



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 06:47 PM UTC

PDB ID : 4V5I / pdb_00004v5i
Title : Structure of the Phage P2 Baseplate in its Activated Conformation with Ca
Authors : Sciara, G.; Bebeacua, C.; Bron, P.; Tremblay, D.; Ortiz-Lombardia, M.;
Lichiere, J.; van Heel, M.; Campanacci, V.; Moineau, S.; Cambillau, C.
Deposited on : 2010-02-05
Resolution : 5.46 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	:	4-5-2 with Phenix2.0
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

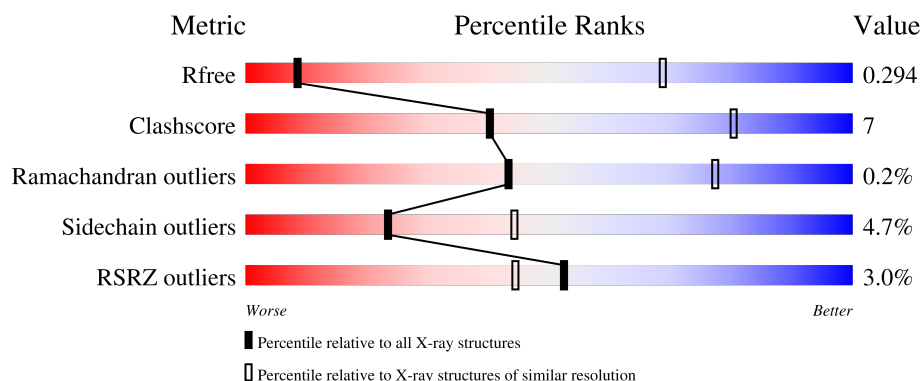
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 5.46 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	1066 (6.92-4.00)
Clashscore	190562	1123 (6.92-4.00)
Ramachandran outliers	187476	1026 (6.92-3.96)
Sidechain outliers	187428	1000 (6.92-3.96)
RSRZ outliers	180081	1059 (6.92-4.00)

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	A0	372	3% 83% 15% .
1	AY	372	3% 84% 14% ..
1	AZ	372	5% 80% 18% .
1	B0	372	2% 84% 14% .
1	BY	372	2% 84% 14% ..

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Mol	Chain	Length	Quality of chain
1	BZ	372	
2	AA	263	
2	AB	263	
2	AC	263	
2	AD	263	
2	AE	263	
2	AF	263	
2	AG	263	
2	AH	263	
2	AI	263	
2	AJ	263	
2	AK	263	
2	AL	263	
2	AM	263	
2	AN	263	
2	AO	263	
2	AP	263	
2	AQ	263	
2	AR	263	
2	BA	263	
2	BB	263	
2	BC	263	
2	BD	263	
2	BE	263	
2	BF	263	

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Mol	Chain	Length	Quality of chain
2	BG	263	
2	BH	263	
2	BI	263	
2	BJ	263	
2	BK	263	
2	BL	263	
2	BM	263	
2	BN	263	
2	BO	263	
2	BP	263	
2	BQ	263	
2	BR	263	
3	AS	298	
3	AT	298	
3	AU	298	
3	AV	298	
3	AW	298	
3	AX	298	
3	BS	298	
3	BT	298	
3	BU	298	
3	BV	298	
3	BW	298	
3	BX	298	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 119484 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 ORF16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A0	372	Total	C	N	O	S	0	0	0
			3000	1918	493	581	8			
1	AY	372	Total	C	N	O	S	0	0	0
			3000	1918	493	581	8			
1	AZ	372	Total	C	N	O	S	0	0	0
			3000	1918	493	581	8			
1	B0	372	Total	C	N	O	S	0	0	0
			3000	1918	493	581	8			
1	BY	372	Total	C	N	O	S	0	0	0
			3000	1918	493	581	8			
1	BZ	372	Total	C	N	O	S	0	0	0
			3000	1918	493	581	8			

- Molecule 2 is a protein called PUTATIVE RECEPTOR BINDING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AA	263	Total	C	N	O	S	0	0	0
			2008	1260	346	396	6			
2	AB	263	Total	C	N	O	S	0	0	0
			2008	1260	346	396	6			
2	AC	263	Total	C	N	O	S	0	0	0
			2008	1260	346	396	6			
2	AD	263	Total	C	N	O	S	0	0	0
			2008	1260	346	396	6			
2	AE	263	Total	C	N	O	S	0	0	0
			2008	1260	346	396	6			
2	AF	263	Total	C	N	O	S	0	0	0
			2008	1260	346	396	6			
2	AG	263	Total	C	N	O	S	0	0	0
			2008	1260	346	396	6			
2	AH	263	Total	C	N	O	S	0	0	0
			2008	1260	346	396	6			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	AI	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	AJ	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	AK	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	AL	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	AM	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	AN	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	AO	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	AP	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	AQ	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	AR	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	BA	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	BB	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	BC	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	BD	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	BE	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	BF	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	BG	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	BH	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	BI	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	BJ	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	BK	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	BL	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	BM	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	BN	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	BO	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	BP	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	BQ	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0
2	BR	263	Total 2008	C 1260	N 346	O 396	S 6	0	0	0

- Molecule 3 is a protein called ORF15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	AS	298	Total 2432	C 1565	N 392	O 469	S 6	0	0	0
3	AT	298	Total 2432	C 1565	N 392	O 469	S 6	0	0	0
3	AU	298	Total 2432	C 1565	N 392	O 469	S 6	0	0	0
3	AV	298	Total 2432	C 1565	N 392	O 469	S 6	0	0	0
3	AW	298	Total 2432	C 1565	N 392	O 469	S 6	0	0	0
3	AX	298	Total 2432	C 1565	N 392	O 469	S 6	0	0	0
3	BS	298	Total 2432	C 1565	N 392	O 469	S 6	0	0	0
3	BT	298	Total 2432	C 1565	N 392	O 469	S 6	0	0	0
3	BU	298	Total 2432	C 1565	N 392	O 469	S 6	0	0	0
3	BV	298	Total 2432	C 1565	N 392	O 469	S 6	0	0	0
3	BW	298	Total 2432	C 1565	N 392	O 469	S 6	0	0	0
3	BX	298	Total 2432	C 1565	N 392	O 469	S 6	0	0	0

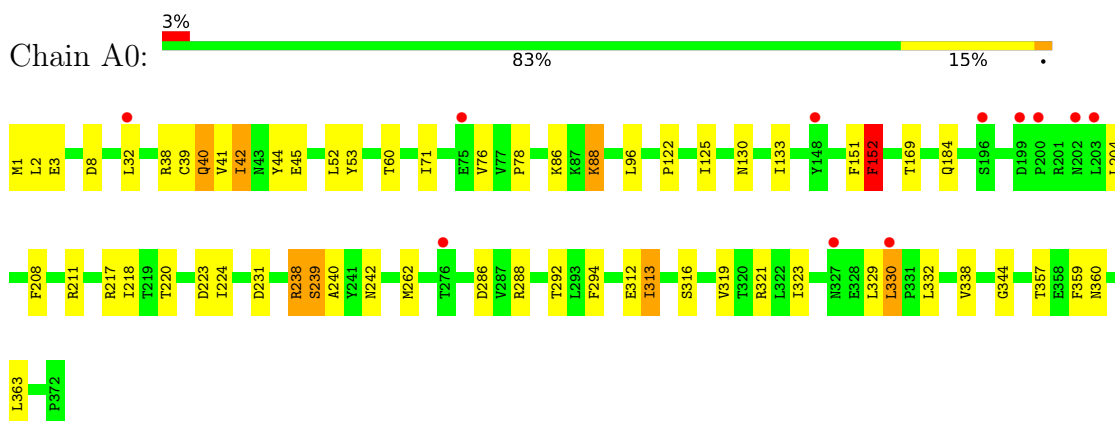
- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	AS	1	Total 1	Ca 1	0	0
4	AT	1	Total 1	Ca 1	0	0
4	AU	1	Total 1	Ca 1	0	0
4	AV	1	Total 1	Ca 1	0	0
4	AW	1	Total 1	Ca 1	0	0
4	AX	1	Total 1	Ca 1	0	0
4	BS	1	Total 1	Ca 1	0	0
4	BT	1	Total 1	Ca 1	0	0
4	BU	1	Total 1	Ca 1	0	0
4	BV	1	Total 1	Ca 1	0	0
4	BW	1	Total 1	Ca 1	0	0
4	BX	1	Total 1	Ca 1	0	0

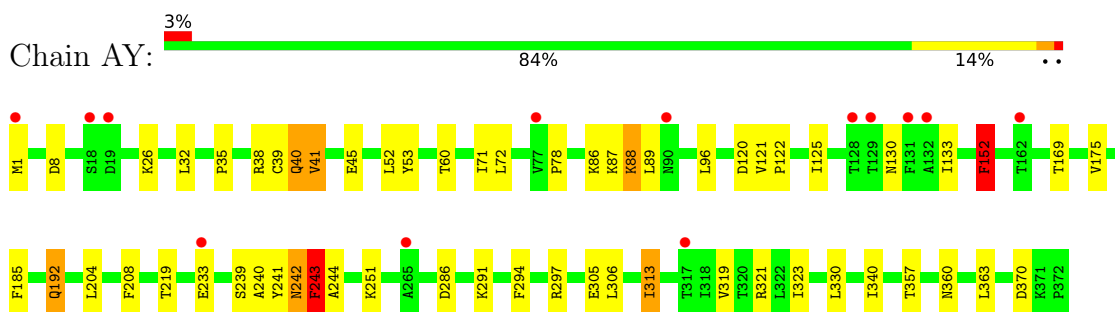
3 Residue-property plots [i](#)

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.

