



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 12:46 PM UTC

PDB ID : 7JLS / pdb_00007jls
Title : RV3666c bound to tripeptide
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Deposited on : 2020-07-30
Resolution : 1.52 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

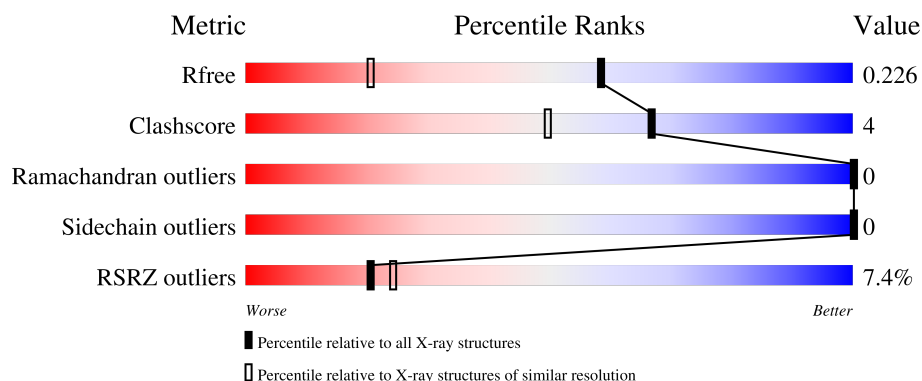
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.52 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	5890 (1.54-1.50)
Clashscore	190562	6116 (1.54-1.50)
Ramachandran outliers	187476	6002 (1.54-1.50)
Sidechain outliers	187428	5999 (1.54-1.50)
RSRZ outliers	180081	5891 (1.54-1.50)

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	553	7% 81% 8% 10%
2	B	3	33% 100%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4254 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 Probable periplasmic dipeptide-binding lipoprotein DppA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	497	Total	C	N	O	S	0	3	0
			3833	2431	675	721	6			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP I6X811
A	2	ALA	-	expression tag	UNP I6X811
A	3	GLY	-	expression tag	UNP I6X811
A	4	LEU	-	expression tag	UNP I6X811
A	5	ASN	-	expression tag	UNP I6X811
A	6	ASP	-	expression tag	UNP I6X811
A	7	ILE	-	expression tag	UNP I6X811
A	8	PHE	-	expression tag	UNP I6X811
A	9	GLU	-	expression tag	UNP I6X811
A	10	ALA	-	expression tag	UNP I6X811
A	11	GLN	-	expression tag	UNP I6X811
A	12	LYS	-	expression tag	UNP I6X811
A	13	ILE	-	expression tag	UNP I6X811
A	14	GLU	-	expression tag	UNP I6X811
A	15	TRP	-	expression tag	UNP I6X811
A	16	HIS	-	expression tag	UNP I6X811
A	17	GLU	-	expression tag	UNP I6X811
A	18	LEU	-	expression tag	UNP I6X811
A	19	GLU	-	expression tag	UNP I6X811
A	20	VAL	-	expression tag	UNP I6X811
A	21	LEU	-	expression tag	UNP I6X811
A	22	PHE	-	expression tag	UNP I6X811
A	23	GLN	-	expression tag	UNP I6X811
A	24	GLY	-	expression tag	UNP I6X811
A	25	PRO	-	expression tag	UNP I6X811
A	26	MET	-	expression tag	UNP I6X811
A	538	GLU	-	expression tag	UNP I6X811

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Chain	Residue	Modelled	Actual	Comment	Reference
A	539	ASN	-	expression tag	UNP I6X811
A	540	LEU	-	expression tag	UNP I6X811
A	541	TYR	-	expression tag	UNP I6X811
A	542	PHE	-	expression tag	UNP I6X811
A	543	GLN	-	expression tag	UNP I6X811
A	544	GLY	-	expression tag	UNP I6X811
A	545	GLY	-	expression tag	UNP I6X811
A	546	HIS	-	expression tag	UNP I6X811
A	547	HIS	-	expression tag	UNP I6X811
A	548	HIS	-	expression tag	UNP I6X811
A	549	HIS	-	expression tag	UNP I6X811
A	550	HIS	-	expression tag	UNP I6X811
A	551	HIS	-	expression tag	UNP I6X811
A	552	HIS	-	expression tag	UNP I6X811
A	553	HIS	-	expression tag	UNP I6X811

- Molecule 2 is a protein called Peptide SER-VAL-ALA.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	3	Total	C	N	O	0	0	0
			18	11	3	4			

