



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 02:04 PM UTC

PDB ID : 4PB6 / pdb_00004pb6
Title : Feline calicivirus VP1 T=1 virus-like particle
Authors : Burmeister, W.P.; Buisson, M.
Deposited on : 2014-04-11
Resolution : 8.00 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:

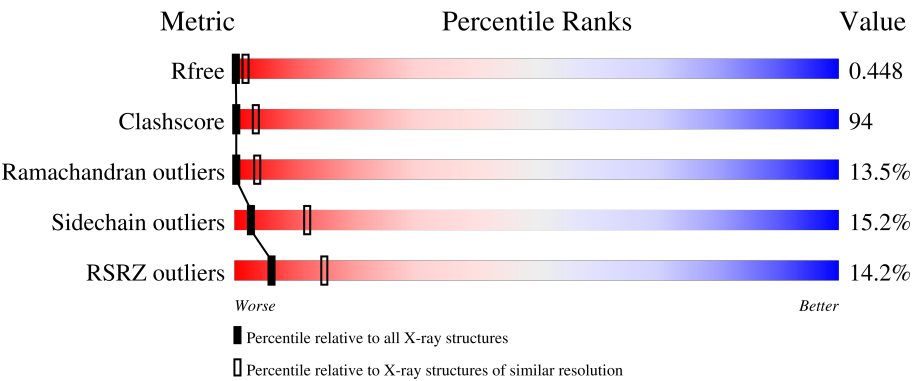
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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 8.00 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	1168 (11.50-4.00)
Clashscore	190562	1001 (11.50-4.06)
Ramachandran outliers	187476	1055 (11.50-4.00)
Sidechain outliers	187428	1018 (11.50-4.00)
RSRZ outliers	180081	1162 (11.50-4.00)

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	A	545	13% 18%52%19%•8%
1	B	545	12% 17%52%19%•8%
1	C	545	15% 16%53%19%•8%
1	D	545	13% 17%53%19%•8%
1	E	545	13% 17%52%19%•8%

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Mol	Chain	Length	Quality of chain
1	F	545	
1	G	545	
1	H	545	
1	I	545	
1	J	545	
1	K	545	
1	L	545	
1	M	545	
1	N	545	
1	O	545	
1	P	545	
1	Q	545	
1	R	545	
1	S	545	
1	T	545	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 77840 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 VP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	502	Total	C	N	O	S	0	0	0
			3892	2491	651	742	8			
1	B	502	Total	C	N	O	S	0	0	0
			3892	2491	651	742	8			
1	C	502	Total	C	N	O	S	0	0	0
			3892	2491	651	742	8			
1	D	502	Total	C	N	O	S	0	0	0
			3892	2491	651	742	8			
1	E	502	Total	C	N	O	S	0	0	0
			3892	2491	651	742	8			
1	F	502	Total	C	N	O	S	0	0	0
			3892	2491	651	742	8			
1	G	502	Total	C	N	O	S	0	0	0
			3892	2491	651	742	8			
1	H	502	Total	C	N	O	S	0	0	0
			3892	2491	651	742	8			
1	I	502	Total	C	N	O	S	0	0	0
			3892	2491	651	742	8			
1	J	502	Total	C	N	O	S	0	0	0
			3892	2491	651	742	8			
1	K	502	Total	C	N	O	S	0	0	0
			3892	2491	651	742	8			
1	L	502	Total	C	N	O	S	0	0	0
			3892	2491	651	742	8			
1	M	502	Total	C	N	O	S	0	0	0
			3892	2491	651	742	8			
1	N	502	Total	C	N	O	S	0	0	0
			3892	2491	651	742	8			
1	O	502	Total	C	N	O	S	0	0	0
			3892	2491	651	742	8			
1	P	502	Total	C	N	O	S	0	0	0
			3892	2491	651	742	8			

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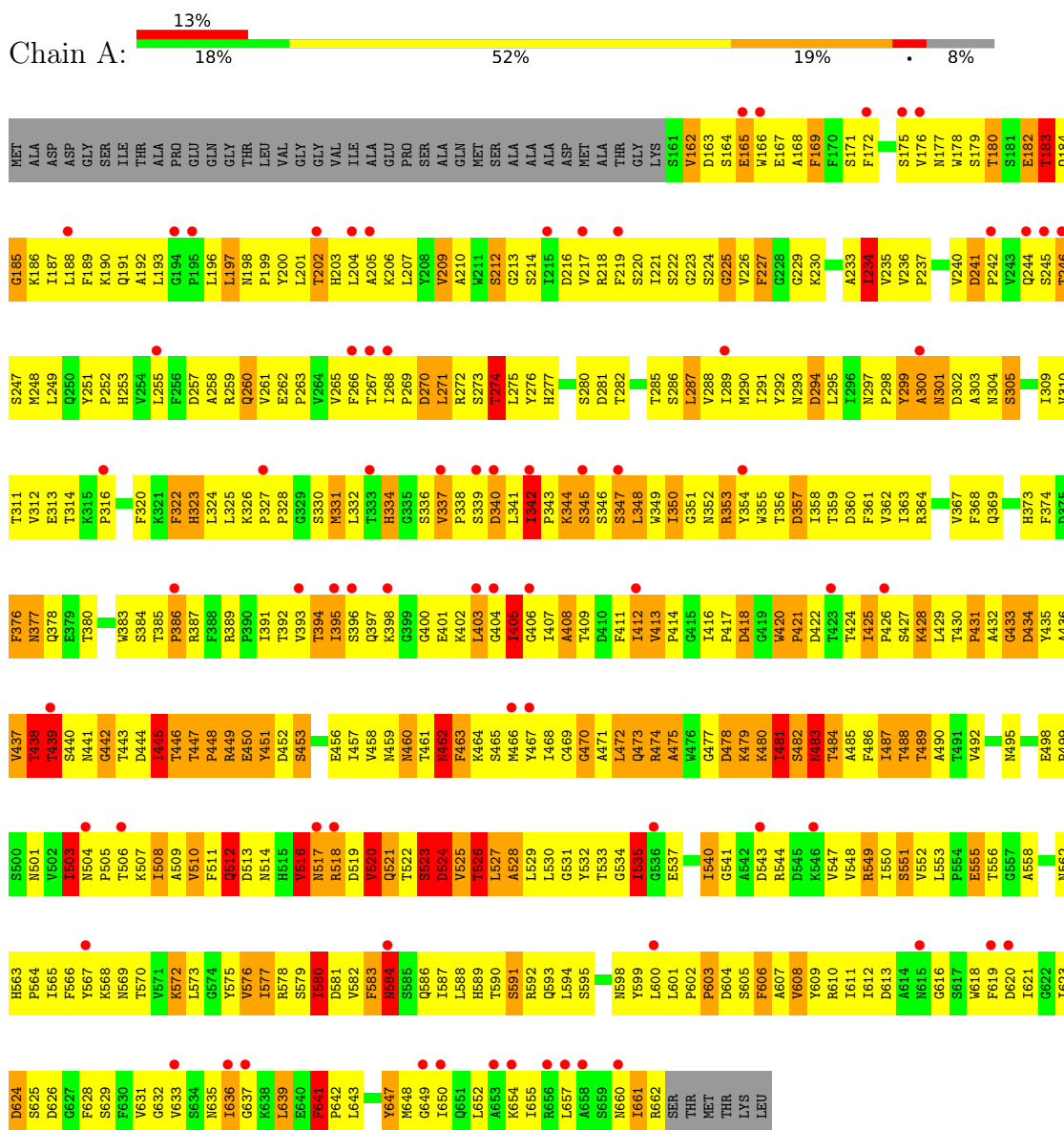
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	502	Total	C	N	O	S	0	0	0
			3892	2491	651	742	8			
1	R	502	Total	C	N	O	S	0	0	0
			3892	2491	651	742	8			
1	S	502	Total	C	N	O	S	0	0	0
			3892	2491	651	742	8			
1	T	502	Total	C	N	O	S	0	0	0
			3892	2491	651	742	8			

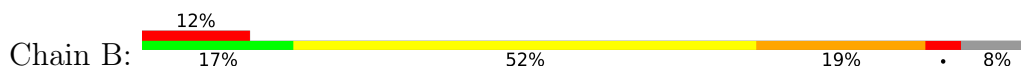
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