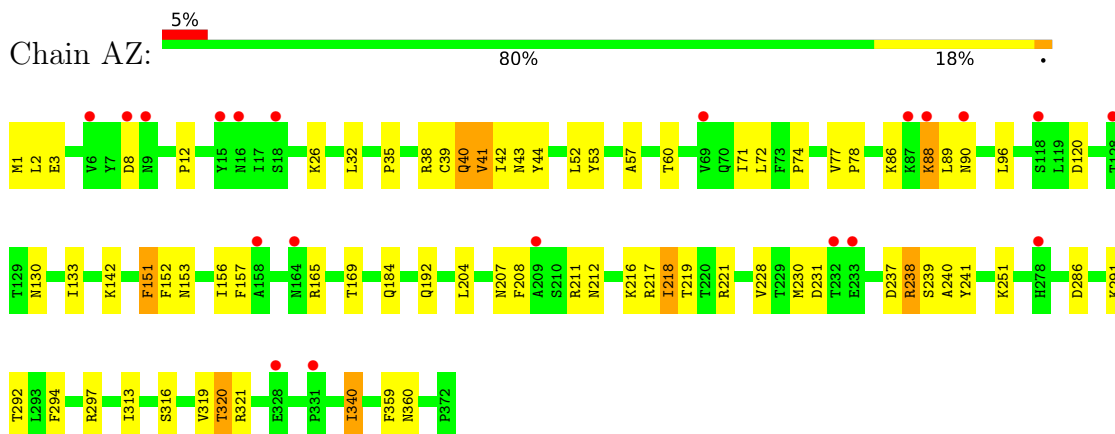
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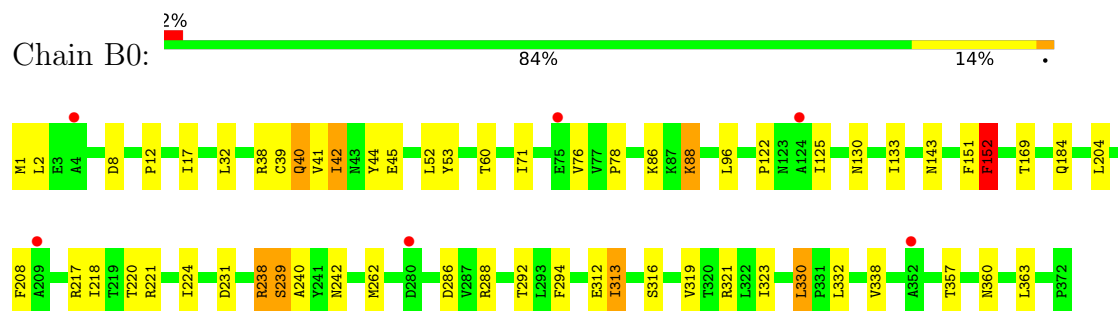
- Molecule 1: ORF16



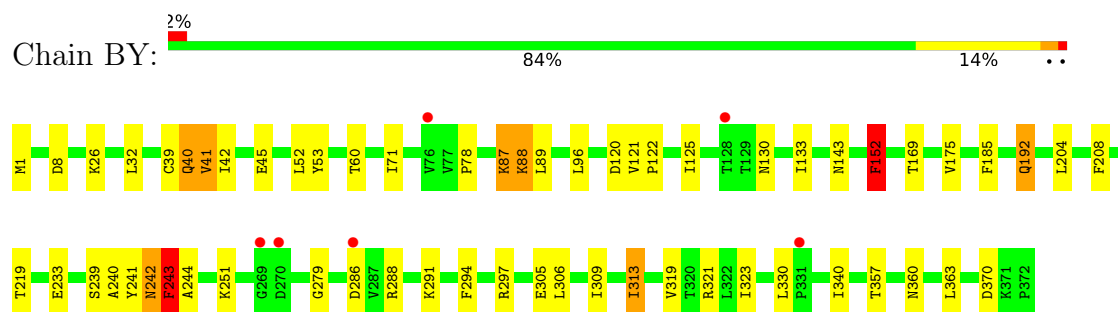
- Molecule 1: ORF16



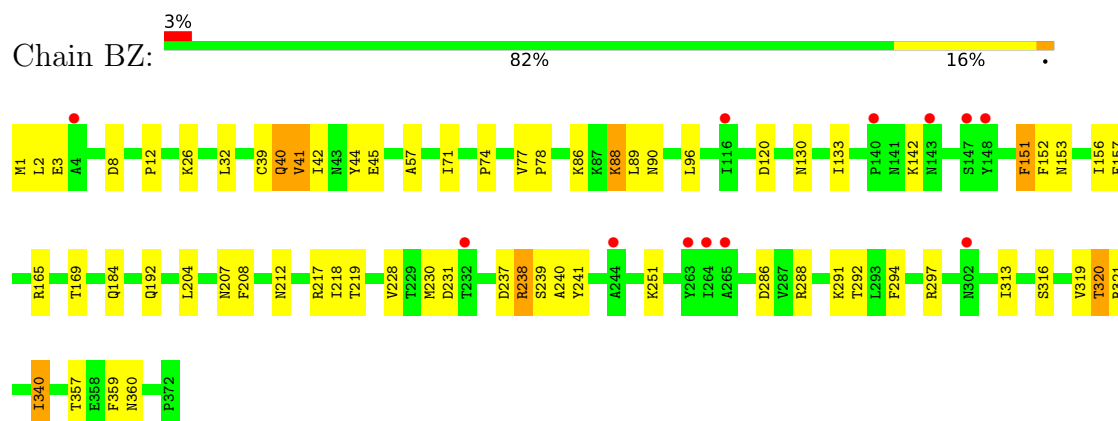
● Molecule 1: ORF16



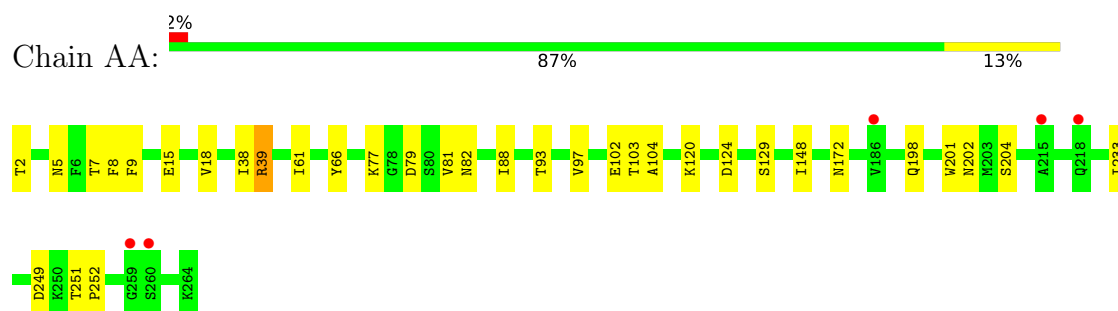
● Molecule 1: ORF16



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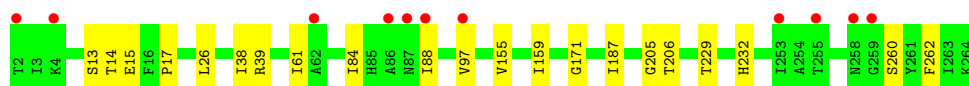


● Molecule 2: PUTATIVE RECEPTOR BINDING PROTEIN

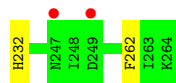
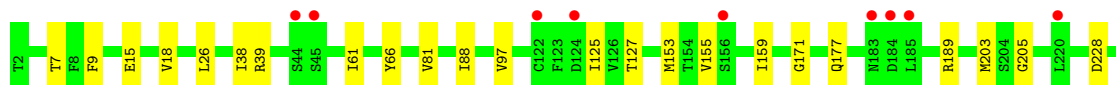


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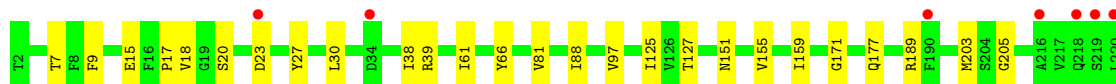
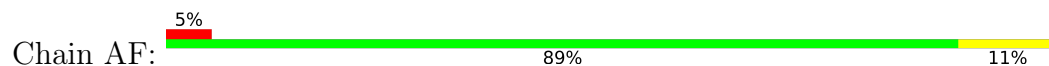
● Molecule 2: PUTATIVE RECEPTOR BINDING PROTEIN



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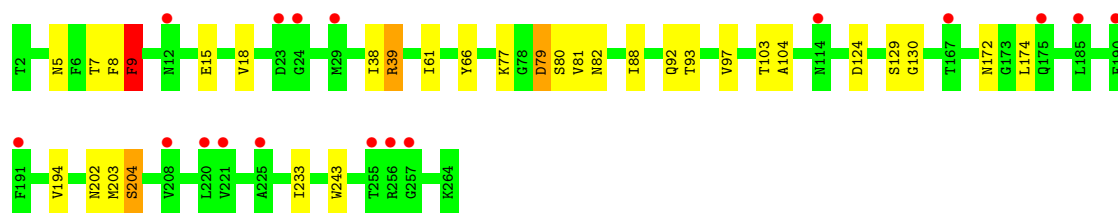


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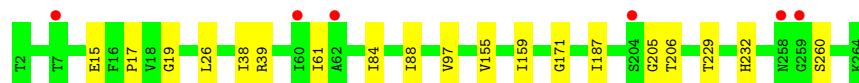


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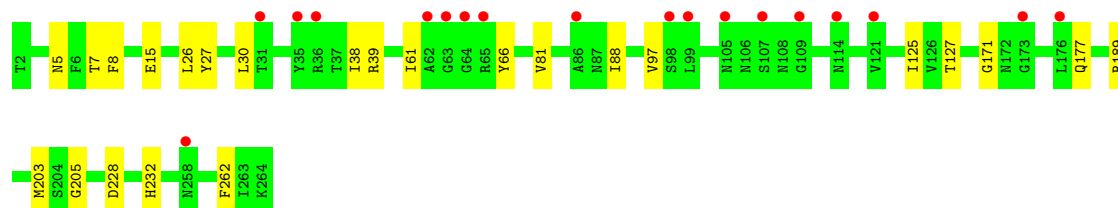




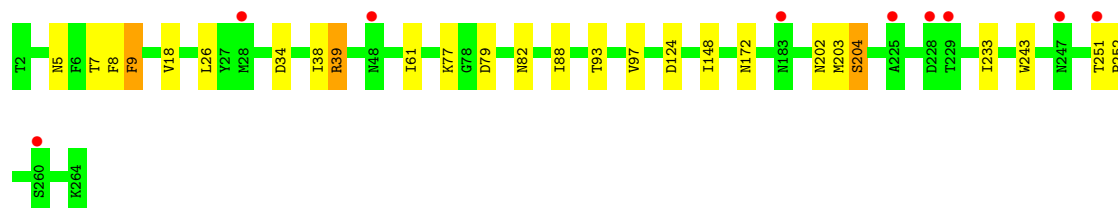
● Molecule 2: PUTATIVE RECEPTOR BINDING PROTEIN



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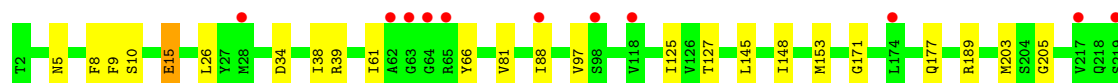
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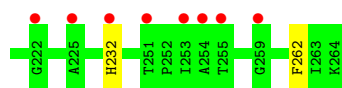