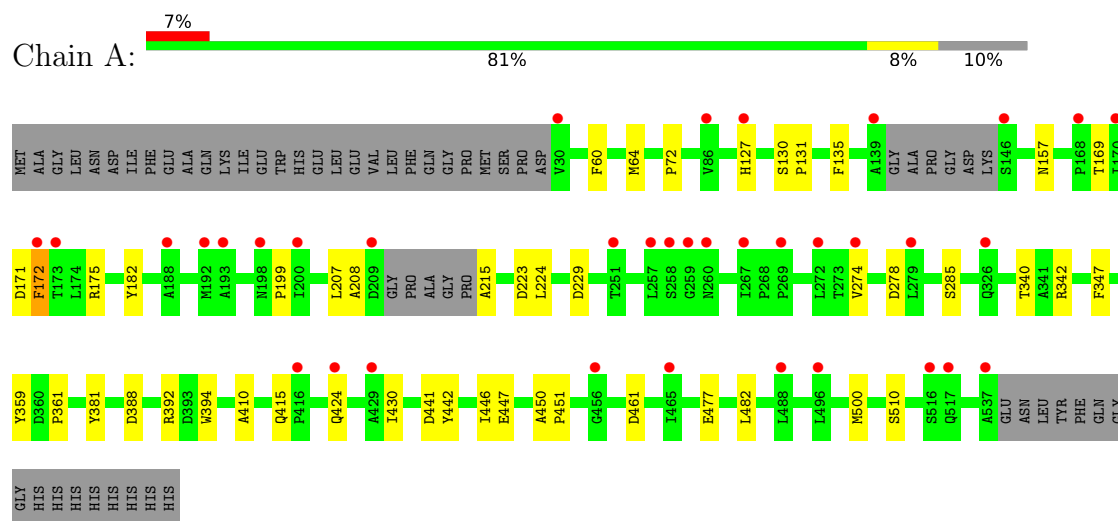
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	401	Total	O	0	0
			401	401		
3	B	2	Total	O	0	0
			2	2		

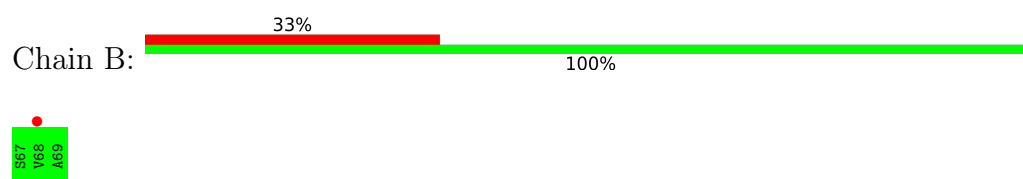
3 Residue-property plots

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: Probable periplasmic dipeptide-binding lipoprotein DppA



- Molecule 2: Peptide SER-VAL-ALA



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	54.05Å 69.96Å 65.39Å 90.00° 109.50° 90.00°	Depositor
Resolution (Å)	50.00 – 1.52 50.00 – 1.52	Depositor EDS
% Data completeness (in resolution range)	94.6 (50.00-1.52) 95.2 (50.00-1.52)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	49.92 (at 1.51Å)	Xtriage
Refinement program	REFMAC 5.8.0257	Depositor
R, R_{free}	0.185 , 0.221 0.192 , 0.226	Depositor DCC
R_{free} test set	3433 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	20.2	Xtriage
Anisotropy	0.055	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 24.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4254	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.13% 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](#)

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	1.12	1/3937 (0.0%)	1.26	7/5387 (0.1%)
2	B	1.24	0/17	0.99	0/22
All	All	1.12	1/3954 (0.0%)	1.25	7/5409 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	340	THR	N-CA	6.04	1.50	1.46

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	461	ASP	CA-CB-CG	7.31	119.91	112.60
1	A	388	ASP	CA-CB-CG	7.13	119.73	112.60
1	A	229	ASP	CA-CB-CG	6.89	119.49	112.60
1	A	415	GLN	O-C-N	-5.89	116.74	121.80
1	A	172	PHE	CA-C-O	-5.85	114.86	121.00
1	A	394	TRP	N-CA-CB	5.60	118.45	110.16
1	A	500	MET	O-C-N	-5.49	119.00	121.53

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	3833	0	3664	28	0
2	B	18	0	18	0	0
3	A	401	0	0	7	0
3	B	2	0	0	0	0
All	All	4254	0	3682	28	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 4.