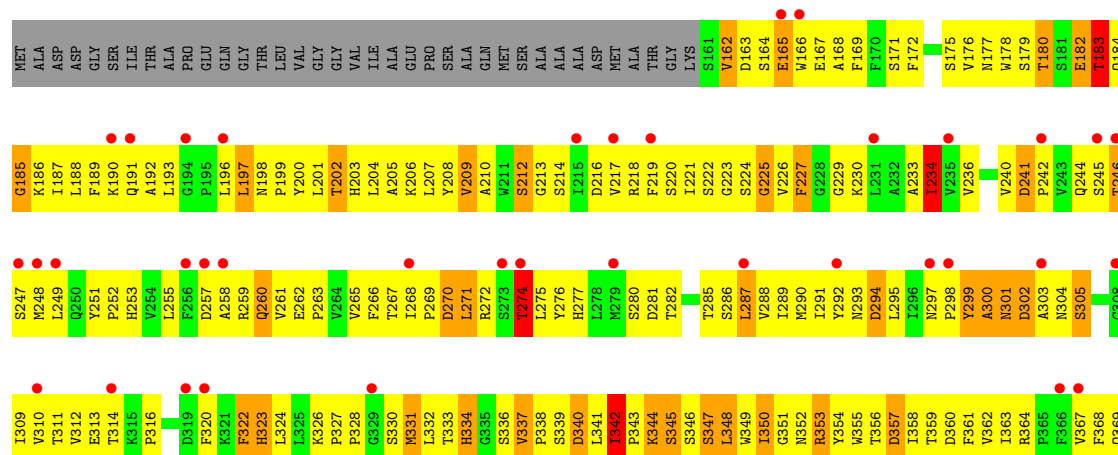
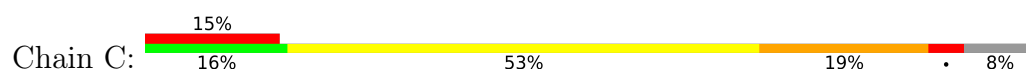
• Molecule 1: VP1

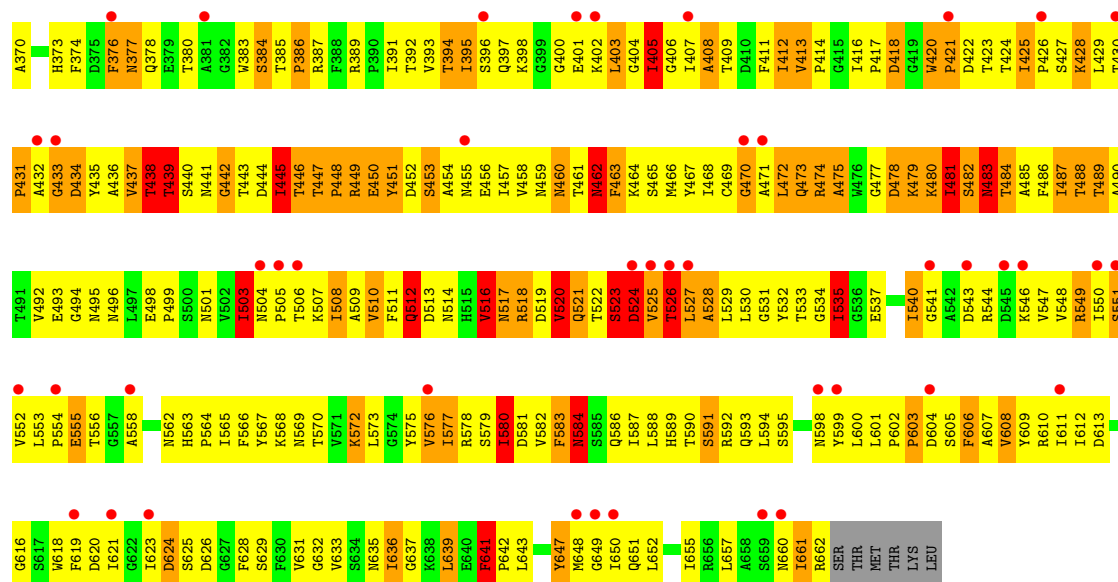


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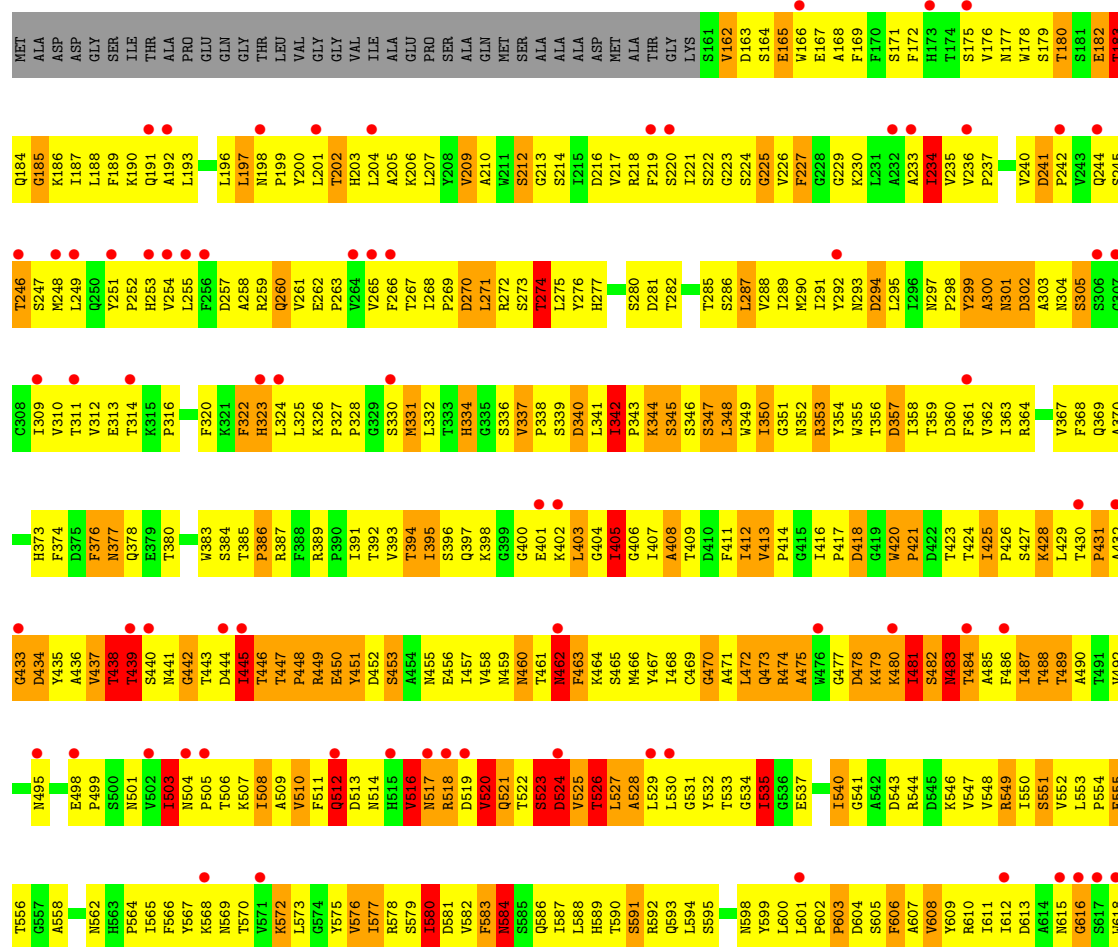
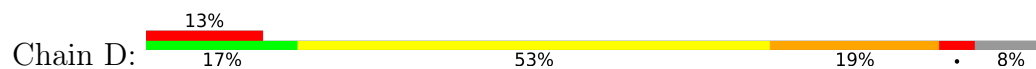


- Molecule 1: VP1



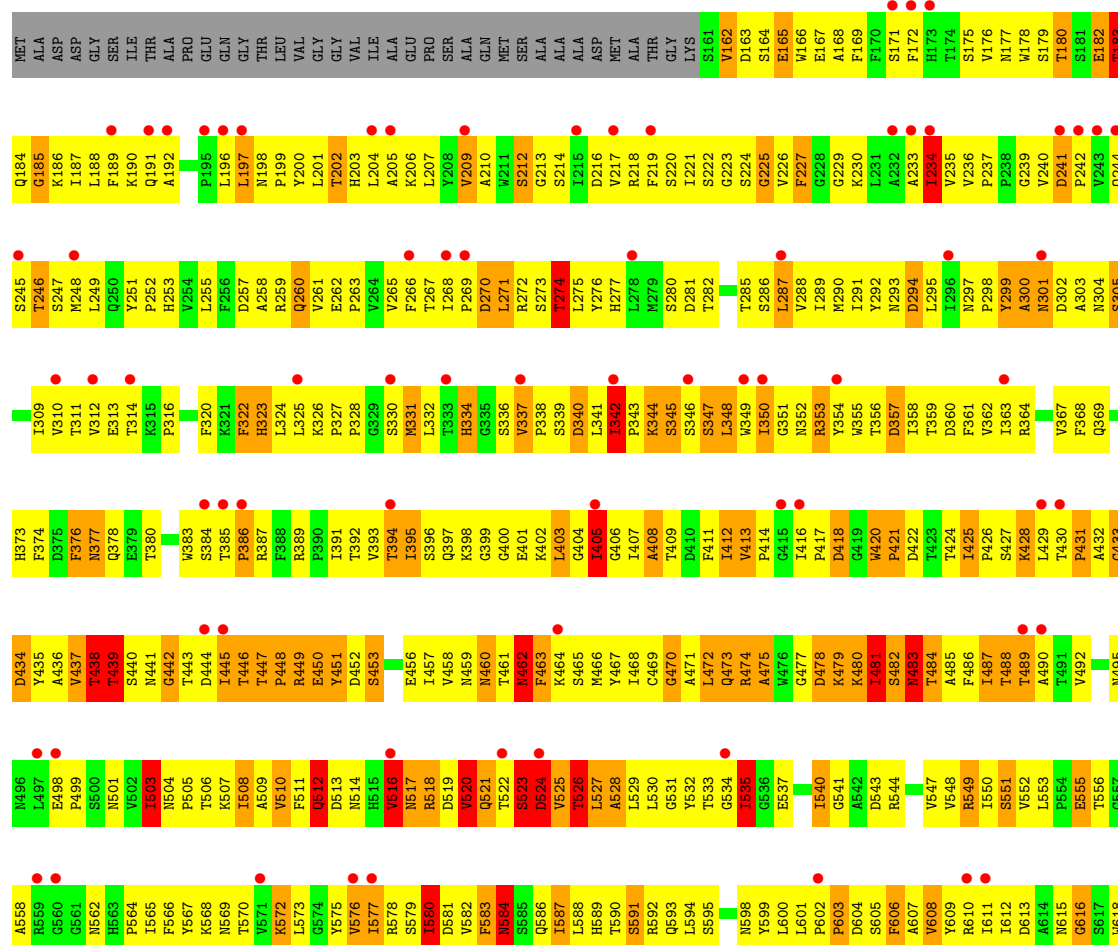
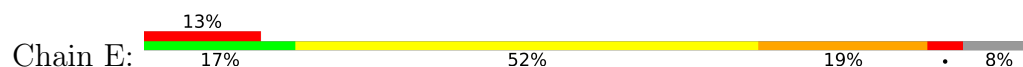