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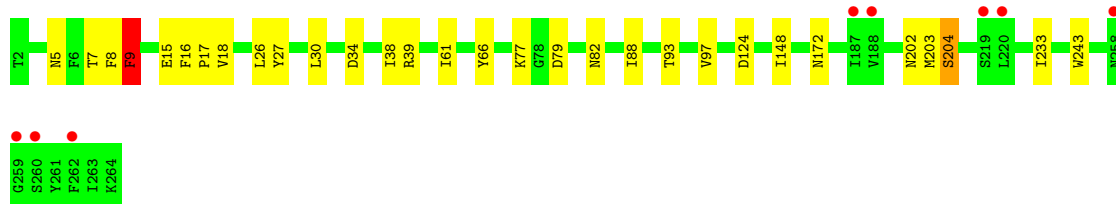
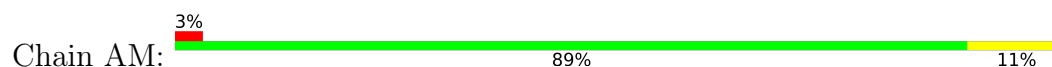


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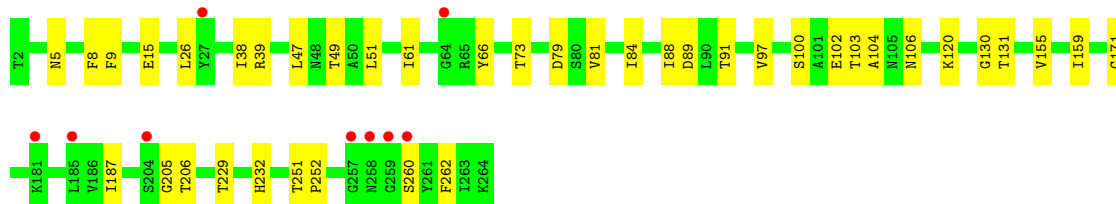
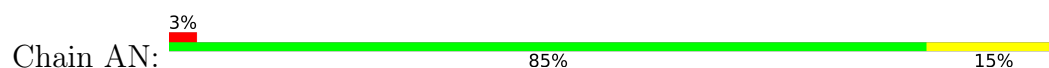




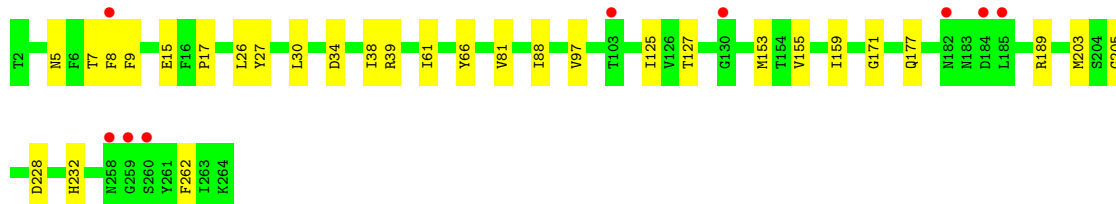
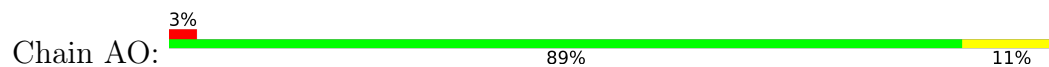
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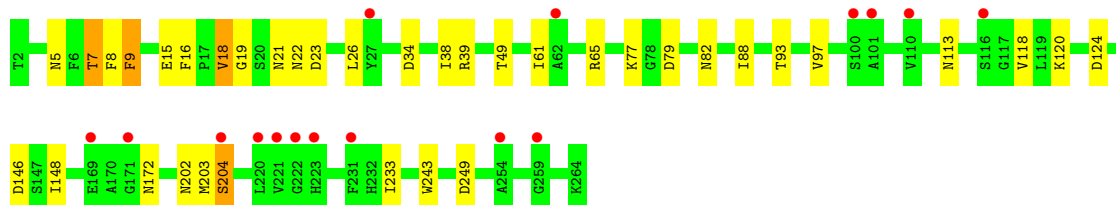
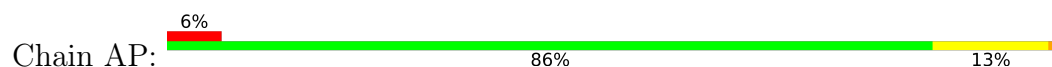
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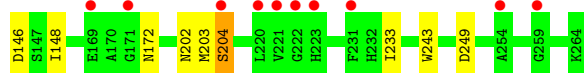
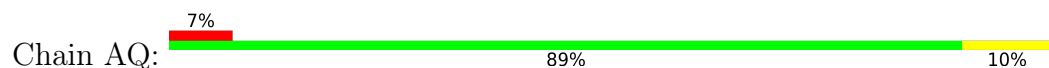
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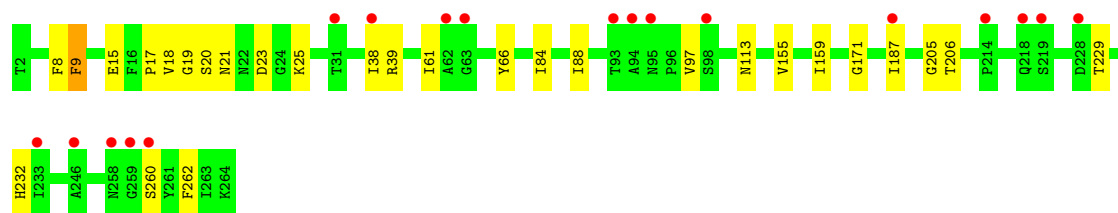


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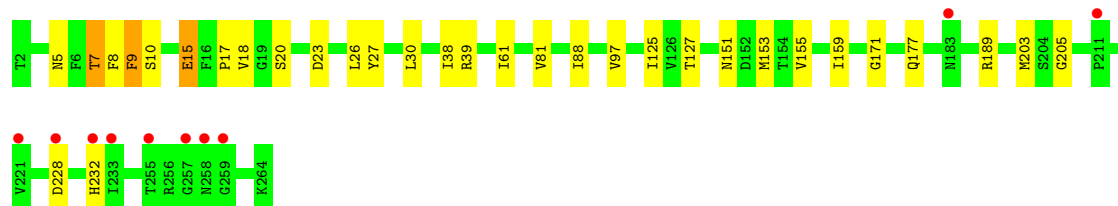


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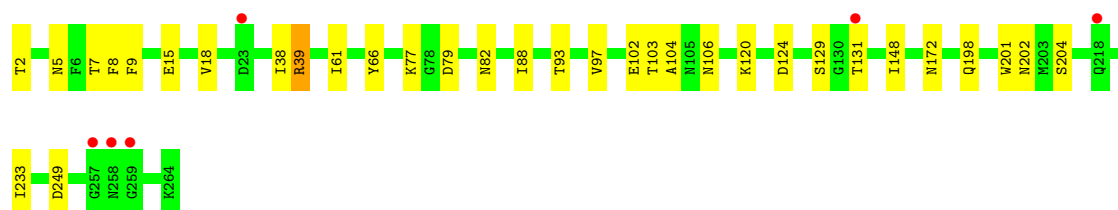
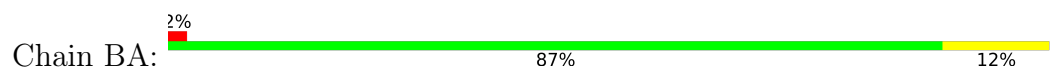




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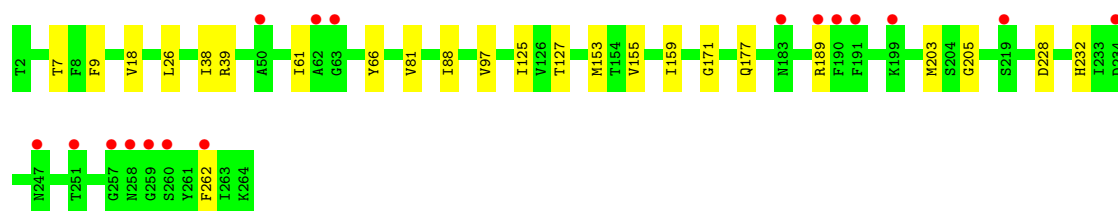
● Molecule 2: PUTATIVE RECEPTOR BINDING PROTEIN



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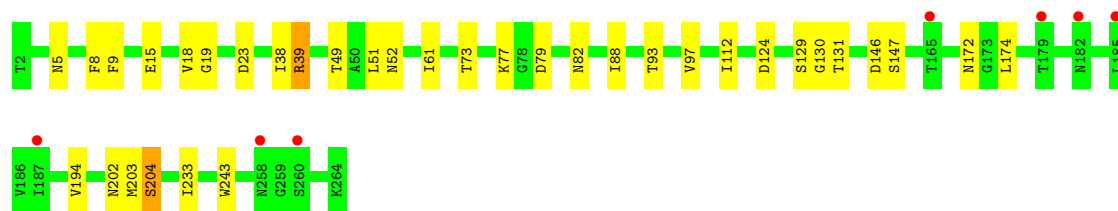


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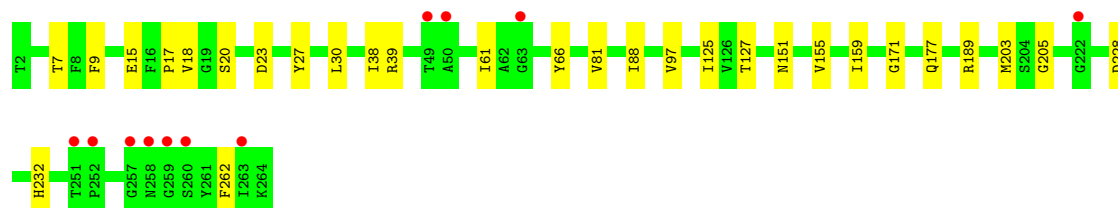
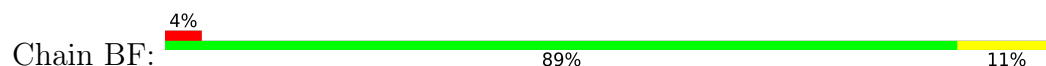




