	KZ	130/130 (100%)	0.62	8 (6%) 26 23	111, 164, 226, 246	0
1	LA	130/130 (100%)	0.43	5 (3%) 44 32	110, 166, 236, 289	0
1	LB	130/130 (100%)	0.64	11 (8%) 16 17	110, 168, 223, 278	0
1	LC	130/130 (100%)	0.68	8 (6%) 26 23	111, 164, 226, 246	0
1	LD	130/130 (100%)	0.78	16 (12%) 8 11	110, 166, 236, 289	0
1	LE	130/130 (100%)	0.80	15 (11%) 9 12	110, 168, 223, 278	0
1	LF	130/130 (100%)	0.71	15 (11%) 9 12	111, 164, 226, 246	0
1	LG	130/130 (100%)	0.82	14 (10%) 11 14	110, 166, 236, 289	0
1	LH	130/130 (100%)	0.94	23 (17%) 4 6	110, 168, 223, 278	0
1	LI	130/130 (100%)	0.66	14 (10%) 11 14	111, 164, 226, 246	0
1	LJ	130/130 (100%)	0.83	13 (10%) 12 15	110, 166, 236, 289	0
1	LK	130/130 (100%)	1.06	29 (22%) 2 4	110, 168, 223, 278	0
1	LL	130/130 (100%)	0.78	16 (12%) 8 11	111, 164, 226, 246	0
1	LM	130/130 (100%)	0.78	16 (12%) 8 11	110, 166, 236, 289	0
1	LN	130/130 (100%)	0.54	8 (6%) 26 23	110, 168, 223, 278	0
1	LO	130/130 (100%)	0.66	13 (10%) 12 15	111, 164, 226, 246	0
1	LP	130/130 (100%)	0.57	12 (9%) 14 16	110, 166, 236, 289	0
1	LQ	130/130 (100%)	0.64	14 (10%) 11 14	110, 168, 223, 278	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	LR	130/130 (100%)	0.69	16 (12%) 8 11	111, 164, 226, 246	0
1	LS	130/130 (100%)	0.53	10 (7%) 19 18	110, 166, 236, 289	0
1	LT	130/130 (100%)	0.73	12 (9%) 14 16	110, 168, 223, 278	0
1	LU	130/130 (100%)	0.65	9 (6%) 23 20	111, 164, 226, 246	0
1	LV	130/130 (100%)	0.73	13 (10%) 12 15	110, 166, 236, 289	0
1	LW	130/130 (100%)	0.64	12 (9%) 14 16	110, 168, 223, 278	0
1	LX	130/130 (100%)	0.65	13 (10%) 12 15	111, 164, 226, 246	0
1	LY	130/130 (100%)	0.61	8 (6%) 26 23	110, 166, 236, 289	0
1	LZ	130/130 (100%)	0.68	14 (10%) 11 14	110, 168, 223, 278	0
1	MA	130/130 (100%)	0.86	18 (13%) 6 10	111, 164, 226, 246	0
1	MB	130/130 (100%)	0.52	9 (6%) 23 20	110, 166, 236, 289	0
1	MC	130/130 (100%)	0.60	9 (6%) 23 20	110, 168, 223, 278	0
1	MD	130/130 (100%)	0.52	6 (4%) 37 28	111, 164, 226, 246	0
1	ME	130/130 (100%)	0.60	11 (8%) 16 17	110, 166, 236, 289	0
1	MF	130/130 (100%)	0.67	16 (12%) 8 11	110, 168, 223, 278	0
1	MG	130/130 (100%)	0.53	10 (7%) 19 18	111, 164, 226, 246	0
1	MH	130/130 (100%)	0.60	7 (5%) 31 25	110, 166, 236, 289	0
1	MI	130/130 (100%)	0.76	12 (9%) 14 16	110, 168, 223, 278	0
1	MJ	130/130 (100%)	0.41	9 (6%) 23 20	111, 164, 226, 246	0
1	MK	130/130 (100%)	0.59	10 (7%) 19 18	110, 166, 236, 289	0
1	ML	130/130 (100%)	0.61	10 (7%) 19 18	110, 168, 223, 278	0
1	MM	130/130 (100%)	0.54	13 (10%) 12 15	111, 164, 226, 246	0
1	MN	130/130 (100%)	0.71	10 (7%) 19 18	110, 166, 236, 289	0
1	MO	130/130 (100%)	0.68	12 (9%) 14 16	110, 168, 223, 278	0
1	MP	130/130 (100%)	0.46	9 (6%) 23 20	111, 164, 226, 246	0
