



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 11:10 AM UTC

PDB ID : 7NXQ / pdb_00007nxq
Title : Structure of the pentameric C-terminal domain of the capsid protein from Kaposi's sarcoma-associated herpesvirus (KSHV)
Authors : Naniima, P.; Legrand, P.; Krey, T.
Deposited on : 2021-03-19
Resolution : 2.42 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

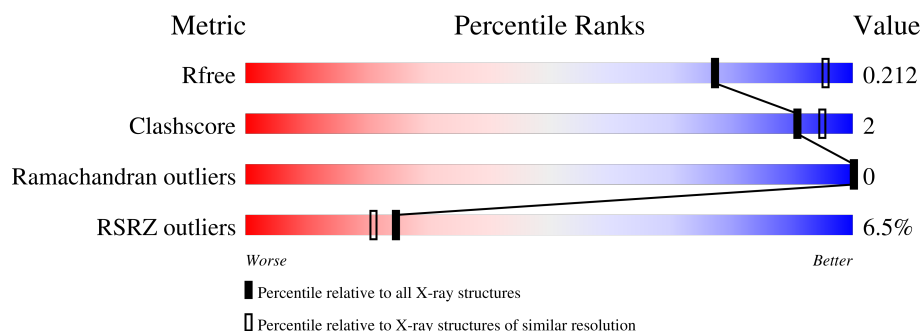
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.42 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	6062 (2.44-2.40)
Clashscore	190562	6562 (2.44-2.40)
Ramachandran outliers	187476	6481 (2.44-2.40)
RSRZ outliers	180081	6066 (2.44-2.40)

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	443	7% 89% 7%
1	B	443	4% 87% 5% 9%
1	C	443	5% 88% 5% 7%
1	D	443	6% 87% 9%
1	E	443	7% 87% 5% 8%
1	F	443	6% 86% 5% 9%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	G	443	8% 87% 5% 9%
1	H	443	5% 87% • 9%
1	I	443	6% 86% 5% 9%
1	J	443	6% 87% • 9%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 33920 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 Capsid vertex component 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	412	Total	C	N	O	S	0	0	0
			3230	2086	551	581	12			
1	B	404	Total	C	N	O	S	0	0	0
			3174	2051	541	570	12			
1	C	411	Total	C	N	O	S	0	0	0
			3221	2080	549	580	12			
1	D	404	Total	C	N	O	S	0	0	0
			3174	2052	541	569	12			
1	E	406	Total	C	N	O	S	0	0	0
			3189	2060	544	573	12			
1	F	405	Total	C	N	O	S	0	0	0
			3188	2060	545	571	12			
1	G	405	Total	C	N	O	S	0	0	0
			3181	2056	542	571	12			
1	H	403	Total	C	N	O	S	0	0	0
			3167	2047	540	568	12			
1	I	404	Total	C	N	O	S	0	0	0
			3176	2052	542	570	12			
1	J	402	Total	C	N	O	S	0	0	0
			3160	2043	538	567	12			

There are 160 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	122	MET	-	initiating methionine	UNP Q76RI7
A	550	PRO	-	expression tag	UNP Q76RI7
A	551	ALA	-	expression tag	UNP Q76RI7
A	552	ALA	-	expression tag	UNP Q76RI7
A	553	ALA	-	expression tag	UNP Q76RI7
A	554	LEU	-	expression tag	UNP Q76RI7
A	555	GLU	-	expression tag	UNP Q76RI7
A	556	HIS	-	expression tag	UNP Q76RI7
A	557	HIS	-	expression tag	UNP Q76RI7