• Molecule 1: VP1

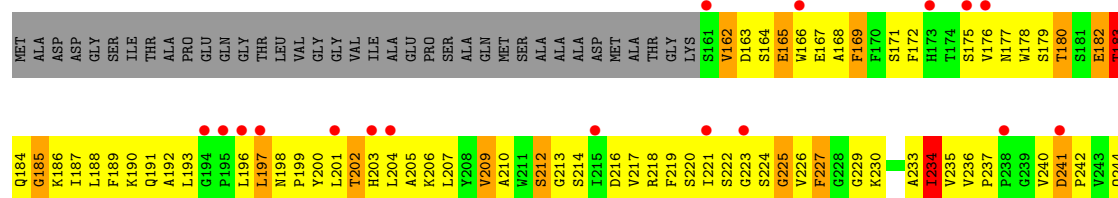
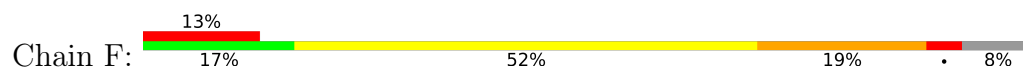




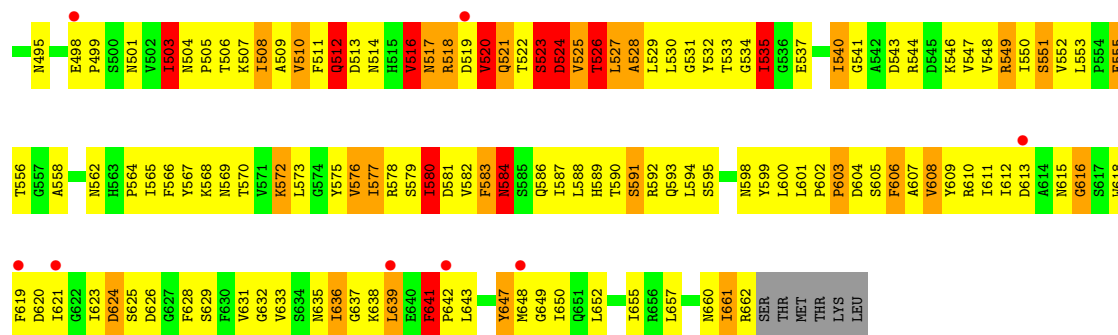
● Molecule 1: VP1



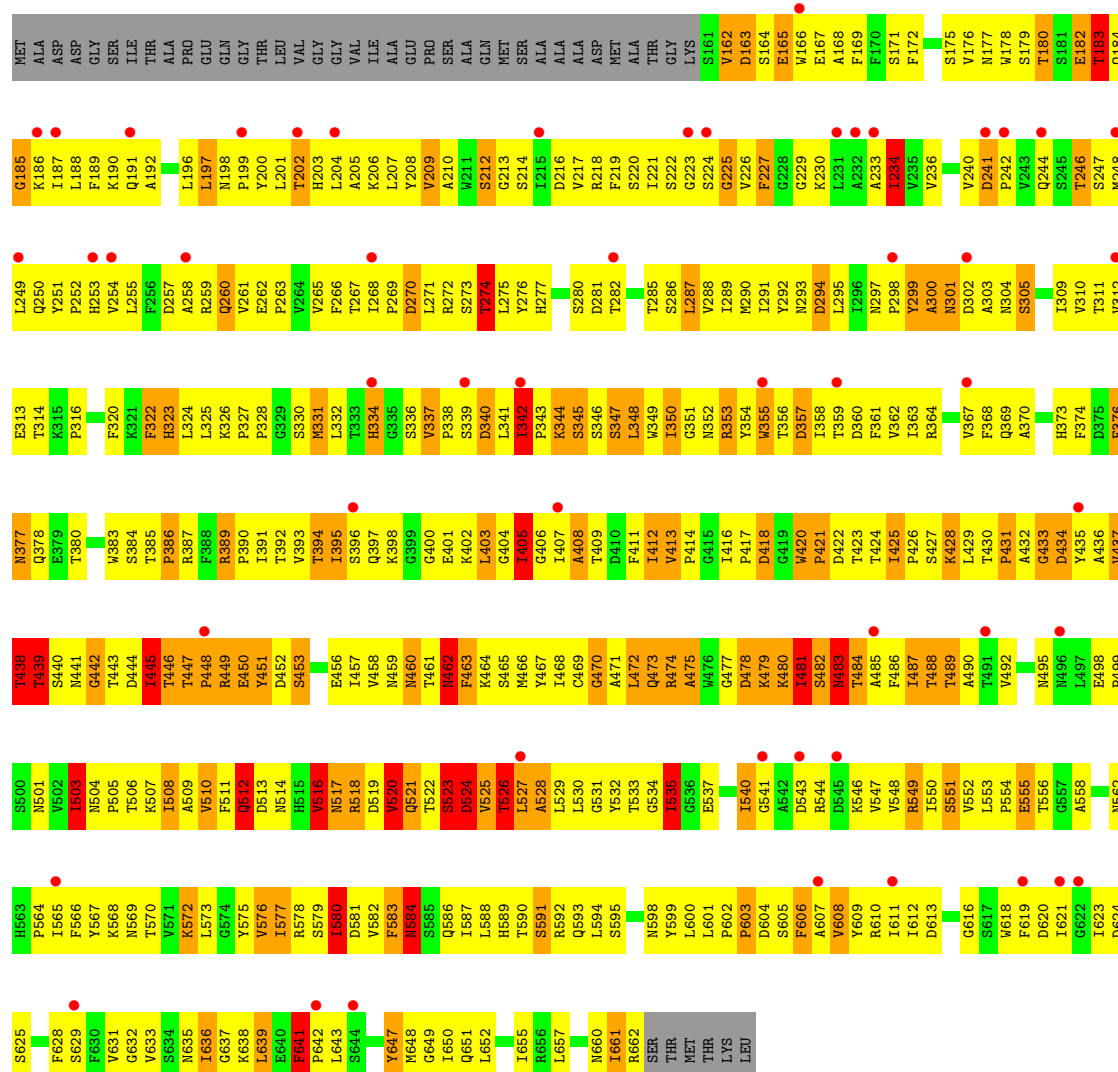
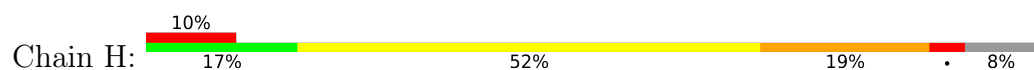
● Molecule 1: VP1