1	MQ	130/130 (100%)	0.43	6 (4%) 37 28	110, 166, 236, 289	0
1	MR	130/130 (100%)	0.91	18 (13%) 6 10	110, 168, 223, 278	0
1	MS	130/130 (100%)	0.67	10 (7%) 19 18	111, 164, 226, 246	0
1	MT	130/130 (100%)	0.50	8 (6%) 26 23	110, 166, 236, 289	0
1	MU	130/130 (100%)	0.56	9 (6%) 23 20	110, 168, 223, 278	0
1	MV	130/130 (100%)	0.56	13 (10%) 12 15	111, 164, 226, 246	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	MW	130/130 (100%)	0.70	10 (7%) 19 18	110, 166, 236, 289	0
1	MX	130/130 (100%)	0.59	8 (6%) 26 23	110, 168, 223, 278	0
1	MY	130/130 (100%)	0.44	7 (5%) 31 25	111, 164, 226, 246	0
1	MZ	130/130 (100%)	0.55	11 (8%) 16 17	110, 166, 236, 289	0
1	NA	130/130 (100%)	0.65	10 (7%) 19 18	110, 168, 223, 278	0
1	NB	130/130 (100%)	0.48	5 (3%) 44 32	111, 164, 226, 246	0
1	NC	130/130 (100%)	0.81	15 (11%) 9 12	110, 166, 236, 289	0
1	ND	130/130 (100%)	0.79	14 (10%) 11 14	110, 168, 223, 278	0
1	NE	130/130 (100%)	0.79	14 (10%) 11 14	111, 164, 226, 246	0
1	NF	130/130 (100%)	0.58	7 (5%) 31 25	110, 166, 236, 289	0
1	NG	130/130 (100%)	0.83	19 (14%) 6 9	110, 168, 223, 278	0
1	NH	130/130 (100%)	0.81	20 (15%) 5 8	111, 164, 226, 246	0
1	NI	130/130 (100%)	0.64	8 (6%) 26 23	110, 166, 236, 289	0
1	NJ	130/130 (100%)	0.76	12 (9%) 14 16	110, 168, 223, 278	0
1	NK	130/130 (100%)	0.69	13 (10%) 12 15	111, 164, 226, 246	0
1	NL	130/130 (100%)	0.81	15 (11%) 9 12	110, 166, 236, 289	0
1	NM	130/130 (100%)	0.77	14 (10%) 11 14	110, 168, 223, 278	0
1	NN	130/130 (100%)	0.58	8 (6%) 26 23	111, 164, 226, 246	0
1	NO	130/130 (100%)	0.71	15 (11%) 9 12	110, 166, 236, 289	0
1	NP	130/130 (100%)	0.52	10 (7%) 19 18	110, 168, 223, 278	0
1	NQ	130/130 (100%)	0.73	15 (11%) 9 12	111, 164, 226, 246	0
1	NR	130/130 (100%)	0.71	13 (10%) 12 15	110, 166, 236, 289	0
1	NS	130/130 (100%)	0.81	12 (9%) 14 16	110, 168, 223, 278	0
1	NT	130/130 (100%)	0.69	10 (7%) 19 18	111, 164, 226, 246	0
1	NU	130/130 (100%)	0.74	15 (11%) 9 12	110, 166, 236, 289	0
1	NV	130/130 (100%)	0.63	9 (6%) 23 20	110, 168, 223, 278	0
All	All	46800/46800 (100%)	0.64	4070 (8%) 16 17	110, 166, 232, 289	0

The worst 5 of 4070 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	HQ	116	TYR	10.4
1	CB	43	LYS	9.0

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Mol	Chain	Res	Type	RSRZ
1	MS	44	GLY	7.9
1	MA	5	ALA	7.5
1	IQ	43	LYS	7.4

5.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	CA	FV	201	1/1	0.90	0.10	148,148,148,148	0
2	CA	NO	201	1/1	0.90	0.12	148,148,148,148	0
2	CA	IA	201	1/1	0.91	0.09	148,148,148,148	0
2	CA	FM	201	1/1	0.91	0.09	148,148,148,148	0
2	CA	BF	201	1/1	0.92	0.09	148,148,148,148	0
2	CA	HR	201	1/1	0.92	0.15	148,148,148,148	0