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	558	HIS	-	expression tag	UNP Q76RI7
A	559	HIS	-	expression tag	UNP Q76RI7
A	560	HIS	-	expression tag	UNP Q76RI7
A	561	HIS	-	expression tag	UNP Q76RI7
A	562	HIS	-	expression tag	UNP Q76RI7
A	563	HIS	-	expression tag	UNP Q76RI7
A	564	HIS	-	expression tag	UNP Q76RI7
B	122	MET	-	initiating methionine	UNP Q76RI7
B	550	PRO	-	expression tag	UNP Q76RI7
B	551	ALA	-	expression tag	UNP Q76RI7
B	552	ALA	-	expression tag	UNP Q76RI7
B	553	ALA	-	expression tag	UNP Q76RI7
B	554	LEU	-	expression tag	UNP Q76RI7
B	555	GLU	-	expression tag	UNP Q76RI7
B	556	HIS	-	expression tag	UNP Q76RI7
B	557	HIS	-	expression tag	UNP Q76RI7
B	558	HIS	-	expression tag	UNP Q76RI7
B	559	HIS	-	expression tag	UNP Q76RI7
B	560	HIS	-	expression tag	UNP Q76RI7
B	561	HIS	-	expression tag	UNP Q76RI7
B	562	HIS	-	expression tag	UNP Q76RI7
B	563	HIS	-	expression tag	UNP Q76RI7
B	564	HIS	-	expression tag	UNP Q76RI7
C	122	MET	-	initiating methionine	UNP Q76RI7
C	550	PRO	-	expression tag	UNP Q76RI7
C	551	ALA	-	expression tag	UNP Q76RI7
C	552	ALA	-	expression tag	UNP Q76RI7
C	553	ALA	-	expression tag	UNP Q76RI7
C	554	LEU	-	expression tag	UNP Q76RI7
C	555	GLU	-	expression tag	UNP Q76RI7
C	556	HIS	-	expression tag	UNP Q76RI7
C	557	HIS	-	expression tag	UNP Q76RI7
C	558	HIS	-	expression tag	UNP Q76RI7
C	559	HIS	-	expression tag	UNP Q76RI7
C	560	HIS	-	expression tag	UNP Q76RI7
C	561	HIS	-	expression tag	UNP Q76RI7
C	562	HIS	-	expression tag	UNP Q76RI7
C	563	HIS	-	expression tag	UNP Q76RI7
C	564	HIS	-	expression tag	UNP Q76RI7
D	122	MET	-	initiating methionine	UNP Q76RI7
D	550	PRO	-	expression tag	UNP Q76RI7
D	551	ALA	-	expression tag	UNP Q76RI7

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	552	ALA	-	expression tag	UNP Q76RI7
D	553	ALA	-	expression tag	UNP Q76RI7
D	554	LEU	-	expression tag	UNP Q76RI7
D	555	GLU	-	expression tag	UNP Q76RI7
D	556	HIS	-	expression tag	UNP Q76RI7
D	557	HIS	-	expression tag	UNP Q76RI7
D	558	HIS	-	expression tag	UNP Q76RI7
D	559	HIS	-	expression tag	UNP Q76RI7
D	560	HIS	-	expression tag	UNP Q76RI7
D	561	HIS	-	expression tag	UNP Q76RI7
D	562	HIS	-	expression tag	UNP Q76RI7
D	563	HIS	-	expression tag	UNP Q76RI7
D	564	HIS	-	expression tag	UNP Q76RI7
E	122	MET	-	initiating methionine	UNP Q76RI7
E	550	PRO	-	expression tag	UNP Q76RI7
E	551	ALA	-	expression tag	UNP Q76RI7
E	552	ALA	-	expression tag	UNP Q76RI7
E	553	ALA	-	expression tag	UNP Q76RI7
E	554	LEU	-	expression tag	UNP Q76RI7
E	555	GLU	-	expression tag	UNP Q76RI7
E	556	HIS	-	expression tag	UNP Q76RI7
E	557	HIS	-	expression tag	UNP Q76RI7
E	558	HIS	-	expression tag	UNP Q76RI7
E	559	HIS	-	expression tag	UNP Q76RI7
E	560	HIS	-	expression tag	UNP Q76RI7
E	561	HIS	-	expression tag	UNP Q76RI7
E	562	HIS	-	expression tag	UNP Q76RI7
E	563	HIS	-	expression tag	UNP Q76RI7
E	564	HIS	-	expression tag	UNP Q76RI7
F	122	MET	-	initiating methionine	UNP Q76RI7
F	550	PRO	-	expression tag	UNP Q76RI7
F	551	ALA	-	expression tag	UNP Q76RI7
F	552	ALA	-	expression tag	UNP Q76RI7
F	553	ALA	-	expression tag	UNP Q76RI7
F	554	LEU	-	expression tag	UNP Q76RI7
F	555	GLU	-	expression tag	UNP Q76RI7
F	556	HIS	-	expression tag	UNP Q76RI7
F	557	HIS	-	expression tag	UNP Q76RI7
F	558	HIS	-	expression tag	UNP Q76RI7
F	559	HIS	-	expression tag	UNP Q76RI7
F	560	HIS	-	expression tag	UNP Q76RI7
F	561	HIS	-	expression tag	UNP Q76RI7