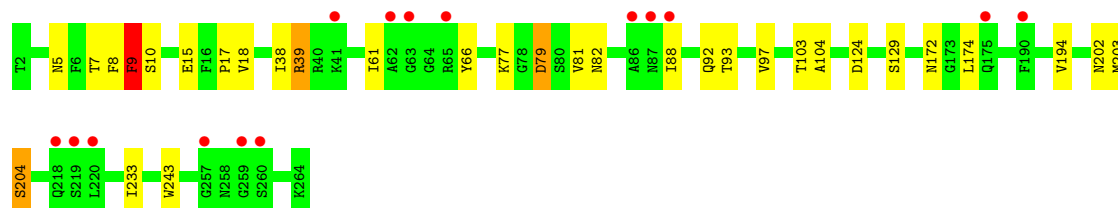
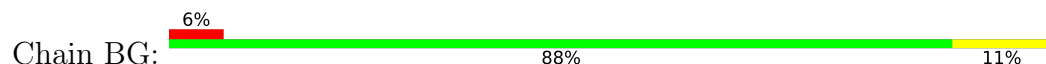
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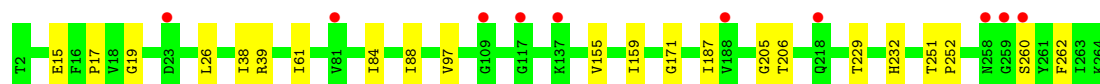
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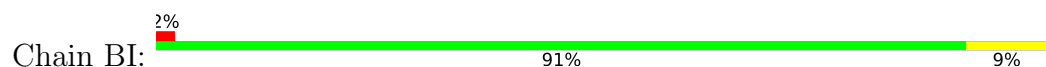
● Molecule 2: PUTATIVE RECEPTOR BINDING PROTEIN



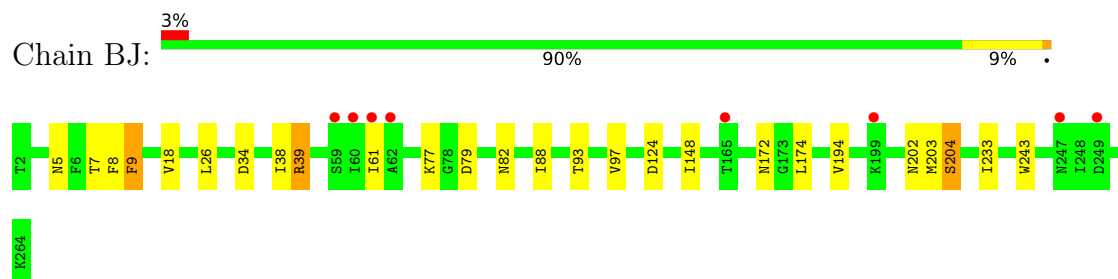
● Molecule 2: PUTATIVE RECEPTOR BINDING PROTEIN



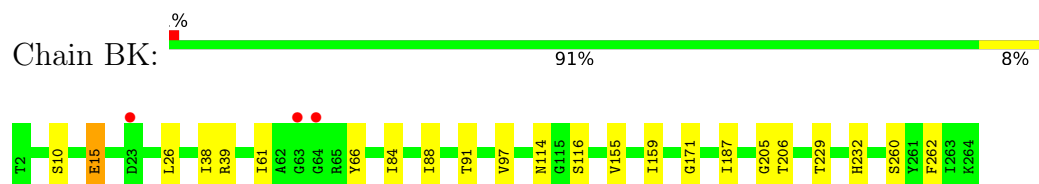
● Molecule 2: PUTATIVE RECEPTOR BINDING PROTEIN



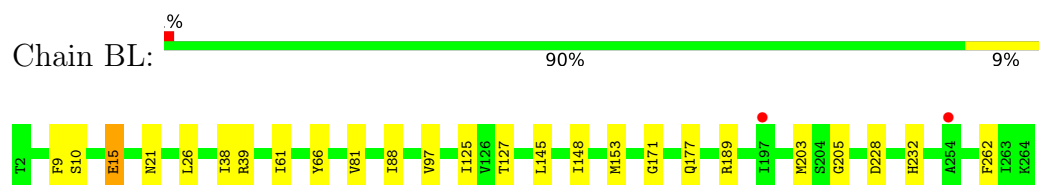
- Molecule 2: PUTATIVE RECEPTOR BINDING PROTEIN



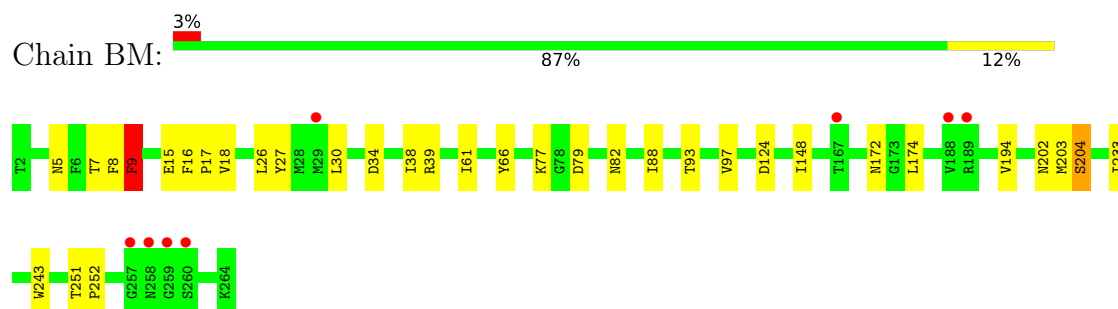
- Molecule 2: PUTATIVE RECEPTOR BINDING PROTEIN



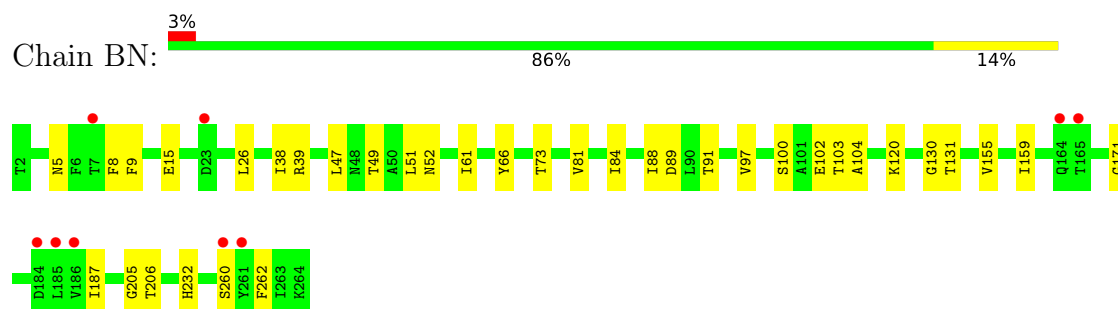
- Molecule 2: PUTATIVE RECEPTOR BINDING PROTEIN



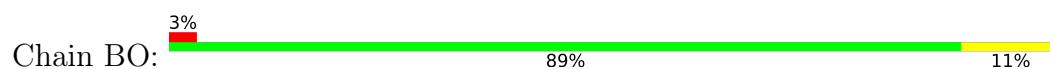
- Molecule 2: PUTATIVE RECEPTOR BINDING PROTEIN

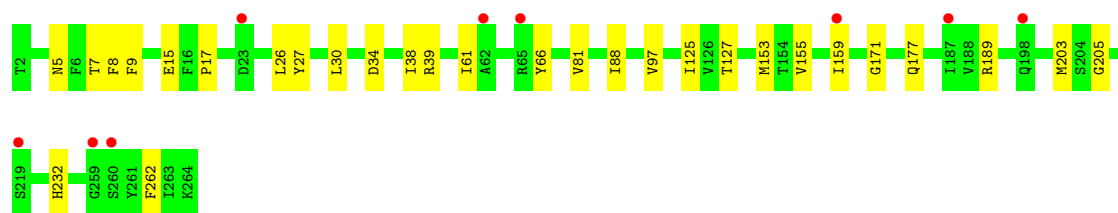


- Molecule 2: PUTATIVE RECEPTOR BINDING PROTEIN

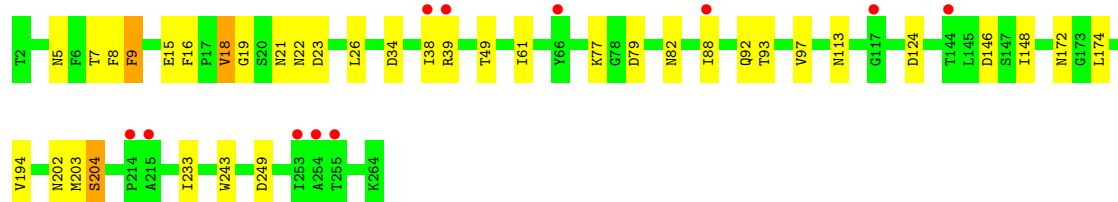
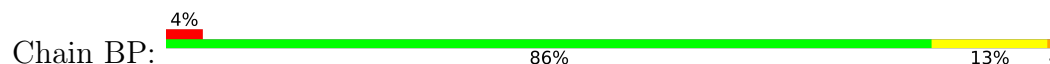


- Molecule 2: PUTATIVE RECEPTOR BINDING PROTEIN

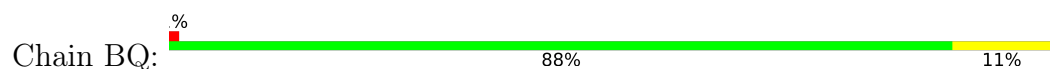




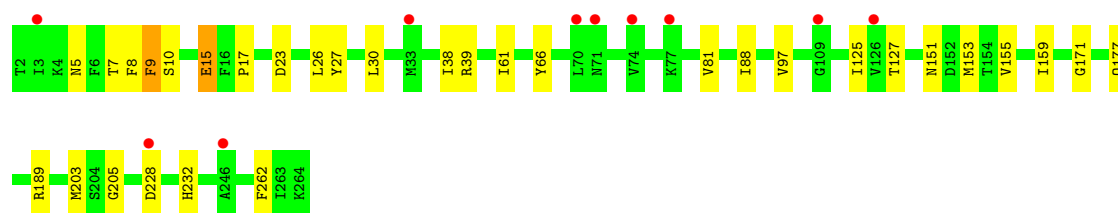
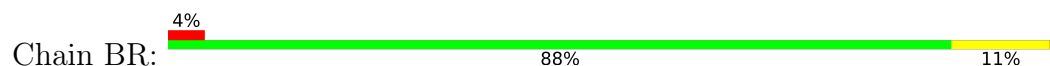
● Molecule 2: PUTATIVE RECEPTOR BINDING PROTEIN