2	CA	NU	201	1/1	0.92	0.10	148,148,148,148	0
2	CA	EO	201	1/1	0.93	0.14	148,148,148,148	0
2	CA	FA	201	1/1	0.93	0.12	148,148,148,148	0
2	CA	DH	201	1/1	0.93	0.15	148,148,148,148	0
2	CA	EC	201	1/1	0.93	0.06	148,148,148,148	0
2	CA	EB	201	1/1	0.94	0.07	148,148,148,148	0
2	CA	HI	201	1/1	0.94	0.06	148,148,148,148	0
2	CA	CG	201	1/1	0.94	0.09	148,148,148,148	0
2	CA	CY	201	1/1	0.94	0.06	148,148,148,148	0
2	CA	LA	201	1/1	0.94	0.07	148,148,148,148	0
2	CA	LJ	201	1/1	0.94	0.07	148,148,148,148	0
2	CA	LV	201	1/1	0.94	0.08	148,148,148,148	0
2	CA	NF	201	1/1	0.94	0.13	148,148,148,148	0
2	CA	AZ	201	1/1	0.94	0.12	148,148,148,148	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CA	DT	201	1/1	0.94	0.08	148,148,148,148	0
2	CA	BL	201	1/1	0.95	0.06	148,148,148,148	0
2	CA	FJ	201	1/1	0.95	0.06	148,148,148,148	0
2	CA	ID	201	1/1	0.95	0.10	148,148,148,148	0
2	CA	IV	201	1/1	0.95	0.05	148,148,148,148	0
2	CA	CD	201	1/1	0.95	0.07	148,148,148,148	0
2	CA	EI	201	1/1	0.95	0.07	148,148,148,148	0
2	CA	LP	201	1/1	0.95	0.07	148,148,148,148	0
2	CA	FY	201	1/1	0.95	0.06	148,148,148,148	0
2	CA	GQ	201	1/1	0.95	0.06	148,148,148,148	0
2	CA	GW	201	1/1	0.95	0.07	148,148,148,148	0
2	CA	AW	201	1/1	0.95	0.14	148,148,148,148	0
2	CA	GB	201	1/1	0.96	0.10	148,148,148,148	0
2	CA	IJ	201	1/1	0.96	0.08	148,148,148,148	0
2	CA	AJ	201	1/1	0.96	0.08	148,148,148,148	0
2	CA	JB	201	1/1	0.96	0.09	148,148,148,148	0
2	CA	JN	201	1/1	0.96	0.07	148,148,148,148	0
2	CA	JQ	201	1/1	0.96	0.07	148,148,148,148	0
2	CA	KR	201	1/1	0.96	0.06	148,148,148,148	0
2	CA	KZ	201	1/1	0.96	0.08	148,148,148,148	0
2	CA	CM	201	1/1	0.96	0.12	148,148,148,148	0
2	CA	GZ	201	1/1	0.96	0.17	148,148,148,148	0
2	CA	HC	201	1/1	0.96	0.17	148,148,148,148	0
2	CA	EL	201	1/1	0.96	0.09	148,148,148,148	0
2	CA	ME	201	1/1	0.96	0.11	148,148,148,148	0
2	CA	MQ	201	1/1	0.96	0.05	148,148,148,148	0
2	CA	HL	201	1/1	0.96	0.07	148,148,148,148	0
2	CA	AH	201	1/1	0.96	0.11	148,148,148,148	0
2	CA	EX	201	1/1	0.96	0.09	148,148,148,148	0
2	CA	EF	201	1/1	0.97	0.10	148,148,148,148	0
2	CA	CS	201	1/1	0.97	0.09	148,148,148,148	0
2	CA	GH	201	1/1	0.97	0.06	148,148,148,148	0
2	CA	JH	201	1/1	0.97	0.05	148,148,148,148	0
2	CA	GK	201	1/1	0.97	0.11	148,148,148,148	0
2	CA	CA	201	1/1	0.97	0.06	148,148,148,148	0
2	CA	JW	201	1/1	0.97	0.04	148,148,148,148	0
2	CA	JZ	201	1/1	0.97	0.13	148,148,148,148	0
2	CA	KF	201	1/1	0.97	0.07	148,148,148,148	0
2	CA	KO	201	1/1	0.97	0.04	148,148,148,148	0
2	CA	GT	201	1/1	0.97	0.12	148,148,148,148	0
2	CA	KU	201	1/1	0.97	0.09	148,148,148,148	0
2	CA	BI	201	1/1	0.97	0.12	148,148,148,148	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CA	ER	201	1/1	0.97	0.14	148,148,148,148	0