Continued on next page...

Continued from previous page...

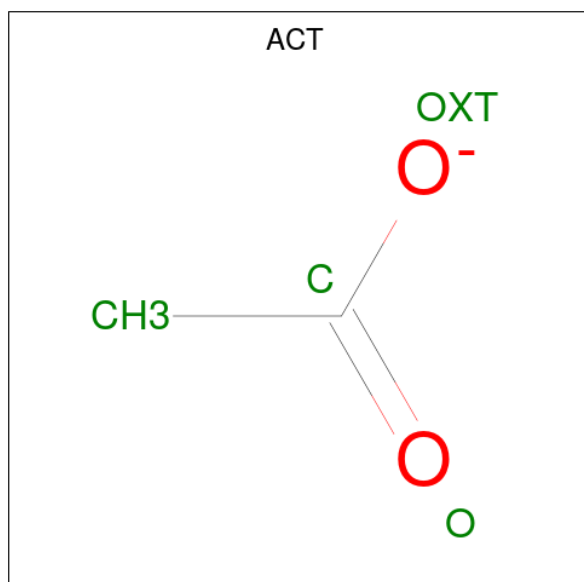
Chain	Residue	Modelled	Actual	Comment	Reference
F	562	HIS	-	expression tag	UNP Q76RI7
F	563	HIS	-	expression tag	UNP Q76RI7
F	564	HIS	-	expression tag	UNP Q76RI7
G	122	MET	-	initiating methionine	UNP Q76RI7
G	550	PRO	-	expression tag	UNP Q76RI7
G	551	ALA	-	expression tag	UNP Q76RI7
G	552	ALA	-	expression tag	UNP Q76RI7
G	553	ALA	-	expression tag	UNP Q76RI7
G	554	LEU	-	expression tag	UNP Q76RI7
G	555	GLU	-	expression tag	UNP Q76RI7
G	556	HIS	-	expression tag	UNP Q76RI7
G	557	HIS	-	expression tag	UNP Q76RI7
G	558	HIS	-	expression tag	UNP Q76RI7
G	559	HIS	-	expression tag	UNP Q76RI7
G	560	HIS	-	expression tag	UNP Q76RI7
G	561	HIS	-	expression tag	UNP Q76RI7
G	562	HIS	-	expression tag	UNP Q76RI7
G	563	HIS	-	expression tag	UNP Q76RI7
G	564	HIS	-	expression tag	UNP Q76RI7
H	122	MET	-	initiating methionine	UNP Q76RI7
H	550	PRO	-	expression tag	UNP Q76RI7
H	551	ALA	-	expression tag	UNP Q76RI7
H	552	ALA	-	expression tag	UNP Q76RI7
H	553	ALA	-	expression tag	UNP Q76RI7
H	554	LEU	-	expression tag	UNP Q76RI7
H	555	GLU	-	expression tag	UNP Q76RI7
H	556	HIS	-	expression tag	UNP Q76RI7
H	557	HIS	-	expression tag	UNP Q76RI7
H	558	HIS	-	expression tag	UNP Q76RI7
H	559	HIS	-	expression tag	UNP Q76RI7
H	560	HIS	-	expression tag	UNP Q76RI7
H	561	HIS	-	expression tag	UNP Q76RI7
H	562	HIS	-	expression tag	UNP Q76RI7
H	563	HIS	-	expression tag	UNP Q76RI7
H	564	HIS	-	expression tag	UNP Q76RI7
I	122	MET	-	initiating methionine	UNP Q76RI7
I	550	PRO	-	expression tag	UNP Q76RI7
I	551	ALA	-	expression tag	UNP Q76RI7
I	552	ALA	-	expression tag	UNP Q76RI7
I	553	ALA	-	expression tag	UNP Q76RI7
I	554	LEU	-	expression tag	UNP Q76RI7
I	555	GLU	-	expression tag	UNP Q76RI7