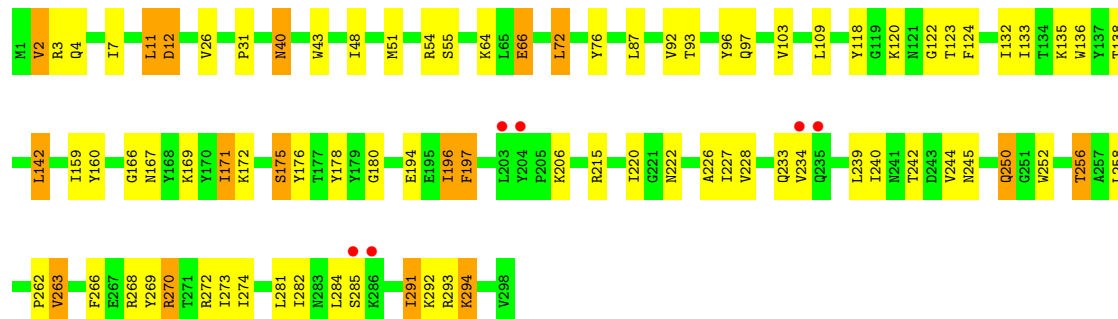
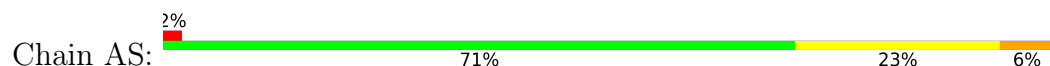
● Molecule 2: PUTATIVE RECEPTOR BINDING PROTEIN



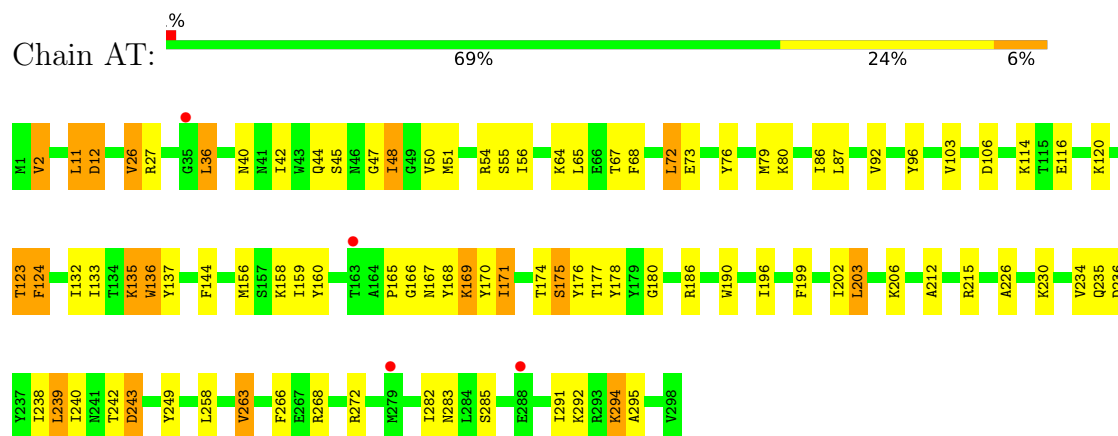
● Molecule 2: PUTATIVE RECEPTOR BINDING PROTEIN



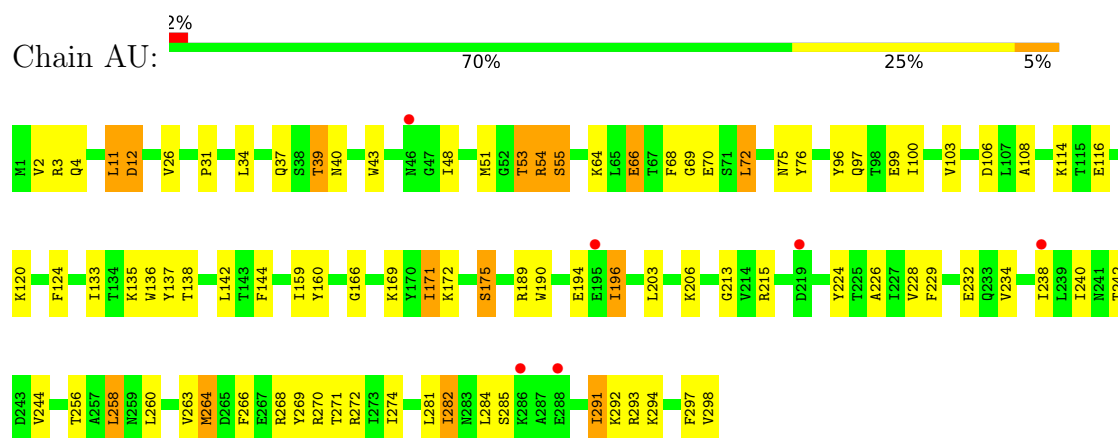
● Molecule 3: ORF15



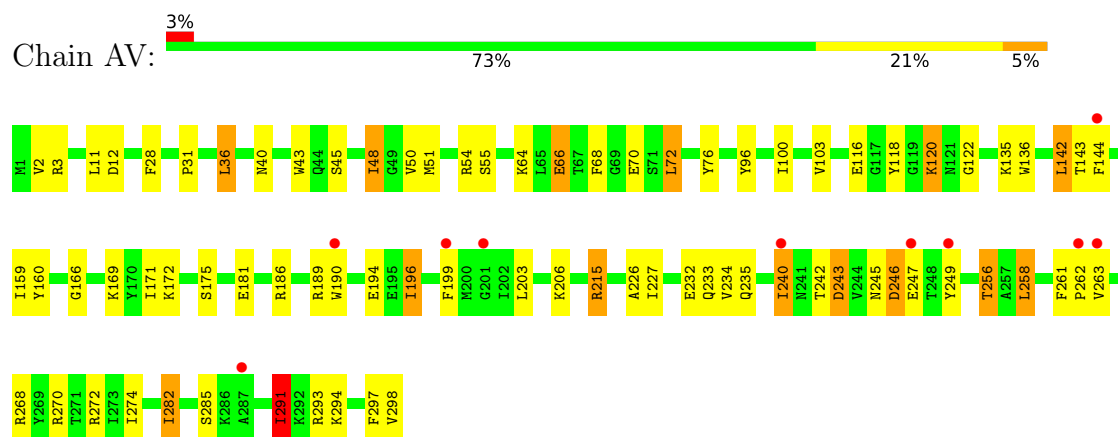
- Molecule 3: ORF15



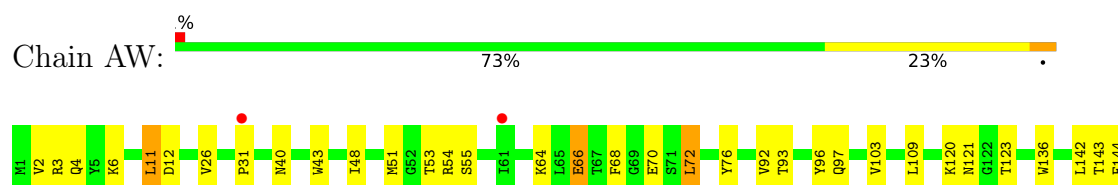
- Molecule 3: ORF15

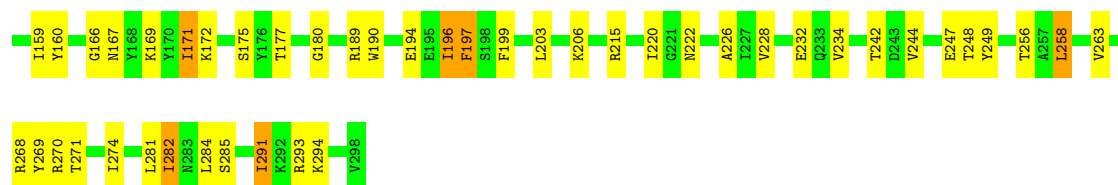


- Molecule 3: ORF15

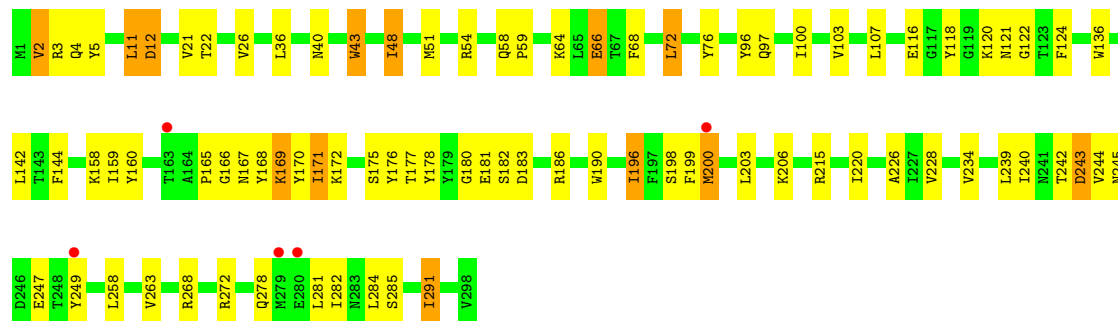
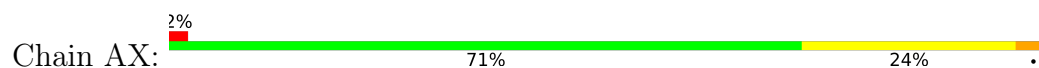


- Molecule 3: ORF15

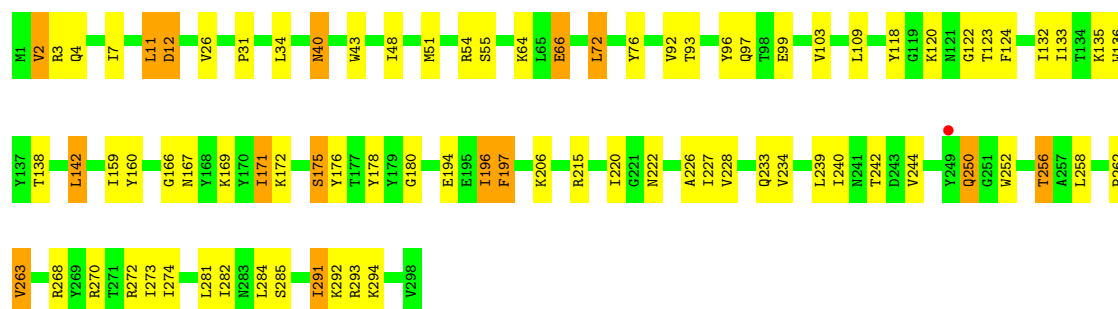




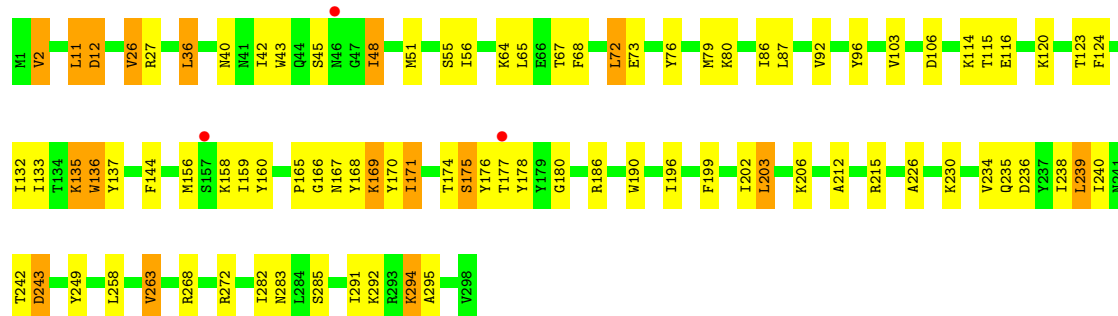
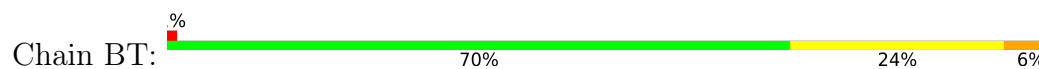
• Molecule 3: ORF15