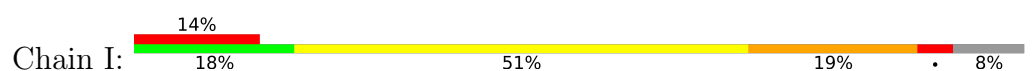


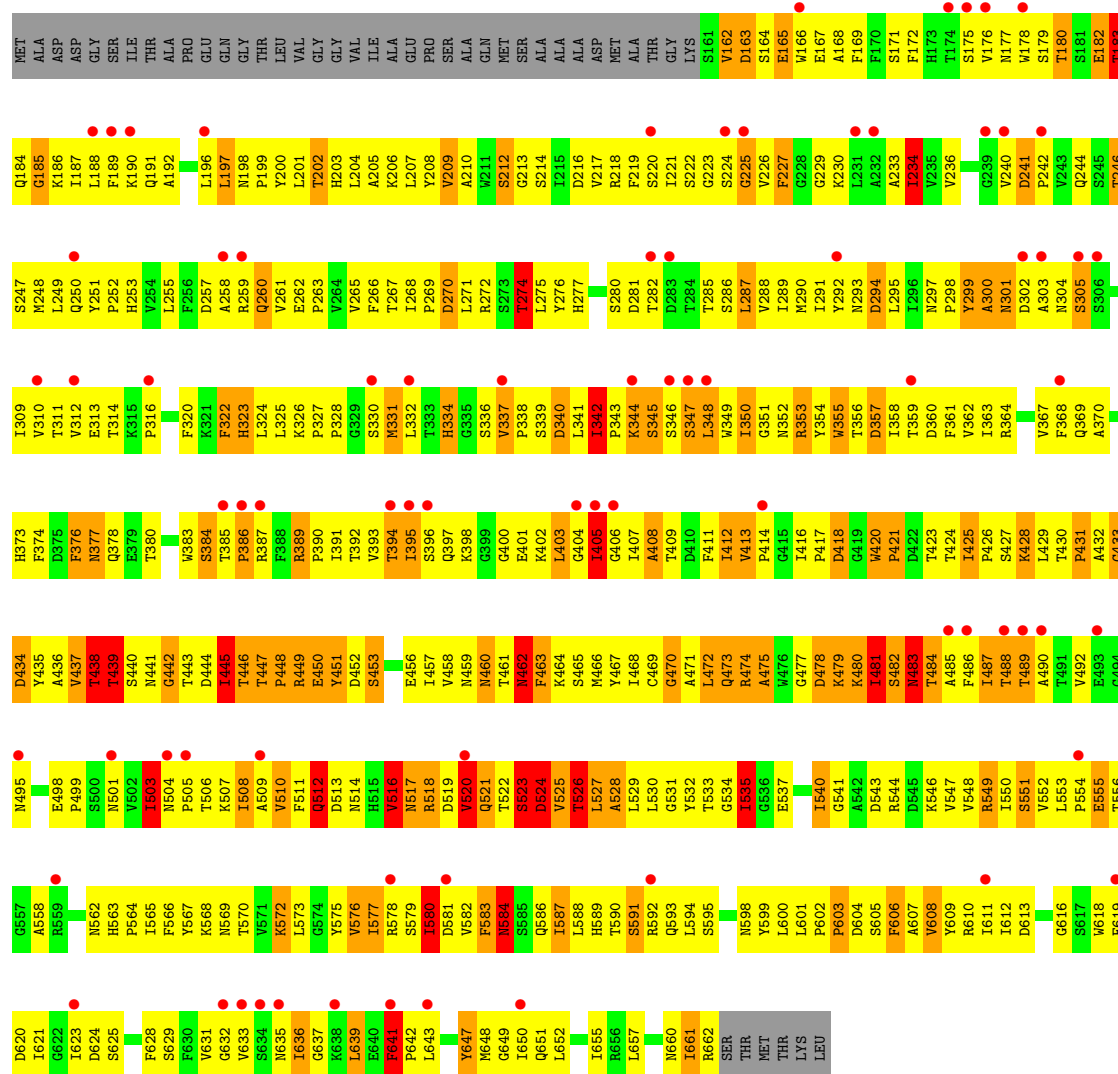


• Molecule 1: VP1

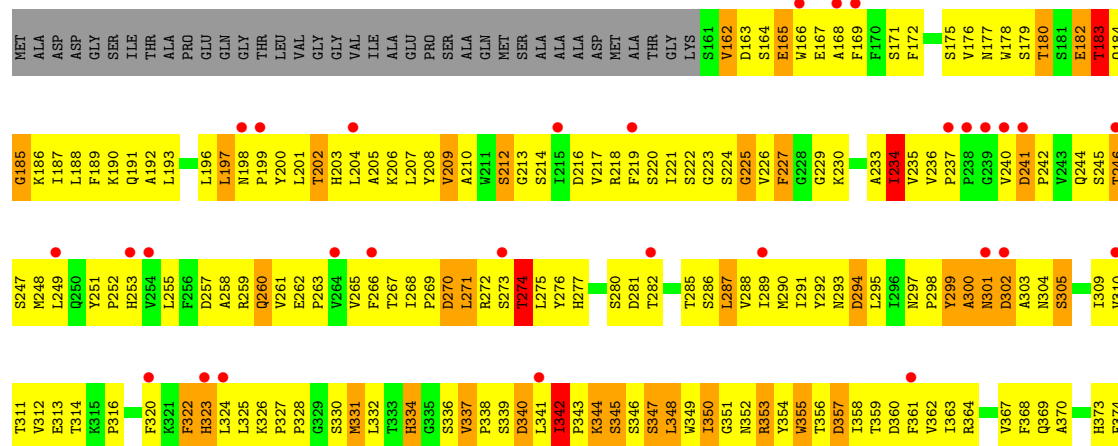
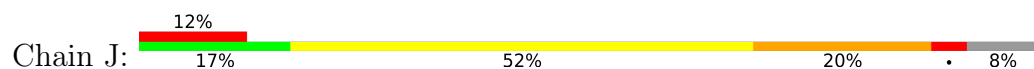