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
I	556	HIS	-	expression tag	UNP Q76RI7
I	557	HIS	-	expression tag	UNP Q76RI7
I	558	HIS	-	expression tag	UNP Q76RI7
I	559	HIS	-	expression tag	UNP Q76RI7
I	560	HIS	-	expression tag	UNP Q76RI7
I	561	HIS	-	expression tag	UNP Q76RI7
I	562	HIS	-	expression tag	UNP Q76RI7
I	563	HIS	-	expression tag	UNP Q76RI7
I	564	HIS	-	expression tag	UNP Q76RI7
J	122	MET	-	initiating methionine	UNP Q76RI7
J	550	PRO	-	expression tag	UNP Q76RI7
J	551	ALA	-	expression tag	UNP Q76RI7
J	552	ALA	-	expression tag	UNP Q76RI7
J	553	ALA	-	expression tag	UNP Q76RI7
J	554	LEU	-	expression tag	UNP Q76RI7
J	555	GLU	-	expression tag	UNP Q76RI7
J	556	HIS	-	expression tag	UNP Q76RI7
J	557	HIS	-	expression tag	UNP Q76RI7
J	558	HIS	-	expression tag	UNP Q76RI7
J	559	HIS	-	expression tag	UNP Q76RI7
J	560	HIS	-	expression tag	UNP Q76RI7
J	561	HIS	-	expression tag	UNP Q76RI7
J	562	HIS	-	expression tag	UNP Q76RI7
J	563	HIS	-	expression tag	UNP Q76RI7
J	564	HIS	-	expression tag	UNP Q76RI7

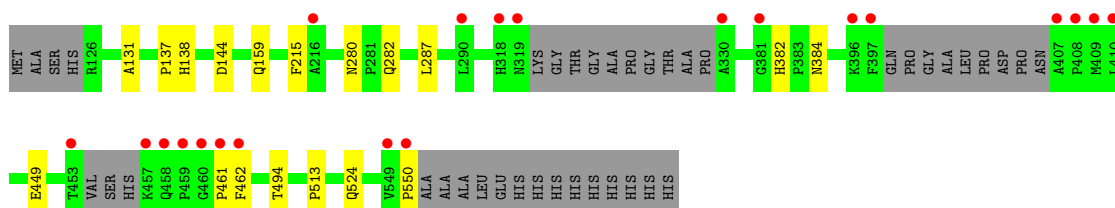
- Molecule 2 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