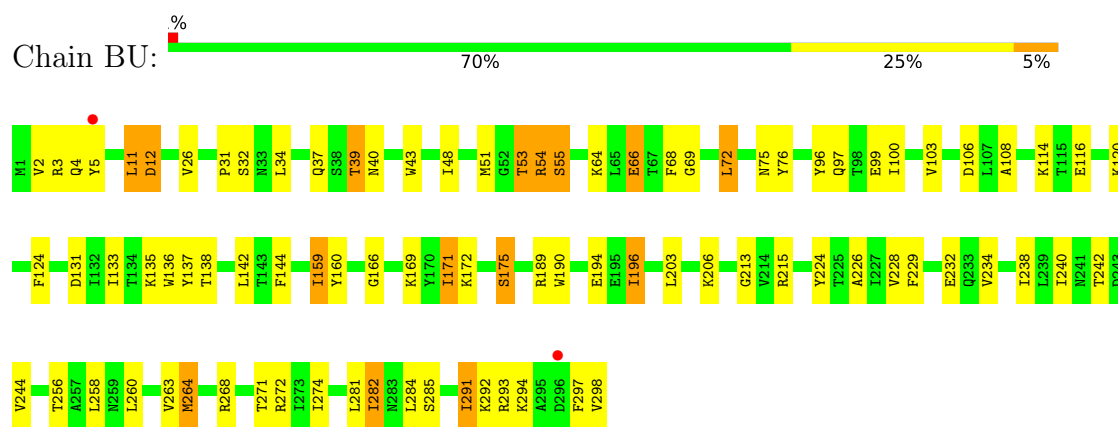
• Molecule 3: ORF15



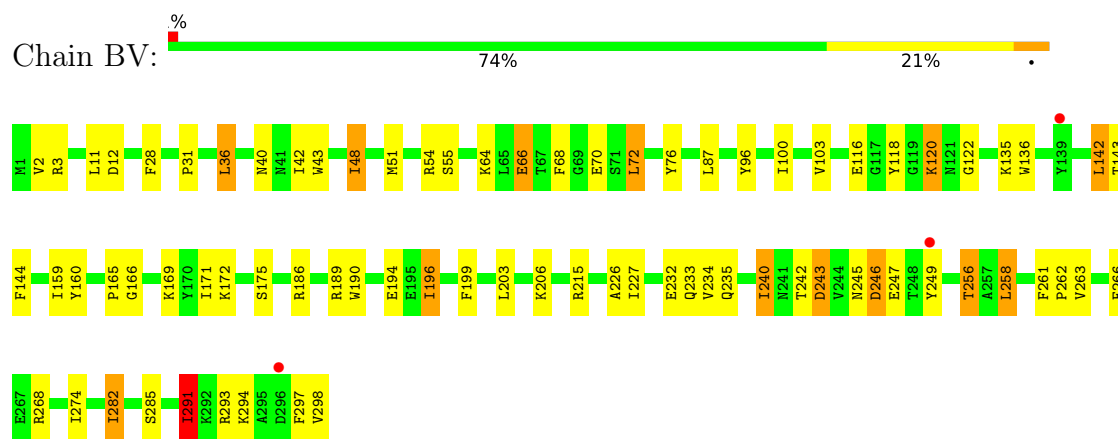
• Molecule 3: ORF15



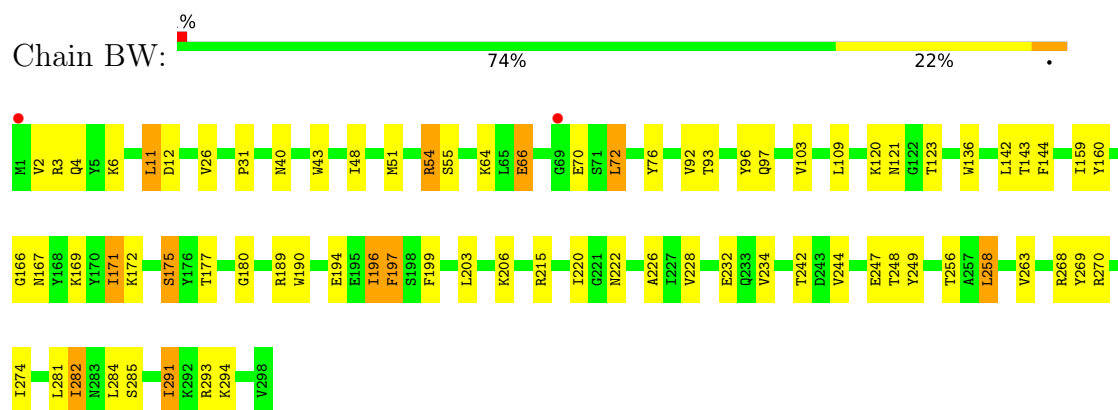
• Molecule 3: ORF15



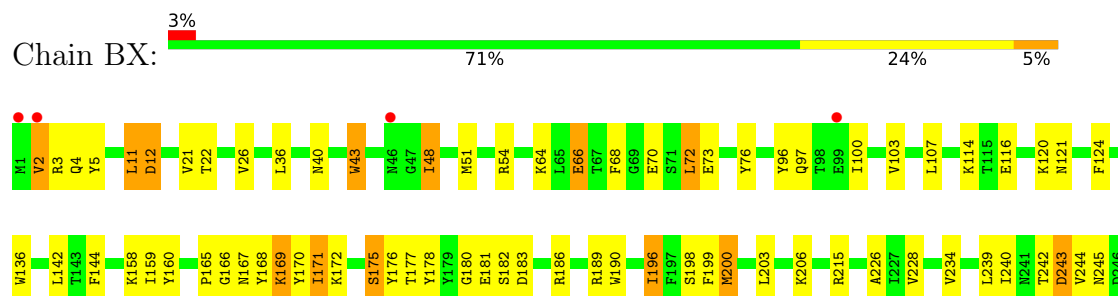
• Molecule 3: ORF15



• Molecule 3: ORF15



• Molecule 3: ORF15





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	219.52Å 219.34Å 392.43Å 90.00° 90.02° 90.00°	Depositor
Resolution (Å)	44.56 – 5.46 44.56 – 5.46	Depositor EDS
% Data completeness (in resolution range)	91.0 (44.56-5.46) 91.0 (44.56-5.46)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.31 (at 5.38Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.291 , 0.297 0.292 , 0.294	Depositor DCC
R_{free} test set	5621 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	205.9	Xtriage
Anisotropy	0.389	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 547.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.409 for k,h,-l 0.399 for -k,-h,-l 0.408 for h,-k,-l	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	119484	wwPDB-VP
Average B, all atoms (Å ²)	343.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.85% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: CA

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	A0	0.72	0/3069	1.26	5/4175 (0.1%)
1	AY	0.72	0/3069	1.26	12/4175 (0.3%)
1	AZ	0.71	0/3069	1.23	7/4175 (0.2%)
1	B0	0.72	0/3069	1.26	5/4175 (0.1%)
1	BY	0.72	0/3069	1.26	14/4175 (0.3%)
1	BZ	0.71	0/3069	1.23	7/4175 (0.2%)
2	AA	0.58	0/2048	1.07	4/2791 (0.1%)
2	AB	0.69	0/2048	1.14	2/2791 (0.1%)
2	AC	0.70	0/2048	1.16	4/2791 (0.1%)
2	AD	0.57	0/2048	1.05	4/2791 (0.1%)
2	AE	0.71	0/2048	1.15	2/2791 (0.1%)
2	AF	0.72	0/2048	1.16	3/2791 (0.1%)
2	AG	0.58	0/2048	1.05	5/2791 (0.2%)
2	AH	0.71	0/2048	1.14	1/2791 (0.0%)
2	AI	0.72	0/2048	1.16	4/2791 (0.1%)
2	AJ	0.61	0/2048	1.10	4/2791 (0.1%)
2	AK	0.69	0/2048	1.15	2/2791 (0.1%)
2	AL	0.71	0/2048	1.16	6/2791 (0.2%)
2	AM	0.62	0/2048	1.11	4/2791 (0.1%)
2	AN	0.70	0/2048	1.15	3/2791 (0.1%)
2	AO	0.71	0/2048	1.16	6/2791 (0.2%)
2	AP	0.62	0/2048	1.11	5/2791 (0.2%)
2	AQ	0.71	0/2048	1.14	3/2791 (0.1%)
2	AR	0.73	0/2048	1.16	4/2791 (0.1%)
2	BA	0.58	0/2048	1.07	4/2791 (0.1%)
2	BB	0.69	0/2048	1.14	2/2791 (0.1%)
2	BC	0.70	0/2048	1.16	3/2791 (0.1%)
2	BD	0.57	0/2048	1.05	4/2791 (0.1%)
2	BE	0.71	0/2048	1.15	1/2791 (0.0%)
2	BF	0.72	0/2048	1.16	4/2791 (0.1%)
2	BG	0.58	0/2048	1.05	5/2791 (0.2%)
2	BH	0.71	0/2048	1.14	2/2791 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
2	BI	0.72	0/2048	1.16	4/2791 (0.1%)
2	BJ	0.62	0/2048	1.10	4/2791 (0.1%)
2	BK	0.69	0/2048	1.15	2/2791 (0.1%)
2	BL	0.71	0/2048	1.16	5/2791 (0.2%)
2	BM	0.62	0/2048	1.11	4/2791 (0.1%)
2	BN	0.70	0/2048	1.15	3/2791 (0.1%)
2	BO	0.71	0/2048	1.16	6/2791 (0.2%)
2	BP	0.62	0/2048	1.11	5/2791 (0.2%)
2	BQ	0.71	0/2048	1.14	3/2791 (0.1%)
2	BR	0.73	0/2048	1.16	5/2791 (0.2%)
3	AS	0.62	0/2485	1.17	7/3356 (0.2%)
3	AT	0.63	0/2485	1.20	8/3356 (0.2%)
3	AU	0.63	0/2485	1.17	5/3356 (0.1%)
3	AV	0.65	0/2485	1.17	3/3356 (0.1%)
3	AW	0.63	0/2485	1.16	2/3356 (0.1%)
3	AX	0.65	1/2485 (0.0%)	1.18	6/3356 (0.2%)
3	BS	0.62	0/2485	1.17	7/3356 (0.2%)
3	BT	0.63	0/2485	1.20	8/3356 (0.2%)
3	BU	0.63	0/2485	1.17	5/3356 (0.1%)
3	BV	0.65	0/2485	1.17	3/3356 (0.1%)
3	BW	0.63	0/2485	1.16	2/3356 (0.1%)
3	BX	0.65	1/2485 (0.0%)	1.18	6/3356 (0.2%)
All	All	0.67	2/121962 (0.0%)	1.16	244/165798 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	AX	22	THR	CA-C	6.82	1.61	1.53
3	BX	22	THR	CA-C	6.77	1.61	1.53