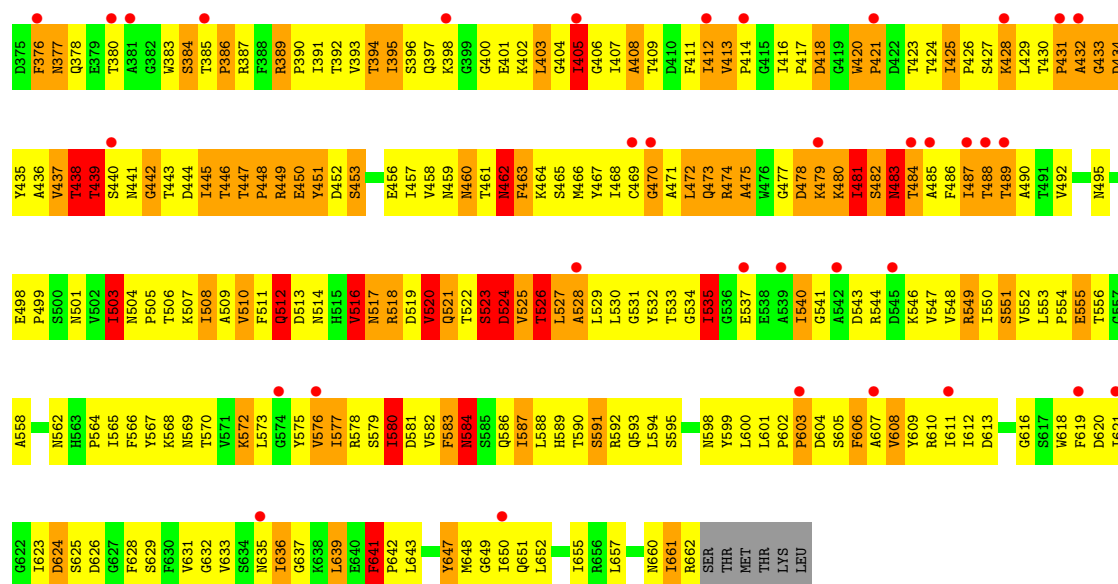
• Molecule 1: VP1



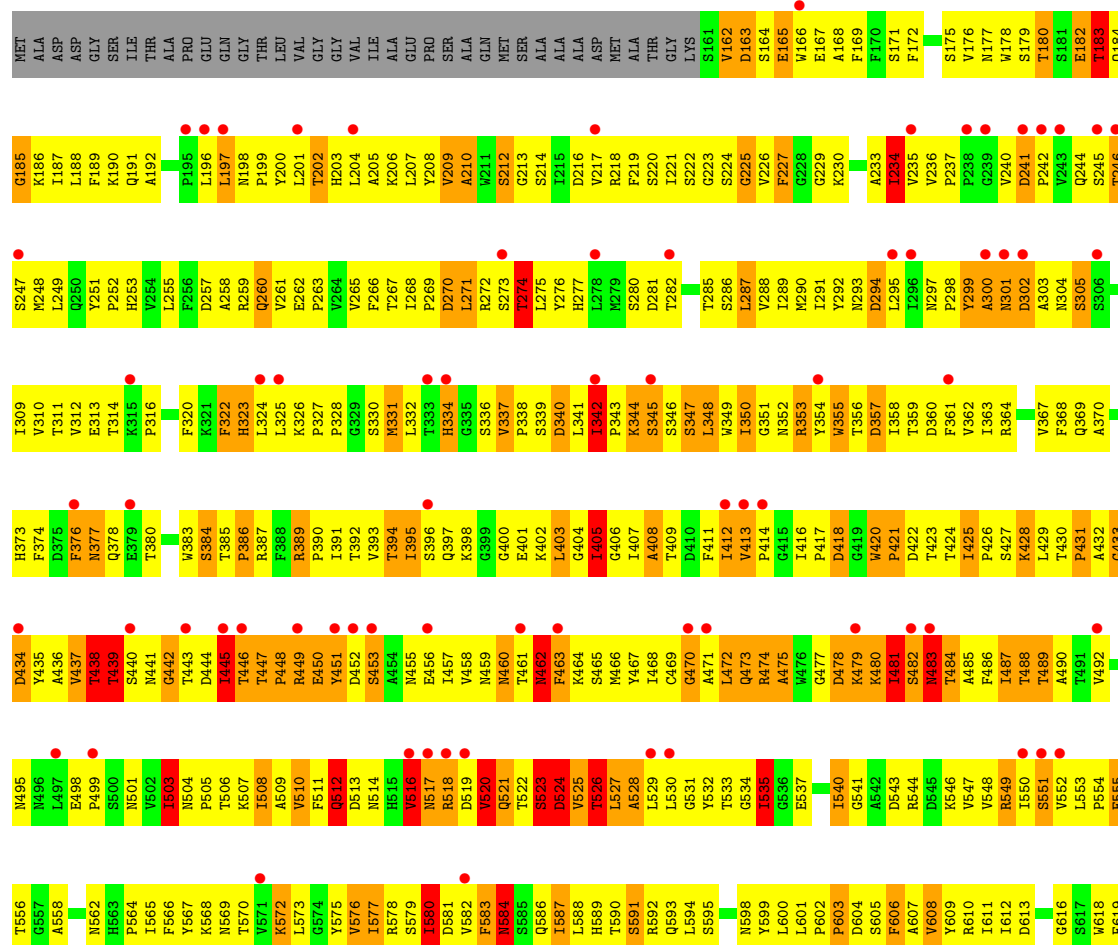
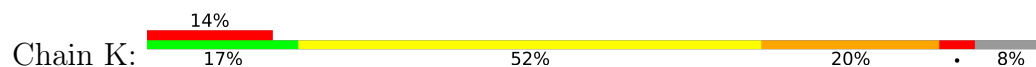


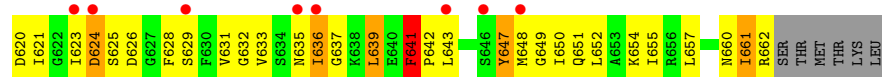
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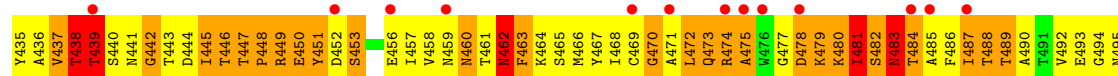
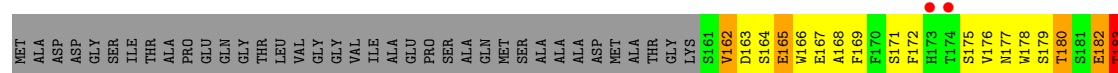
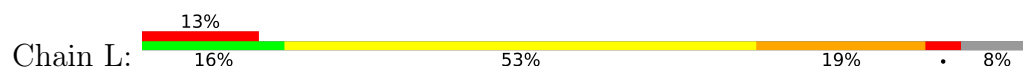


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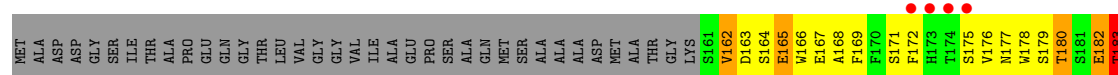
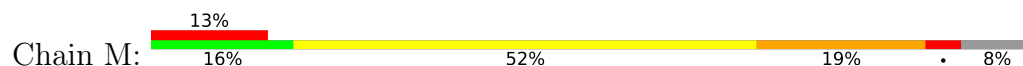