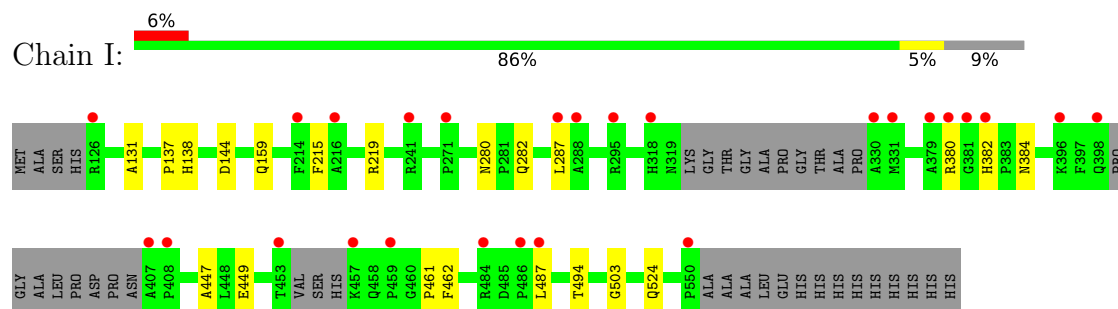
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 4 2 2	0	0
2	A	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0
2	B	1	Total C O 4 2 2	0	0
2	C	1	Total C O 4 2 2	0	0
2	C	1	Total C O 4 2 2	0	0
2	D	1	Total C O 4 2 2	0	0
2	D	1	Total C O 4 2 2	0	0
2	E	1	Total C O 4 2 2	0	0
2	E	1	Total C O 4 2 2	0	0
2	F	1	Total C O 4 2 2	0	0
2	F	1	Total C O 4 2 2	0	0
2	G	1	Total C O 4 2 2	0	0
2	G	1	Total C O 4 2 2	0	0
2	H	1	Total C O 4 2 2	0	0
2	H	1	Total C O 4 2 2	0	0
2	I	1	Total C O 4 2 2	0	0
2	I	1	Total C O 4 2 2	0	0
2	J	1	Total C O 4 2 2	0	0
2	J	1	Total C O 4 2 2	0	0

- Molecule 3 is water.

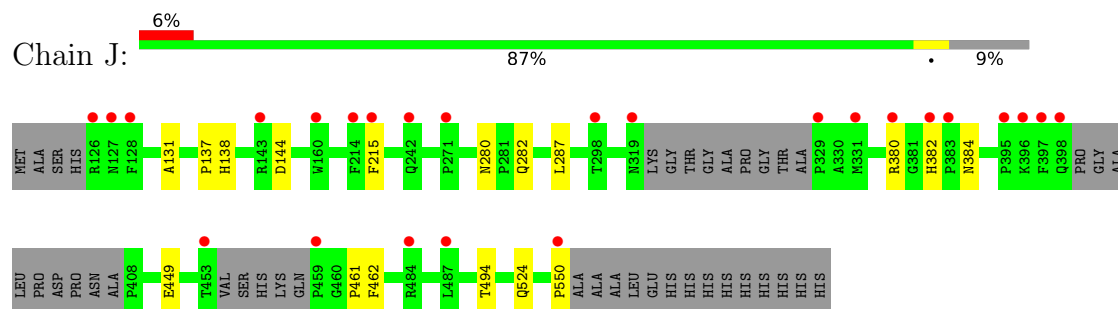
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	254	Total 254	O 254	0	0
3	B	213	Total 213	O 213	0	0
3	C	229	Total 229	O 229	0	0
3	D	193	Total 193	O 193	0	0
3	E	154	Total 154	O 154	0	0
3	F	211	Total 211	O 211	0	0
3	G	185	Total 185	O 185	0	0
3	H	158	Total 158	O 158	0	0
3	I	199	Total 199	O 199	0	0
3	J	184	Total 184	O 184	0	0



● Molecule 1: Capsid vertex component 2



● Molecule 1: Capsid vertex component 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	95.51Å 239.14Å 264.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.36 – 2.42 48.36 – 2.42	Depositor EDS
% Data completeness (in resolution range)	75.8 (48.36-2.42) 75.7 (48.36-2.42)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.80 (at 2.42Å)	Xtriage
Refinement program	BUSTER 2.10.4	Depositor
R, R_{free}	0.207 , 0.235 (Not available) , 0.212	Depositor DCC
R_{free} test set	8712 reflections (3.76%)	wwPDB-VP
Wilson B-factor (Å ²)	48.7	Xtriage
Anisotropy	0.082	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 61.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	33920	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.42% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.61	0/3315	1.00	3/4514 (0.1%)
1	B	0.61	0/3256	0.99	4/4431 (0.1%)
1	C	0.61	0/3306	0.99	3/4503 (0.1%)
1	D	0.59	0/3256	0.98	3/4429 (0.1%)
1	E	0.59	0/3272	0.98	4/4453 (0.1%)
1	F	0.59	0/3271	1.00	3/4449 (0.1%)
1	G	0.59	0/3264	0.99	4/4442 (0.1%)
1	H	0.58	0/3248	0.99	4/4418 (0.1%)
1	I	0.59	0/3257	0.99	3/4430 (0.1%)
1	J	0.60	0/3242	0.99	3/4409 (0.1%)
All	All	0.60	0/32687	0.99	34/44478 (0.1%)

There are no bond length outliers.