The worst 5 of 244 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AY	152	PHE	CA-CB-CG	11.97	125.77	113.80
1	BY	152	PHE	CA-CB-CG	11.97	125.77	113.80
1	B0	152	PHE	CA-CB-CG	11.56	125.36	113.80
1	A0	152	PHE	CA-CB-CG	11.53	125.33	113.80
2	BK	15	GLU	N-CA-C	7.50	119.14	110.97

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A0	3000	0	2956	57	0
1	AY	3000	0	2956	38	0
1	AZ	3000	0	2956	75	0
1	B0	3000	0	2956	47	0
1	BY	3000	0	2956	38	0
1	BZ	3000	0	2956	54	0
2	AA	2008	0	1971	22	0
2	AB	2008	0	1971	16	0
2	AC	2008	0	1971	15	0
2	AD	2008	0	1971	57	0
2	AE	2008	0	1971	34	0
2	AF	2008	0	1971	20	0
2	AG	2008	0	1971	35	0
2	AH	2008	0	1971	9	0
2	AI	2008	0	1971	10	0
2	AJ	2008	0	1971	11	0
2	AK	2008	0	1971	14	0
2	AL	2008	0	1971	10	0
2	AM	2008	0	1971	15	0
2	AN	2008	0	1971	38	0
2	AO	2008	0	1971	13	0
2	AP	2008	0	1971	36	0
2	AQ	2008	0	1971	43	0
2	AR	2008	0	1971	34	0
2	BA	2008	0	1971	18	0
2	BB	2008	0	1971	17	0
2	BC	2008	0	1971	15	0
2	BD	2008	0	1971	46	0
2	BE	2008	0	1971	35	0
2	BF	2008	0	1971	21	0
2	BG	2008	0	1971	25	0
2	BH	2008	0	1971	11	0
2	BI	2008	0	1971	10	0
2	BJ	2008	0	1971	10	0
2	BK	2008	0	1971	12	0
2	BL	2008	0	1971	11	0
2	BM	2008	0	1971	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	BN	2008	0	1971	37	0
2	BO	2008	0	1971	12	0
2	BP	2008	0	1971	23	0
2	BQ	2008	0	1971	32	0
2	BR	2008	0	1971	23	0
3	AS	2432	0	2392	122	0
3	AT	2432	0	2392	111	0
3	AU	2432	0	2392	100	0
3	AV	2432	0	2392	101	0
3	AW	2432	0	2392	75	0
3	AX	2432	0	2392	151	0
3	BS	2432	0	2392	99	0
3	BT	2432	0	2392	106	0
3	BU	2432	0	2392	96	0
3	BV	2432	0	2392	94	0
3	BW	2432	0	2392	76	0
3	BX	2432	0	2392	117	0
4	AS	1	0	0	0	0
4	AT	1	0	0	0	0
4	AU	1	0	0	0	0
4	AV	1	0	0	0	0
4	AW	1	0	0	0	0
4	AX	1	0	0	0	0
4	BS	1	0	0	0	0
4	BT	1	0	0	0	0
4	BU	1	0	0	0	0
4	BV	1	0	0	0	0
4	BW	1	0	0	0	0
4	BX	1	0	0	0	0
All	All	119484	0	117396	1553	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 7.

The worst 5 of 1553 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)
3:AW:120:LYS:HD3	3:BV:68:PHE:CE1	1.26	1.65
3:AV:68:PHE:CD1	3:BW:120:LYS:HD3	1.30	1.61
3:AV:68:PHE:CE1	3:BW:120:LYS:HD3	1.28	1.58
3:AU:68:PHE:CE1	3:BX:120:LYS:HD3	1.37	1.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:AW:120:LYS:HD3	3:BV:68:PHE:CD1	1.42	1.54

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	A0	370/372 (100%)	358 (97%)	12 (3%)	0	100	100
1	AY	370/372 (100%)	355 (96%)	15 (4%)	0	100	100
1	AZ	370/372 (100%)	358 (97%)	12 (3%)	0	100	100
1	B0	370/372 (100%)	358 (97%)	12 (3%)	0	100	100
1	BY	370/372 (100%)	355 (96%)	15 (4%)	0	100	100
1	BZ	370/372 (100%)	357 (96%)	13 (4%)	0	100	100
2	AA	261/263 (99%)	254 (97%)	7 (3%)	0	100	100
2	AB	261/263 (99%)	245 (94%)	16 (6%)	0	100	100
2	AC	261/263 (99%)	247 (95%)	14 (5%)	0	100	100
2	AD	261/263 (99%)	255 (98%)	6 (2%)	0	100	100
2	AE	261/263 (99%)	246 (94%)	15 (6%)	0	100	100
2	AF	261/263 (99%)	246 (94%)	15 (6%)	0	100	100
2	AG	261/263 (99%)	255 (98%)	6 (2%)	0	100	100
2	AH	261/263 (99%)	246 (94%)	15 (6%)	0	100	100
2	AI	261/263 (99%)	246 (94%)	15 (6%)	0	100	100
2	AJ	261/263 (99%)	255 (98%)	6 (2%)	0	100	100
2	AK	261/263 (99%)	246 (94%)	15 (6%)	0	100	100
2	AL	261/263 (99%)	247 (95%)	14 (5%)	0	100	100
2	AM	261/263 (99%)	255 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AN	261/263 (99%)	247 (95%)	14 (5%)	0	100	100
2	AO	261/263 (99%)	246 (94%)	15 (6%)	0	100	100
2	AP	261/263 (99%)	254 (97%)	7 (3%)	0	100	100
2	AQ	261/263 (99%)	245 (94%)	16 (6%)	0	100	100
2	AR	261/263 (99%)	247 (95%)	14 (5%)	0	100	100
2	BA	261/263 (99%)	254 (97%)	7 (3%)	0	100	100
2	BB	261/263 (99%)	245 (94%)	16 (6%)	0	100	100
2	BC	261/263 (99%)	247 (95%)	14 (5%)	0	100	100
2	BD	261/263 (99%)	255 (98%)	6 (2%)	0	100	100
2	BE	261/263 (99%)	246 (94%)	15 (6%)	0	100	100
2	BF	261/263 (99%)	246 (94%)	15 (6%)	0	100	100
2	BG	261/263 (99%)	254 (97%)	7 (3%)	0	100	100
2	BH	261/263 (99%)	246 (94%)	15 (6%)	0	100	100
2	BI	261/263 (99%)	246 (94%)	15 (6%)	0	100	100
2	BJ	261/263 (99%)	255 (98%)	6 (2%)	0	100	100
2	BK	261/263 (99%)	246 (94%)	15 (6%)	0	100	100
2	BL	261/263 (99%)	247 (95%)	14 (5%)	0	100	100
2	BM	261/263 (99%)	255 (98%)	6 (2%)	0	100	100
2	BN	261/263 (99%)	247 (95%)	14 (5%)	0	100	100
2	BO	261/263 (99%)	246 (94%)	15 (6%)	0	100	100
2	BP	261/263 (99%)	255 (98%)	6 (2%)	0	100	100
2	BQ	261/263 (99%)	245 (94%)	16 (6%)	0	100	100
2	BR	261/263 (99%)	247 (95%)	14 (5%)	0	100	100
3	AS	296/298 (99%)	277 (94%)	17 (6%)	2 (1%)	18	55
3	AT	296/298 (99%)	273 (92%)	21 (7%)	2 (1%)	18	55
3	AU	296/298 (99%)	274 (93%)	20 (7%)	2 (1%)	18	55
3	AV	296/298 (99%)	275 (93%)	19 (6%)	2 (1%)	18	55
3	AW	296/298 (99%)	280 (95%)	14 (5%)	2 (1%)	18	55
3	AX	296/298 (99%)	277 (94%)	17 (6%)	2 (1%)	18	55
3	BS	296/298 (99%)	278 (94%)	16 (5%)	2 (1%)	18	55
3	BT	296/298 (99%)	273 (92%)	21 (7%)	2 (1%)	18	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	BU	296/298 (99%)	274 (93%)	20 (7%)	2 (1%)	18	55
3	BV	296/298 (99%)	275 (93%)	19 (6%)	2 (1%)	18	55
3	BW	296/298 (99%)	280 (95%)	14 (5%)	2 (1%)	18	55
3	BX	296/298 (99%)	277 (94%)	17 (6%)	2 (1%)	18	55
All	All	15168/15276 (99%)	14418 (95%)	726 (5%)	24 (0%)	43	77

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	AS	175	SER
3	AT	175	SER
3	AU	175	SER
3	AV	175	SER
3	AW	175	SER