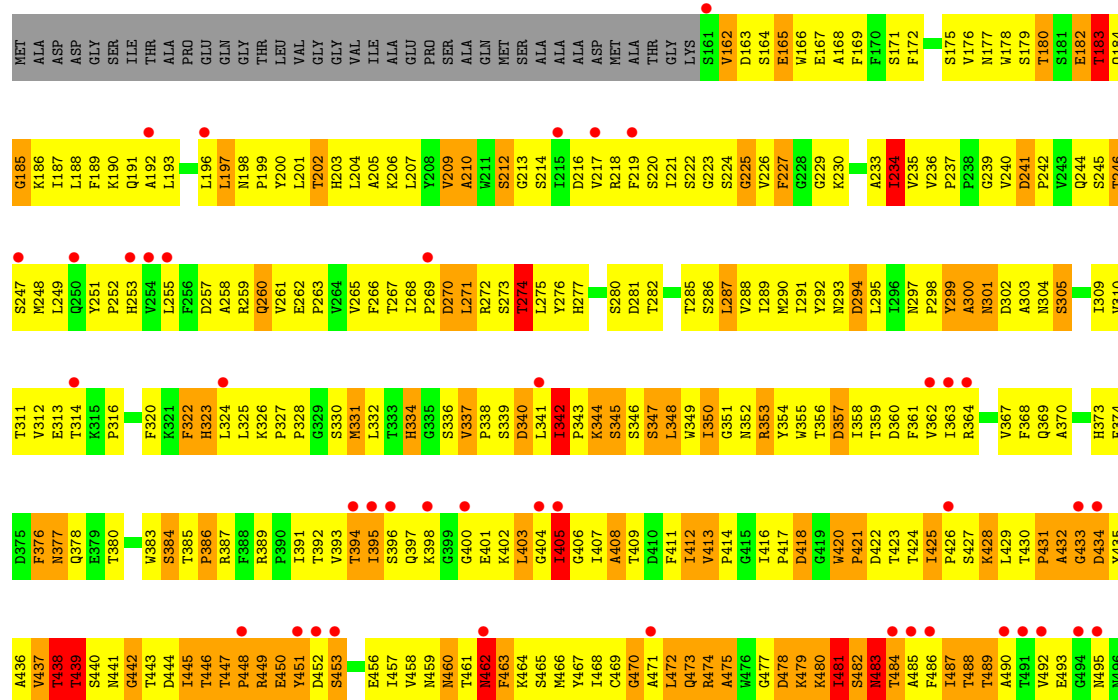


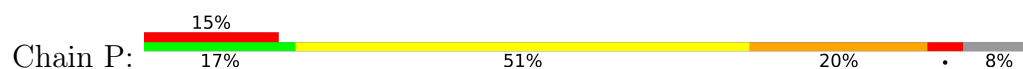
● Molecule 1: VP1

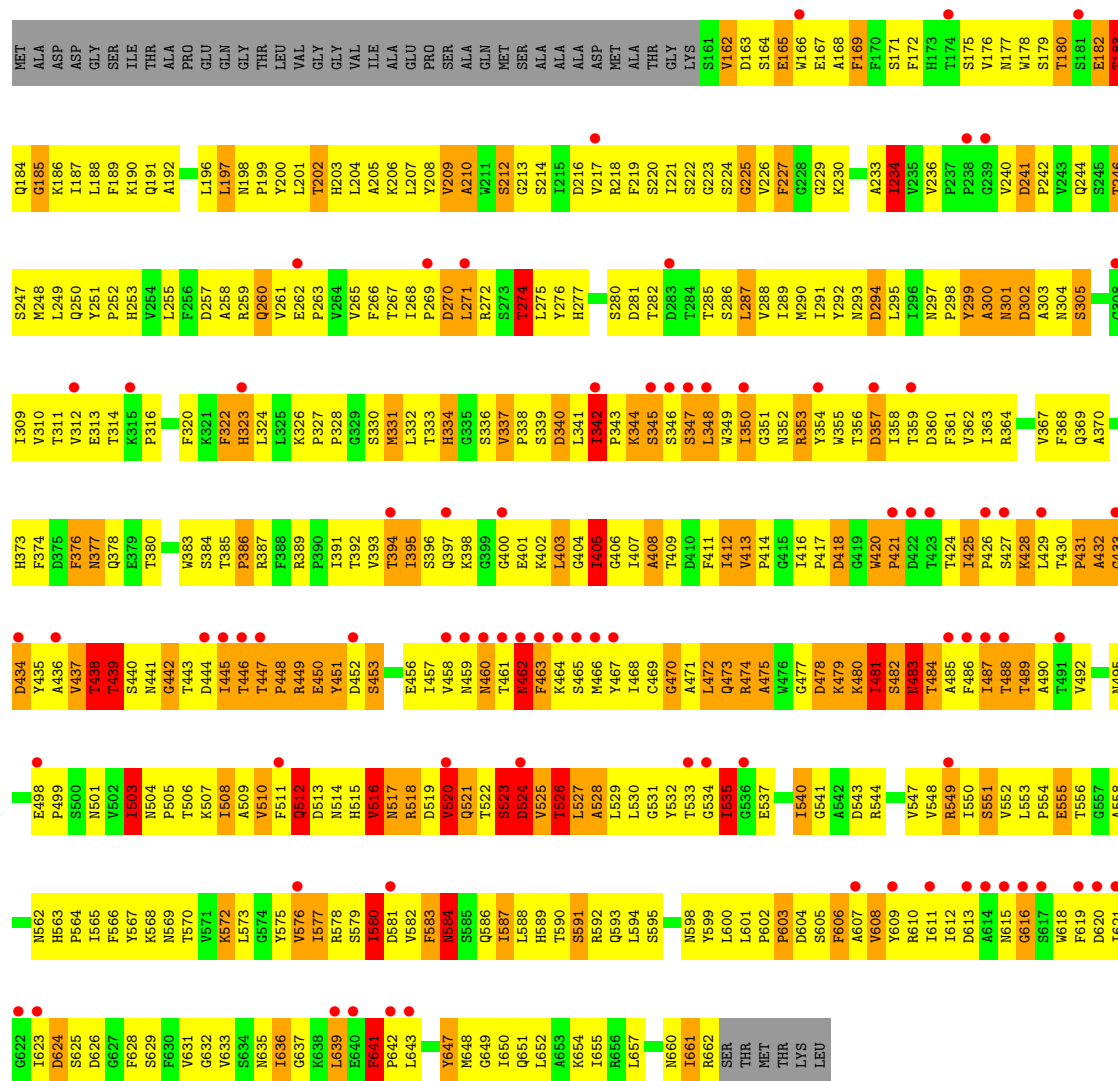


● Molecule 1: VP1

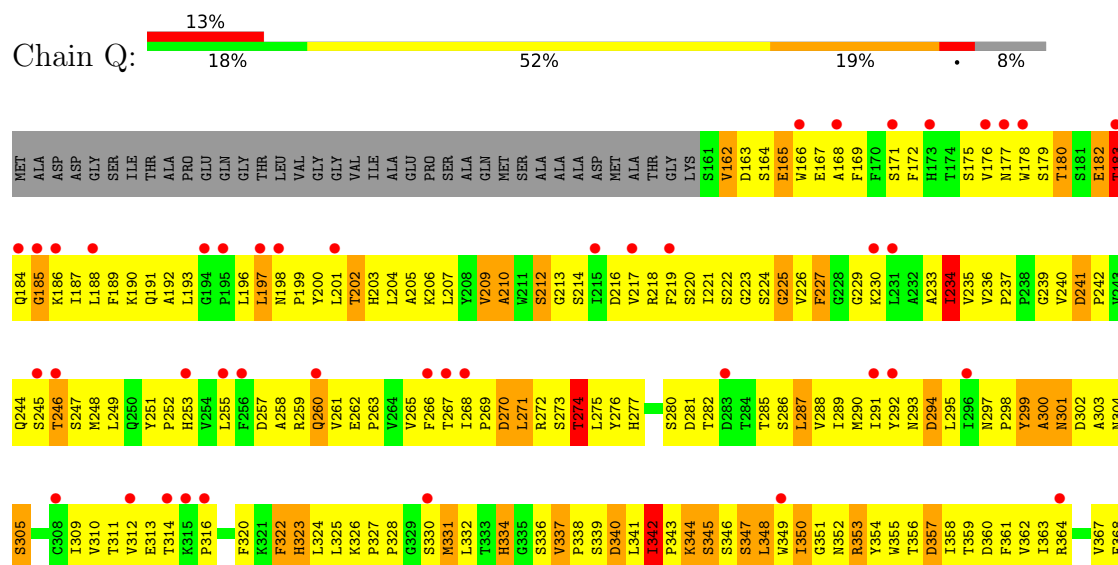


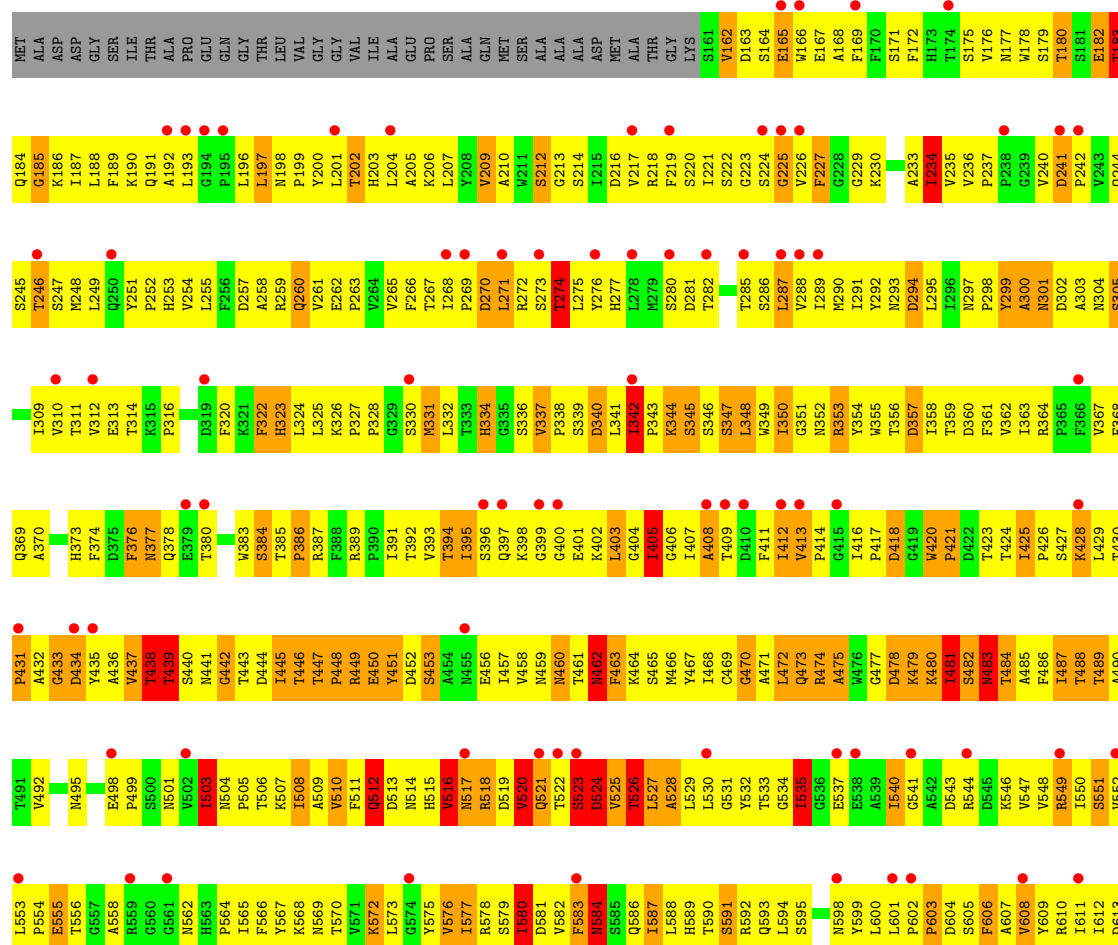


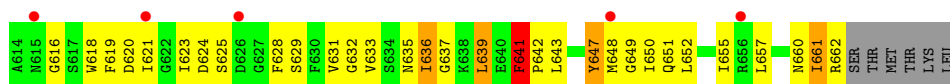




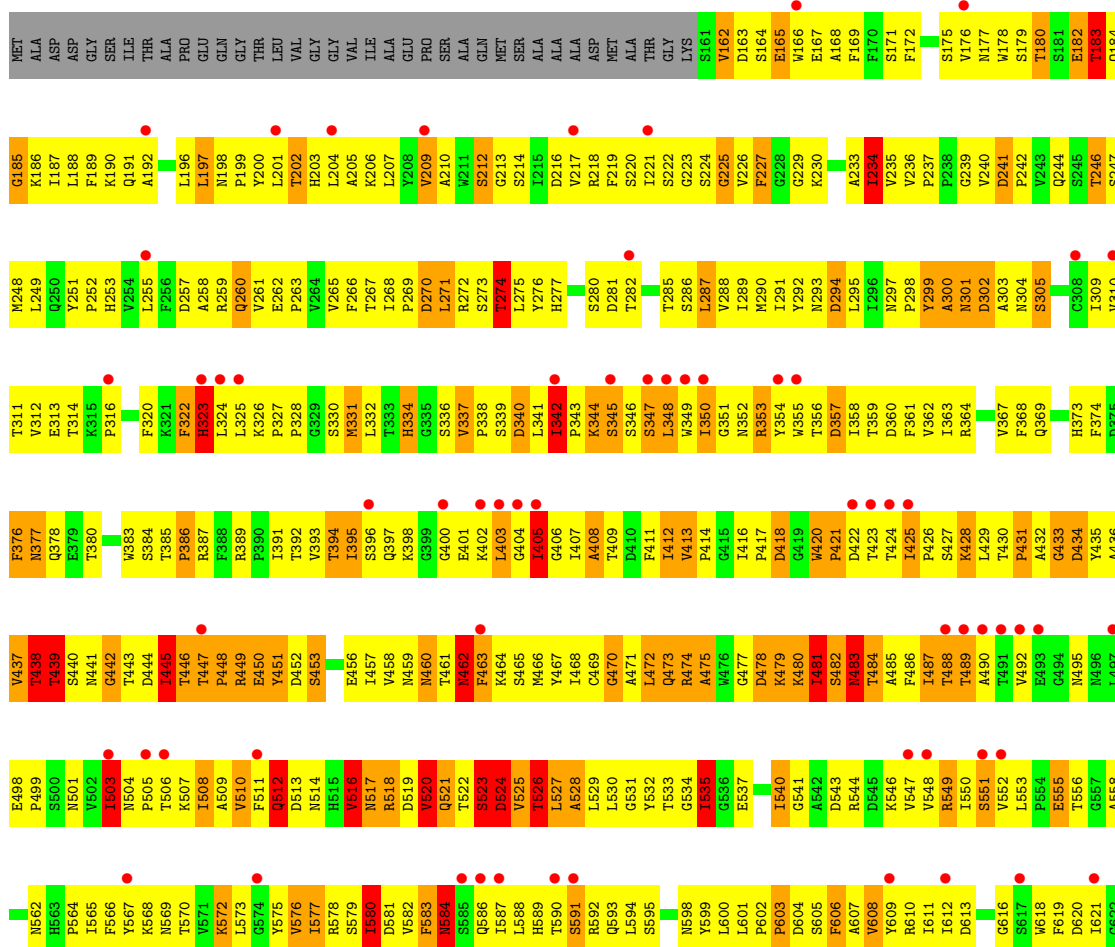
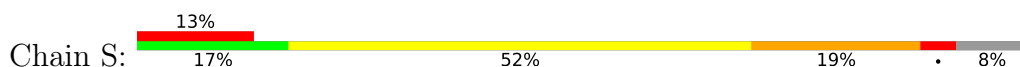
• Molecule 1: VP1