All (28) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:208:ALA:O	1:A:215:ALA:HB2	1.96	0.66
1:A:169:THR:HG22	3:A:602:HOH:O	1.97	0.64
1:A:172:PHE:O	1:A:175:ARG:HG2	1.99	0.63
1:A:274:VAL:HG12	1:A:278:ASP:OD2	2.01	0.60
1:A:446:ILE:HD13	1:A:477:GLU:HG2	1.82	0.60
1:A:441:ASP:OD2	1:A:447:GLU:OE2	2.21	0.59
1:A:207:LEU:HD23	1:A:224[B]:LEU:CD2	2.38	0.53
1:A:64:MET:HE3	1:A:72:PRO:HB2	1.90	0.53
1:A:285:SER:HA	1:A:510:SER:O	2.10	0.52
1:A:172:PHE:N	3:A:602:HOH:O	2.41	0.52
1:A:442:TYR:CZ	1:A:447:GLU:HG3	2.46	0.50
1:A:392:ARG:NH1	3:A:608:HOH:O	2.40	0.47
1:A:130:SER:HA	1:A:135:PHE:CG	2.50	0.47
1:A:274:VAL:HG12	1:A:278:ASP:CG	2.40	0.47
1:A:127:HIS:ND1	3:A:601:HOH:O	2.20	0.46
1:A:223:ASP:C	1:A:224[A]:LEU:HD12	2.41	0.46
1:A:342:ARG:HA	1:A:347:PHE:CG	2.50	0.46
1:A:424[A]:GLN:HE21	1:A:430:ILE:HG13	1.80	0.46
1:A:171:ASP:C	3:A:602:HOH:O	2.59	0.45
1:A:381:TYR:O	1:A:410:ALA:HA	2.17	0.44
1:A:359:TYR:CZ	1:A:361:PRO:HG3	2.53	0.43
1:A:450:ALA:HB3	1:A:451:PRO:HD3	2.00	0.42
1:A:60:PHE:HB2	1:A:182:TYR:CD2	2.55	0.41
1:A:130:SER:N	1:A:131:PRO:CD	2.84	0.41
1:A:157:ASN:HB2	3:A:925:HOH:O	2.21	0.41
1:A:342:ARG:HD2	3:A:754:HOH:O	2.20	0.41
1:A:482:LEU:HD12	1:A:482:LEU:HA	1.93	0.41
1:A:199:PRO:HD2	1:A:207:LEU:CD1	2.52	0.40

There are no symmetry-related clashes.

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	494/553 (89%)	487 (99%)	7 (1%)	0	100	100
2	B	1/3 (33%)	1 (100%)	0	0	100	100
All	All	495/556 (89%)	488 (99%)	7 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	396/446 (89%)	396 (100%)	0	100	100
2	B	2/2 (100%)	2 (100%)	0	100	100
All	All	398/448 (89%)	398 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	123	GLN
1	A	370	GLN
1	A	498	HIS

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](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	497/553 (89%)	0.71	36 (7%) 21 25	8, 23, 36, 60	3 (0%)
2	B	3/3 (100%)	1.61	1 (33%) 1 1	23, 23, 27, 28	0
All	All	500/556 (89%)	0.72	37 (7%) 20 24	8, 23, 36, 60	3 (0%)

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	170	ILE	3.8
1	A	259	GLY	3.6
1	A	537	ALA	3.6
1	A	274	VAL	3.5
1	A	269	PRO	3.3
1	A	416	PRO	3.0
1	A	172	PHE	2.9
1	A	209	ASP	2.8
2	B	68	VAL	2.8
1	A	139	ALA	2.8
1	A	127	HIS	2.8
1	A	193	ALA	2.7
1	A	257	LEU	2.7
1	A	168	PRO	2.6
1	A	516	SER	2.6
1	A	272	LEU	2.5
1	A	260	ASN	2.5
1	A	429	ALA	2.5
1	A	488	LEU	2.5
1	A	258	SER	2.4
1	A	517	GLN	2.4
1	A	30	VAL	2.3
1	A	456	GLY	2.3
1	A	86	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	279	LEU	2.3
1	A	465	ILE	2.3
1	A	424[A]	GLN	2.2
1	A	267	ILE	2.1
1	A	173	THR	2.1
1	A	251	THR	2.1
1	A	146	SER	2.1
1	A	496	LEU	2.1
1	A	200	ILE	2.1
1	A	188	ALA	2.1
1	A	326	GLN	2.1
1	A	192	MET	2.1
1	A	198	ASN	2.0

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.