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	A0	337/337 (100%)	323 (96%)	14 (4%)	26	48
1	AY	337/337 (100%)	319 (95%)	18 (5%)	20	40
1	AZ	337/337 (100%)	318 (94%)	19 (6%)	19	39
1	B0	337/337 (100%)	323 (96%)	14 (4%)	26	48
1	BY	337/337 (100%)	319 (95%)	18 (5%)	20	40
1	BZ	337/337 (100%)	318 (94%)	19 (6%)	19	39
2	AA	227/227 (100%)	217 (96%)	10 (4%)	25	46
2	AB	227/227 (100%)	223 (98%)	4 (2%)	51	66
2	AC	227/227 (100%)	223 (98%)	4 (2%)	51	66
2	AD	227/227 (100%)	219 (96%)	8 (4%)	32	53
2	AE	227/227 (100%)	223 (98%)	4 (2%)	51	66
2	AF	227/227 (100%)	223 (98%)	4 (2%)	51	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
2	AG	227/227 (100%)	218 (96%)	9 (4%)	28	48	
2	AH	227/227 (100%)	223 (98%)	4 (2%)	51	66	
2	AI	227/227 (100%)	223 (98%)	4 (2%)	51	66	
2	AJ	227/227 (100%)	218 (96%)	9 (4%)	28	48	
2	AK	227/227 (100%)	223 (98%)	4 (2%)	51	66	
2	AL	227/227 (100%)	223 (98%)	4 (2%)	51	66	
2	AM	227/227 (100%)	218 (96%)	9 (4%)	28	48	
2	AN	227/227 (100%)	223 (98%)	4 (2%)	51	66	
2	AO	227/227 (100%)	223 (98%)	4 (2%)	51	66	
2	AP	227/227 (100%)	218 (96%)	9 (4%)	28	48	
2	AQ	227/227 (100%)	223 (98%)	4 (2%)	51	66	
2	AR	227/227 (100%)	222 (98%)	5 (2%)	45	63	
2	BA	227/227 (100%)	217 (96%)	10 (4%)	25	46	
2	BB	227/227 (100%)	223 (98%)	4 (2%)	51	66	
2	BC	227/227 (100%)	223 (98%)	4 (2%)	51	66	
2	BD	227/227 (100%)	219 (96%)	8 (4%)	32	53	
2	BE	227/227 (100%)	223 (98%)	4 (2%)	51	66	
2	BF	227/227 (100%)	223 (98%)	4 (2%)	51	66	
2	BG	227/227 (100%)	218 (96%)	9 (4%)	28	48	
2	BH	227/227 (100%)	223 (98%)	4 (2%)	51	66	
2	BI	227/227 (100%)	223 (98%)	4 (2%)	51	66	
2	BJ	227/227 (100%)	218 (96%)	9 (4%)	28	48	
2	BK	227/227 (100%)	223 (98%)	4 (2%)	51	66	
2	BL	227/227 (100%)	223 (98%)	4 (2%)	51	66	
2	BM	227/227 (100%)	218 (96%)	9 (4%)	28	48	
2	BN	227/227 (100%)	223 (98%)	4 (2%)	51	66	
2	BO	227/227 (100%)	223 (98%)	4 (2%)	51	66	
2	BP	227/227 (100%)	218 (96%)	9 (4%)	28	48	
2	BQ	227/227 (100%)	223 (98%)	4 (2%)	51	66	
2	BR	227/227 (100%)	222 (98%)	5 (2%)	45	63	
3	AS	264/265 (100%)	240 (91%)	24 (9%)	9	27	

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	AT	264/265 (100%)	242 (92%)	22 (8%)	10	30
3	AU	264/265 (100%)	235 (89%)	29 (11%)	6	20
3	AV	264/265 (100%)	234 (89%)	30 (11%)	5	19
3	AW	264/265 (100%)	231 (88%)	33 (12%)	4	16
3	AX	264/265 (100%)	240 (91%)	24 (9%)	9	27
3	BS	264/265 (100%)	240 (91%)	24 (9%)	9	27
3	BT	264/265 (100%)	242 (92%)	22 (8%)	10	30
3	BU	264/265 (100%)	235 (89%)	29 (11%)	6	20
3	BV	264/265 (100%)	235 (89%)	29 (11%)	6	20
3	BW	264/265 (100%)	231 (88%)	33 (12%)	4	16
3	BX	264/265 (100%)	240 (91%)	24 (9%)	9	27
All	All	13362/13374 (100%)	12731 (95%)	631 (5%)	23	44

5 of 631 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	BT	64	LYS
3	BX	36	LEU
3	BT	243	ASP
3	BT	55	SER
3	BV	143	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 318 such sidechains are listed below:

Mol	Chain	Res	Type
2	BM	71	ASN
3	BV	250	GLN
2	BN	92	GLN
2	BR	71	ASN
1	BY	24	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 12 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.

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	A0	372/372 (100%)	0.00	11 (2%)	52	44	351, 388, 435, 523	0
1	AY	372/372 (100%)	0.06	13 (3%)	47	42	359, 396, 449, 555	0
1	AZ	372/372 (100%)	0.08	20 (5%)	31	32	364, 394, 444, 557	0
1	B0	372/372 (100%)	0.03	6 (1%)	70	58	337, 377, 425, 485	0
1	BY	372/372 (100%)	-0.08	6 (1%)	70	58	331, 361, 429, 557	0
1	BZ	372/372 (100%)	-0.04	12 (3%)	50	43	332, 360, 422, 502	0
2	AA	263/263 (100%)	-0.13	5 (1%)	66	55	248, 312, 407, 435	0
2	AB	263/263 (100%)	-0.05	11 (4%)	40	38	284, 350, 440, 481	0
2	AC	263/263 (100%)	-0.02	11 (4%)	40	38	257, 345, 417, 473	0
2	AD	263/263 (100%)	0.02	8 (3%)	52	44	258, 320, 441, 485	0
2	AE	263/263 (100%)	-0.07	8 (3%)	52	44	277, 344, 466, 480	0
2	AF	263/263 (100%)	-0.02	12 (4%)	37	36	265, 367, 471, 497	0
2	AG	263/263 (100%)	0.11	17 (6%)	25	28	265, 348, 500, 556	0
2	AH	263/263 (100%)	-0.09	6 (2%)	61	51	315, 402, 524, 572	0
2	AI	263/263 (100%)	0.17	18 (6%)	23	27	282, 416, 532, 576	0
2	AJ	263/263 (100%)	-0.05	9 (3%)	48	42	264, 342, 429, 539	0
2	AK	263/263 (100%)	-0.20	4 (1%)	72	59	255, 301, 456, 521	0
2	AL	263/263 (100%)	-0.03	19 (7%)	21	25	277, 345, 485, 575	0
2	AM	263/263 (100%)	-0.05	8 (3%)	52	44	266, 358, 425, 467	0
2	AN	263/263 (100%)	-0.03	9 (3%)	48	42	252, 313, 386, 420	0
2	AO	263/263 (100%)	0.03	9 (3%)	48	42	276, 347, 419, 449	0
2	AP	263/263 (100%)	0.12	16 (6%)	27	30	267, 341, 556, 576	0
2	AQ	263/263 (100%)	0.02	18 (6%)	23	27	295, 397, 566, 605	0
2	AR	263/263 (100%)	0.12	10 (3%)	44	40	298, 417, 541, 571	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
2	BA	263/263 (100%)	-0.10	6 (2%) 61 51	259, 312, 430, 466	0
2	BB	263/263 (100%)	-0.25	4 (1%) 72 59	282, 346, 455, 506	0
2	BC	263/263 (100%)	-0.02	17 (6%) 25 28	273, 344, 419, 481	0
2	BD	263/263 (100%)	-0.09	7 (2%) 56 47	252, 316, 445, 484	0
2	BE	263/263 (100%)	-0.15	10 (3%) 44 40	274, 342, 448, 477	0
2	BF	263/263 (100%)	0.09	11 (4%) 40 38	258, 361, 457, 487	0
2	BG	263/263 (100%)	0.04	15 (5%) 29 31	252, 346, 496, 557	0
2	BH	263/263 (100%)	-0.15	10 (3%) 44 40	314, 408, 514, 559	0
2	BI	263/263 (100%)	-0.17	4 (1%) 72 59	276, 420, 541, 584	0
2	BJ	263/263 (100%)	-0.19	8 (3%) 52 44	268, 345, 419, 521	0
2	BK	263/263 (100%)	-0.16	3 (1%) 78 65	256, 305, 435, 496	0
2	BL	263/263 (100%)	-0.29	2 (0%) 82 71	283, 341, 452, 534	0
2	BM	263/263 (100%)	-0.10	8 (3%) 52 44	264, 357, 438, 484	0
2	BN	263/263 (100%)	-0.06	9 (3%) 48 42	255, 316, 388, 433	0
2	BO	263/263 (100%)	-0.05	9 (3%) 48 42	276, 348, 418, 453	0
2	BP	263/263 (100%)	0.05	11 (4%) 40 38	261, 365, 541, 549	0
2	BQ	263/263 (100%)	-0.25	3 (1%) 78 65	312, 413, 547, 559	0
2	BR	263/263 (100%)	-0.02	10 (3%) 44 40	308, 418, 537, 556	0
3	AS	298/298 (100%)	-0.06	6 (2%) 65 54	219, 262, 346, 379	0
3	AT	298/298 (100%)	-0.10	4 (1%) 75 62	230, 260, 318, 344	0
3	AU	298/298 (100%)	-0.21	6 (2%) 65 54	228, 269, 334, 364	0
3	AV	298/298 (100%)	-0.06	10 (3%) 48 42	229, 264, 317, 332	0
3	AW	298/298 (100%)	-0.16	2 (0%) 84 72	213, 254, 317, 347	0
3	AX	298/298 (100%)	-0.18	5 (1%) 69 57	216, 255, 347, 401	0
3	BS	298/298 (100%)	-0.17	1 (0%) 90 81	222, 256, 339, 388	0
3	BT	298/298 (100%)	-0.17	3 (1%) 79 66	218, 265, 316, 343	0
3	BU	298/298 (100%)	-0.25	2 (0%) 84 72	228, 262, 338, 382	0
3	BV	298/298 (100%)	-0.14	3 (1%) 79 66	218, 260, 305, 324	0
3	BW	298/298 (100%)	-0.19	2 (0%) 84 72	215, 256, 341, 403	0
3	BX	298/298 (100%)	-0.16	8 (2%) 56 47	228, 272, 370, 407	0
All	All	15276/15276 (100%)	-0.07	465 (3%) 52 44	213, 344, 468, 605	0

The worst 5 of 465 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	AM	259	GLY	8.8
2	BO	260	SER	7.0
2	AO	259	GLY	6.9
2	BH	260	SER	6.6
2	BC	257	GLY	6.5

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	CA	BU	301	1/1	0.96	0.07	269,269,269,269	0
4	CA	BV	301	1/1	0.96	0.12	272,272,272,272	0
4	CA	AW	301	1/1	0.98	0.07	266,266,266,266	0
4	CA	AX	301	1/1	0.98	0.14	275,275,275,275	0
4	CA	BT	301	1/1	0.98	0.07	279,279,279,279	0
4	CA	AS	301	1/1	0.98	0.07	281,281,281,281	0
4	CA	AV	301	1/1	0.98	0.11	276,276,276,276	0
4	CA	BX	301	1/1	0.98	0.10	287,287,287,287	0
4	CA	AT	301	1/1	0.99	0.06	275,275,275,275	0
4	CA	BS	301	1/1	0.99	0.06	267,267,267,267	0
4	CA	BW	301	1/1	0.99	0.05	268,268,268,268	0
4	CA	AU	301	1/1	0.99	0.04	275,275,275,275	0

6.5 Other polymers [i](#)

There are no such residues in this entry.