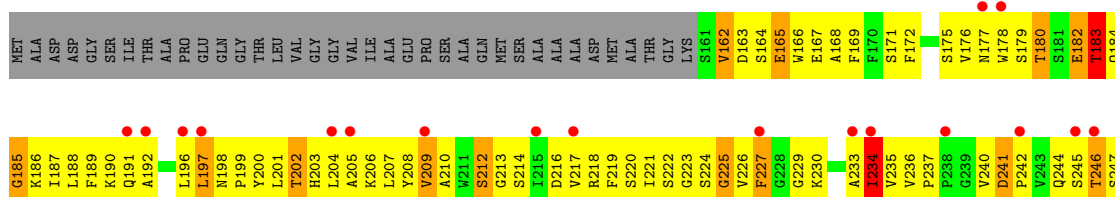
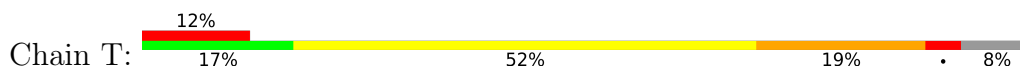


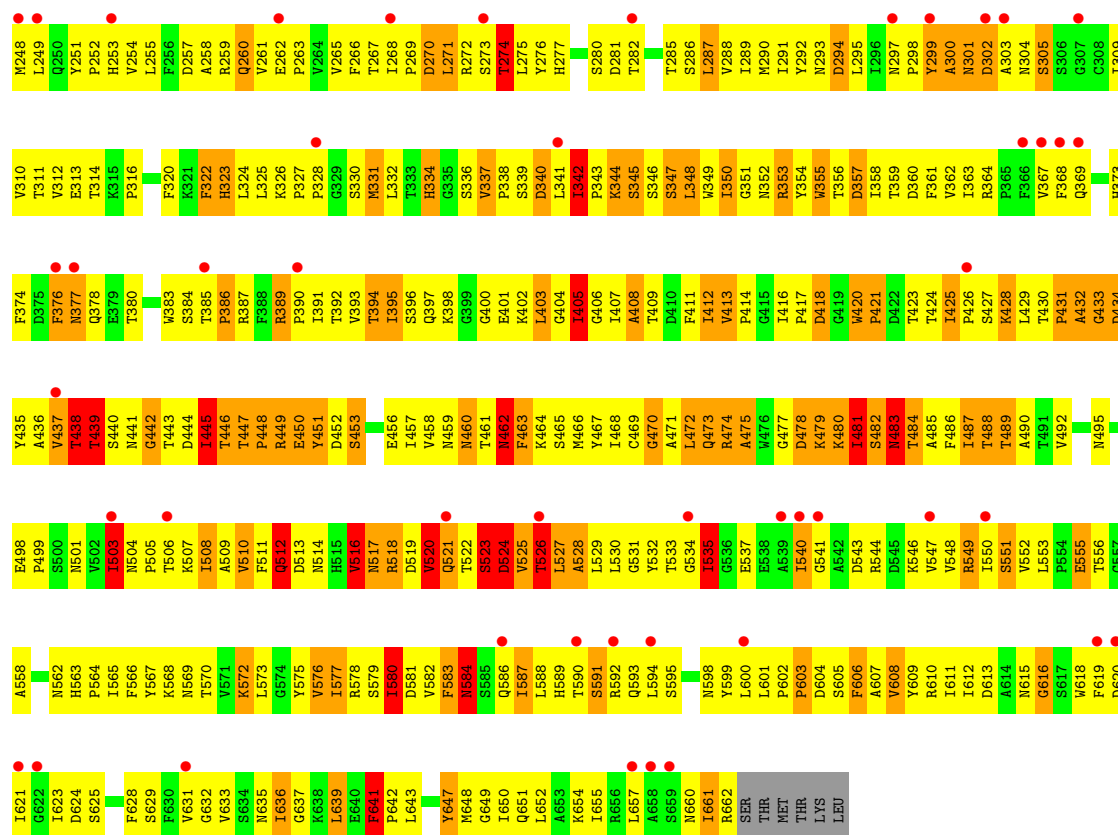


• Molecule 1: VP1



• Molecule 1: VP1





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	358.34Å 358.34Å 358.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	65.51 – 8.00 65.51 – 8.00	Depositor EDS
% Data completeness (in resolution range)	87.8 (65.51-8.00) 88.1 (65.51-8.00)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	0.24	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.41 (at 8.38Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.441 , 0.463 0.426 , 0.448	Depositor DCC
R_{free} test set	710 reflections (4.31%)	wwPDB-VP
Wilson B-factor (Å ²)	426.8	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 0.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.32$, $\langle L^2 \rangle = 0.16$	Xtriage
Estimated twinning fraction	0.108 for l,-k,h	Xtriage
F_o, F_c correlation	0.25	EDS
Total number of atoms	77840	wwPDB-VP
Average B, all atoms (Å ²)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.33% 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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.84	6/3991 (0.2%)	1.26	41/5446 (0.8%)
1	B	0.84	6/3991 (0.2%)	1.26	42/5446 (0.8%)
1	C	0.84	6/3991 (0.2%)	1.26	40/5446 (0.7%)
1	D	0.84	6/3991 (0.2%)	1.26	40/5446 (0.7%)
1	E	0.84	5/3991 (0.1%)	1.26	41/5446 (0.8%)
1	F	0.84	5/3991 (0.1%)	1.26	40/5446 (0.7%)
1	G	0.84	5/3991 (0.1%)	1.26	41/5446 (0.8%)
1	H	0.84	6/3991 (0.2%)	1.26	41/5446 (0.8%)
1	I	0.84	6/3991 (0.2%)	1.26	41/5446 (0.8%)
1	J	0.84	5/3991 (0.1%)	1.26	41/5446 (0.8%)
1	K	0.85	5/3991 (0.1%)	1.26	42/5446 (0.8%)
1	L	0.84	5/3991 (0.1%)	1.26	41/5446 (0.8%)
1	M	0.85	6/3991 (0.2%)	1.26	42/5446 (0.8%)
1	N	0.85	5/3991 (0.1%)	1.26	42/5446 (0.8%)
1	O	0.84	6/3991 (0.2%)	1.26	41/5446 (0.8%)
1	P	0.85	5/3991 (0.1%)	1.26	42/5446 (0.8%)
1	Q	0.84	5/3991 (0.1%)	1.26	42/5446 (0.8%)
1	R	0.84	5/3991 (0.1%)	1.26	41/5446 (0.8%)
1	S	0.84	6/3991 (0.2%)	1.26	39/5446 (0.7%)
1	T	0.84	6/3991 (0.2%)	1.26	41/5446 (0.8%)
All	All	0.84	110/79820 (0.1%)	1.26	821/108920 (0.8%)

The worst 5 of 110 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	520	VAL	CA-CB	7.65	1.63	1.54
1	P	520	VAL	CA-CB	7.65	1.63	1.54
1	H	520	VAL	CA-CB	7.63	1.63	1.54
1	K	520	VAL	CA-CB	7.62	1.63	1.54
1	O	520	VAL	CA-CB	7.61	1.63	1.54

The worst 5 of 821 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	512	GLN	N-CA-C	11.68	123.17	108.45
1	T	512	GLN	N-CA-C	11.66	123.15	108.45
1	L	512	GLN	N-CA-C	11.64	123.12	108.45
1	S	512	GLN	N-CA-C	11.64	123.12	108.45
1	F	512	GLN	N-CA-C	11.64	123.12	108.45

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3892	0	3823	949	5
1	B	3892	0	3823	944	0
1	C	3892	0	3825	713	207
1	D	3892	0	3823	951	3
1	E	3892	0	3824	866	88
1	F	3892	0	3823	951	8
1	G	3892	0	3825	715	143
1	H	3892	0	3825	709	124
1	I	3892	0	3825	714	88
1	J	3892	0	3824	799	91
1	K	3892	0	3824	801	104
1	L	3892	0	3823	951	38
1	M	3892	0	3824	805	123
1	N	3892	0	3824	862	115
1	O	3892	0	3825	709	152
1	P	3892	0	3825	724	149
1	Q	3892	0	3824	879	85
1	R	3892	0	3823	945	14
1	S	3892	0	3824	863	82
1	T	3892	0	3824	794	85
All	All	77840	0	76480	14569	928

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 94.