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	462	PHE	CA-CB-CG	8.41	122.21	113.80
1	J	462	PHE	CA-CB-CG	7.77	121.57	113.80
1	E	462	PHE	CA-CB-CG	7.57	121.37	113.80
1	C	462	PHE	CA-CB-CG	7.54	121.33	113.80
1	D	462	PHE	CA-CB-CG	7.30	121.10	113.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3230	0	3232	18	0
1	B	3174	0	3175	16	0
1	C	3221	0	3219	16	0
1	D	3174	0	3181	14	0
1	E	3189	0	3189	14	0
1	F	3188	0	3191	14	0
1	G	3181	0	3183	15	0
1	H	3167	0	3173	10	0
1	I	3176	0	3181	17	0
1	J	3160	0	3165	9	0
2	A	8	0	6	0	0
2	B	8	0	6	0	0
2	C	8	0	6	0	0
2	D	8	0	6	0	0
2	E	8	0	6	0	0
2	F	8	0	6	0	0
2	G	8	0	6	0	0
2	H	8	0	6	0	0
2	I	8	0	6	0	0
2	J	8	0	6	0	0
3	A	254	0	0	0	0
3	B	213	0	0	0	0
3	C	229	0	0	0	0
3	D	193	0	0	0	0
3	E	154	0	0	1	0
3	F	211	0	0	1	0
3	G	185	0	0	0	0
3	H	158	0	0	0	0
3	I	199	0	0	1	0
3	J	184	0	0	0	0
All	All	33920	0	31949	110	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 2.

The worst 5 of 110 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:E:380:ARG:HA	1:G:486:PRO:HD2	1.38	1.02

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:380:ARG:HA	1:G:486:PRO:CD	2.01	0.91
1:A:380:ARG:HB3	1:B:484:ARG:HE	1.49	0.77
1:A:404:ASP:HB3	1:A:407:ALA:HB2	1.64	0.77
1:E:380:ARG:CA	1:G:486:PRO:HD2	2.17	0.71

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	406/443 (92%)	399 (98%)	7 (2%)	0	100	100
1	B	362/443 (82%)	356 (98%)	6 (2%)	0	100	100
1	C	405/443 (91%)	400 (99%)	5 (1%)	0	100	100
1	D	396/443 (89%)	390 (98%)	6 (2%)	0	100	100
1	E	398/443 (90%)	390 (98%)	8 (2%)	0	100	100
1	F	397/443 (90%)	391 (98%)	6 (2%)	0	100	100
1	G	397/443 (90%)	391 (98%)	6 (2%)	0	100	100
1	H	395/443 (89%)	389 (98%)	6 (2%)	0	100	100
1	I	396/443 (89%)	390 (98%)	6 (2%)	0	100	100
1	J	394/443 (89%)	388 (98%)	6 (2%)	0	100	100
All	All	3946/4430 (89%)	3884 (98%)	62 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