2	CA	DQ	201	1/1	0.97	0.09	148,148,148,148	0
2	CA	BB	201	1/1	0.97	0.20	148,148,148,148	0
2	CA	LS	201	1/1	0.97	0.07	148,148,148,148	0
2	CA	DW	201	1/1	0.97	0.09	148,148,148,148	0
2	CA	LY	201	1/1	0.97	0.14	148,148,148,148	0
2	CA	BX	201	1/1	0.97	0.12	148,148,148,148	0
2	CA	MH	201	1/1	0.97	0.09	148,148,148,148	0
2	CA	MK	201	1/1	0.97	0.11	148,148,148,148	0
2	CA	HX	201	1/1	0.97	0.06	148,148,148,148	0
2	CA	FS	201	1/1	0.97	0.06	148,148,148,148	0
2	CA	NL	201	1/1	0.97	0.06	148,148,148,148	0
2	CA	CP	201	1/1	0.97	0.08	148,148,148,148	0
2	CA	NR	201	1/1	0.97	0.13	148,148,148,148	0
2	CA	IG	201	1/1	0.97	0.09	148,148,148,148	0
2	CA	KX	201	1/1	0.98	0.05	148,148,148,148	0
2	CA	IM	201	1/1	0.98	0.15	148,148,148,148	0
2	CA	IS	201	1/1	0.98	0.07	148,148,148,148	0
2	CA	LD	201	1/1	0.98	0.09	148,148,148,148	0
2	CA	LG	201	1/1	0.98	0.11	148,148,148,148	0
2	CA	FD	201	1/1	0.98	0.08	148,148,148,148	0
2	CA	LM	201	1/1	0.98	0.08	148,148,148,148	0
2	CA	IY	201	1/1	0.98	0.04	148,148,148,148	0
2	CA	GE	201	1/1	0.98	0.13	148,148,148,148	0
2	CA	JE	201	1/1	0.98	0.06	148,148,148,148	0
2	CA	FG	201	1/1	0.98	0.06	148,148,148,148	0
2	CA	HO	201	1/1	0.98	0.05	148,148,148,148	0
2	CA	DE	201	1/1	0.98	0.11	148,148,148,148	0
2	CA	HU	201	1/1	0.98	0.09	148,148,148,148	0
2	CA	MN	201	1/1	0.98	0.05	148,148,148,148	0
2	CA	BC	201	1/1	0.98	0.06	148,148,148,148	0
2	CA	MW	201	1/1	0.98	0.11	148,148,148,148	0
2	CA	MZ	201	1/1	0.98	0.07	148,148,148,148	0
2	CA	KC	201	1/1	0.98	0.04	148,148,148,148	0
2	CA	NI	201	1/1	0.98	0.04	148,148,148,148	0
2	CA	GS	201	1/1	0.98	0.10	148,148,148,148	0
2	CA	EU	201	1/1	0.98	0.07	148,148,148,148	0
2	CA	DZ	201	1/1	0.98	0.09	148,148,148,148	0
2	CA	AQ	201	1/1	0.98	0.11	148,148,148,148	0
2	CA	AN	201	1/1	0.99	0.10	148,148,148,148	0
2	CA	AB	201	1/1	0.99	0.10	148,148,148,148	0
2	CA	CJ	201	1/1	0.99	0.10	148,148,148,148	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CA	MB	201	1/1	0.99	0.07	148,148,148,148	0
2	CA	KI	201	1/1	0.99	0.03	148,148,148,148	0
2	CA	KL	201	1/1	0.99	0.13	148,148,148,148	0
2	CA	HF	201	1/1	0.99	0.11	148,148,148,148	0
2	CA	BO	201	1/1	0.99	0.10	148,148,148,148	0
2	CA	CO	201	1/1	0.99	0.13	148,148,148,148	0
2	CA	MT	201	1/1	0.99	0.08	148,148,148,148	0
2	CA	BU	201	1/1	0.99	0.07	148,148,148,148	0
2	CA	JD	201	1/1	0.99	0.15	148,148,148,148	0
2	CA	NC	201	1/1	0.99	0.04	148,148,148,148	0
2	CA	AT	201	1/1	0.99	0.05	148,148,148,148	0
2	CA	GN	201	1/1	0.99	0.16	148,148,148,148	0
2	CA	CV	201	1/1	0.99	0.04	148,148,148,148	0
2	CA	AK	201	1/1	0.99	0.04	148,148,148,148	0
2	CA	JT	201	1/1	0.99	0.07	148,148,148,148	0
2	CA	DB	201	1/1	0.99	0.05	148,148,148,148	0

5.5 Other polymers [i](#)

There are no such residues in this entry.