The worst 5 of 14569 close contacts within the same asymmetric unit are listed below, sorted by

their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:165:GLU:CD	1:R:325:LEU:HD22	1.20	1.63
1:A:330:SER:C	1:L:240:VAL:HG11	1.21	1.62
1:B:325:LEU:HD22	1:D:165:GLU:CG	1.29	1.62
1:B:325:LEU:HD22	1:D:165:GLU:CD	1.20	1.62
1:Q:325:LEU:HD22	1:R:165:GLU:CG	1.29	1.61

The worst 5 of 928 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:493:GLU:O	1:C:518:ARG:CD[7_564]	0.17	2.03
1:G:251:TYR:CE1	1:M:327:PRO:O[9_555]	0.34	1.86
1:R:435:TYR:CD1	1:R:519:ASP:OD1[11_455]	0.35	1.85
1:O:251:TYR:CE1	1:T:327:PRO:O[5_555]	0.38	1.82
1:H:272:ARG:O	1:H:276:TYR:CE1[9_555]	0.40	1.80

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	498/545 (91%)	316 (64%)	115 (23%)	67 (14%)	0	4
1	B	498/545 (91%)	317 (64%)	114 (23%)	67 (14%)	0	4
1	C	498/545 (91%)	318 (64%)	113 (23%)	67 (14%)	0	4
1	D	498/545 (91%)	316 (64%)	115 (23%)	67 (14%)	0	4
1	E	498/545 (91%)	317 (64%)	114 (23%)	67 (14%)	0	4
1	F	498/545 (91%)	317 (64%)	114 (23%)	67 (14%)	0	4
1	G	498/545 (91%)	317 (64%)	114 (23%)	67 (14%)	0	4
1	H	498/545 (91%)	318 (64%)	113 (23%)	67 (14%)	0	4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	I	498/545 (91%)	316 (64%)	115 (23%)	67 (14%)	0	4
1	J	498/545 (91%)	317 (64%)	114 (23%)	67 (14%)	0	4
1	K	498/545 (91%)	318 (64%)	113 (23%)	67 (14%)	0	4
1	L	498/545 (91%)	316 (64%)	115 (23%)	67 (14%)	0	4
1	M	498/545 (91%)	316 (64%)	115 (23%)	67 (14%)	0	4
1	N	498/545 (91%)	318 (64%)	113 (23%)	67 (14%)	0	4
1	O	498/545 (91%)	317 (64%)	114 (23%)	67 (14%)	0	4
1	P	498/545 (91%)	318 (64%)	113 (23%)	67 (14%)	0	4
1	Q	498/545 (91%)	317 (64%)	114 (23%)	67 (14%)	0	4
1	R	498/545 (91%)	317 (64%)	114 (23%)	67 (14%)	0	4
1	S	498/545 (91%)	318 (64%)	113 (23%)	67 (14%)	0	4
1	T	498/545 (91%)	317 (64%)	114 (23%)	67 (14%)	0	4
All	All	9960/10900 (91%)	6341 (64%)	2279 (23%)	1340 (14%)	0	4

5 of 1340 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	294	ASP
1	A	300	ALA
1	A	301	ASN
1	A	303	ALA
1	A	305	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	A	434/464 (94%)	367 (85%)	67 (15%)	2	12
1	B	434/464 (94%)	368 (85%)	66 (15%)	3	12
1	C	434/464 (94%)	368 (85%)	66 (15%)	3	12
1	D	434/464 (94%)	368 (85%)	66 (15%)	3	12

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	434/464 (94%)	368 (85%)	66 (15%)	3	12
1	F	434/464 (94%)	367 (85%)	67 (15%)	2	12
1	G	434/464 (94%)	368 (85%)	66 (15%)	3	12
1	H	434/464 (94%)	368 (85%)	66 (15%)	3	12
1	I	434/464 (94%)	368 (85%)	66 (15%)	3	12
1	J	434/464 (94%)	368 (85%)	66 (15%)	3	12
1	K	434/464 (94%)	368 (85%)	66 (15%)	3	12
1	L	434/464 (94%)	368 (85%)	66 (15%)	3	12
1	M	434/464 (94%)	368 (85%)	66 (15%)	3	12
1	N	434/464 (94%)	368 (85%)	66 (15%)	3	12
1	O	434/464 (94%)	368 (85%)	66 (15%)	3	12
1	P	434/464 (94%)	367 (85%)	67 (15%)	2	12
1	Q	434/464 (94%)	368 (85%)	66 (15%)	3	12
1	R	434/464 (94%)	368 (85%)	66 (15%)	3	12
1	S	434/464 (94%)	368 (85%)	66 (15%)	3	12
1	T	434/464 (94%)	368 (85%)	66 (15%)	3	12
All	All	8680/9280 (94%)	7357 (85%)	1323 (15%)	3	12

5 of 1323 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	O	163	ASP
1	R	348	LEU
1	O	403	LEU
1	N	647	TYR
1	P	523	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 290 such sidechains are listed below:

Mol	Chain	Res	Type
1	Q	244	GLN
1	T	569	ASN
1	Q	462	ASN
1	S	191	GLN
1	G	514	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1
1	B	1
1	C	1
1	D	1
1	E	1
1	F	1
1	G	1
1	H	1
1	I	1
1	J	1
1	K	1
1	L	1
1	M	1
1	N	1
1	O	1
1	P	1

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Mol	Chain	Number of breaks
1	Q	1
1	R	1
1	S	1
1	T	1

The worst 5 of 20 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	330:SER	C	331:MET	N	3.54
1	B	330:SER	C	331:MET	N	3.54
1	C	330:SER	C	331:MET	N	3.54
1	D	330:SER	C	331:MET	N	3.54
1	E	330:SER	C	331:MET	N	3.54

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2	OWAB(Å ²)	Q < 0.9
1	A	502/545 (92%)	0.64	72 (14%) 6 14	95, 95, 95, 95	0
1	B	502/545 (92%)	0.64	68 (13%) 7 15	95, 95, 95, 95	0
1	C	502/545 (92%)	0.80	80 (15%) 5 13	95, 95, 95, 95	0
1	D	502/545 (92%)	0.58	73 (14%) 6 14	95, 95, 95, 95	0
1	E	502/545 (92%)	0.74	72 (14%) 6 14	95, 95, 95, 95	0
1	F	502/545 (92%)	0.65	69 (13%) 6 15	95, 95, 95, 95	0
1	G	502/545 (92%)	0.58	67 (13%) 7 15	95, 95, 95, 95	0
1	H	502/545 (92%)	0.42	52 (10%) 11 19	95, 95, 95, 95	0
1	I	502/545 (92%)	0.70	77 (15%) 5 14	95, 95, 95, 95	0
1	J	502/545 (92%)	0.58	65 (12%) 7 16	95, 95, 95, 95	0
1	K	502/545 (92%)	0.75	79 (15%) 5 13	95, 95, 95, 95	0
1	L	502/545 (92%)	0.65	73 (14%) 6 14	95, 95, 95, 95	0
1	M	502/545 (92%)	0.54	70 (13%) 6 15	95, 95, 95, 95	0
1	N	502/545 (92%)	0.75	65 (12%) 7 16	95, 95, 95, 95	0
1	O	502/545 (92%)	0.56	72 (14%) 6 14	95, 95, 95, 95	0
1	P	502/545 (92%)	0.92	82 (16%) 4 12	95, 95, 95, 95	0
1	Q	502/545 (92%)	0.64	71 (14%) 6 15	95, 95, 95, 95	0
1	R	502/545 (92%)	0.71	83 (16%) 4 12	95, 95, 95, 95	0
1	S	502/545 (92%)	0.82	69 (13%) 6 15	95, 95, 95, 95	0
1	T	502/545 (92%)	0.60	65 (12%) 7 16	95, 95, 95, 95	0
All	All	10040/10900 (92%)	0.66	1424 (14%) 6 15	95, 95, 95, 95	0

The worst 5 of 1424 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	S	404	GLY	31.3
1	N	492	VAL	24.2
1	P	463	PHE	20.6
1	T	273	SER	19.7
1	L	522	THR	19.4

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.