20 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	ACT	H	601	-	3,3,3	1.10	0	3,3,3	0.98	0
2	ACT	H	602	-	3,3,3	1.08	0	3,3,3	0.97	0
2	ACT	B	601	-	3,3,3	1.10	0	3,3,3	0.82	0
2	ACT	G	602	-	3,3,3	1.15	0	3,3,3	0.85	0
2	ACT	G	601	-	3,3,3	1.17	0	3,3,3	0.85	0
2	ACT	I	602	-	3,3,3	1.10	0	3,3,3	0.86	0
2	ACT	J	601	-	3,3,3	1.04	0	3,3,3	0.97	0
2	ACT	I	601	-	3,3,3	1.09	0	3,3,3	0.84	0
2	ACT	E	602	-	3,3,3	1.07	0	3,3,3	0.97	0
2	ACT	C	601	-	3,3,3	1.09	0	3,3,3	0.88	0
2	ACT	A	602	-	3,3,3	1.17	0	3,3,3	0.83	0
2	ACT	C	602	-	3,3,3	1.13	0	3,3,3	1.04	0
2	ACT	F	602	-	3,3,3	1.15	0	3,3,3	1.04	0
2	ACT	D	601	-	3,3,3	1.07	0	3,3,3	0.84	0
2	ACT	B	602	-	3,3,3	1.14	0	3,3,3	0.86	0
2	ACT	E	601	-	3,3,3	1.08	0	3,3,3	1.02	0
2	ACT	A	601	-	3,3,3	1.17	0	3,3,3	0.86	0
2	ACT	D	602	-	3,3,3	1.13	0	3,3,3	0.86	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	ACT	F	601	-	3,3,3	1.04	0	3,3,3	0.88	0
2	ACT	J	602	-	3,3,3	1.15	0	3,3,3	0.98	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2			OWAB(Å ²)	Q < 0.9
1	A	412/443 (93%)	0.12	29 (7%)	22	19	29, 47, 87, 114	0
1	B	404/443 (91%)	0.22	16 (3%)	42	38	34, 57, 88, 109	0
1	C	411/443 (92%)	0.23	23 (5%)	30	26	30, 54, 96, 112	0
1	D	404/443 (91%)	0.25	28 (6%)	23	19	33, 56, 90, 106	0
1	E	406/443 (91%)	0.39	33 (8%)	18	14	34, 60, 100, 120	0
1	F	405/443 (91%)	0.27	26 (6%)	25	22	28, 57, 108, 127	0
1	G	405/443 (91%)	0.41	37 (9%)	15	12	34, 60, 102, 117	0
1	H	403/443 (90%)	0.31	21 (5%)	33	29	38, 61, 97, 122	0
1	I	404/443 (91%)	0.25	26 (6%)	25	22	31, 54, 94, 112	0
1	J	402/443 (90%)	0.38	25 (6%)	26	23	38, 61, 97, 110	0
All	All	4056/4430 (91%)	0.28	264 (6%)	25	21	28, 57, 98, 127	0

The worst 5 of 264 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	512	SER	5.8
1	E	379	ALA	5.5
1	C	330	ALA	5.3
1	G	453	THR	5.3
1	I	216	ALA	5.2

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 ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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	ACT	F	602	4/4	0.85	0.20	81,81,81,82	0
2	ACT	H	602	4/4	0.85	0.19	87,87,87,88	0
2	ACT	J	602	4/4	0.85	0.22	90,91,91,91	0
2	ACT	C	602	4/4	0.86	0.19	84,84,84,84	0
2	ACT	D	602	4/4	0.87	0.16	76,76,77,77	0
2	ACT	A	602	4/4	0.88	0.15	76,76,76,76	0
2	ACT	E	602	4/4	0.89	0.16	88,88,88,88	0
2	ACT	G	602	4/4	0.89	0.17	79,79,79,79	0
2	ACT	J	601	4/4	0.90	0.14	53,53,53,53	0
2	ACT	B	602	4/4	0.91	0.17	89,89,89,90	0
2	ACT	I	602	4/4	0.91	0.13	70,70,70,70	0
2	ACT	D	601	4/4	0.92	0.13	54,54,55,55	0
2	ACT	H	601	4/4	0.92	0.15	65,65,66,66	0
2	ACT	G	601	4/4	0.92	0.14	52,52,53,54	0
2	ACT	E	601	4/4	0.94	0.10	58,58,58,58	0
2	ACT	F	601	4/4	0.94	0.10	47,48,48,48	0
2	ACT	I	601	4/4	0.96	0.09	54,54,54,55	0
2	ACT	B	601	4/4	0.97	0.07	52,52,52,52	0
2	ACT	A	601	4/4	0.97	0.07	53,53,53,53	0
2	ACT	C	601	4/4	0.97	0.06	42,43,43,43	0

6.5 Other polymers ⓘ

There are no such residues in this entry.