



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 03:19 PM GMT

PDB ID : 4C30
Title : Crystal structure of Deinococcus radiodurans UvrD in complex with DNA, form 2
Authors : Stelter, M.; Acajjaoui, S.; McSweeney, S.; Timmins, J.
Deposited on : 2013-08-21
Resolution : 3.00 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

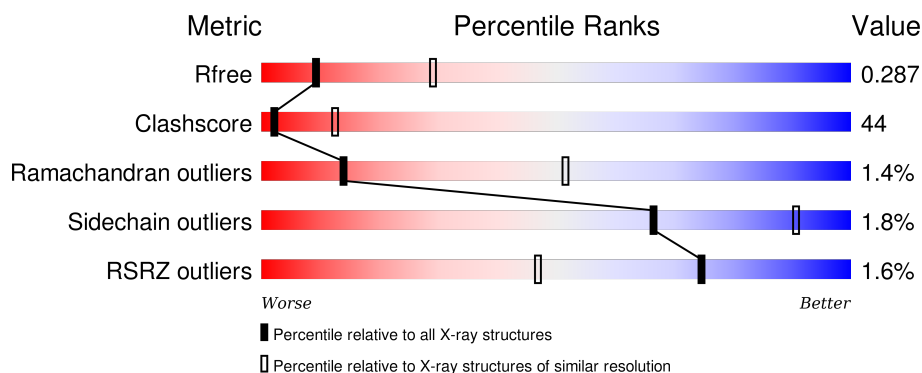
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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.




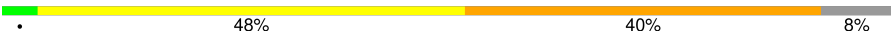

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	665	<div> <div>3%</div> <div>45%</div> <div>47%</div> <div>5%</div> </div>
1	D	665	<div> <div>%</div> <div>48%</div> <div>46%</div> <div>• •</div> </div>
1	F	665	<div> <div>2%</div> <div>45%</div> <div>48%</div> <div>• 5%</div> </div>
1	I	665	<div> <div>%</div> <div>49%</div> <div>45%</div> <div>• •</div> </div>
2	K	25	<div> <div>52%</div> <div>40%</div> <div>8%</div> </div>

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Mol	Chain	Length	Quality of chain
2	X	25	
3	L	25	
3	Y	25	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	ANP	F	1663	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 22073 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 DNA HELICASE II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	631	Total	C	N	O	S	0	0	0
			4970	3112	898	945	15			
1	D	642	Total	C	N	O	S	0	2	0
			5059	3168	916	961	14			
1	F	632	Total	C	N	O	S	0	0	0
			4978	3118	899	946	15			
1	I	638	Total	C	N	O	S	0	1	0
			5025	3145	909	957	14			

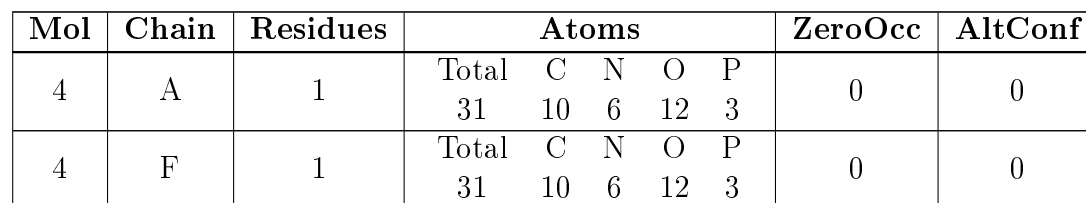
- Molecule 2 is a DNA chain called DNA STRAND FOR25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	K	23	Total	C	N	O	P	0	0	0
			471	225	78	145	23			
2	X	23	Total	C	N	O	P	0	0	0
			471	225	78	145	23			

- Molecule 3 is a DNA chain called DNA STRAND REV25.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	23	Total	C	N	O	P	0	0	0
			467	223	80	141	23			
3	Y	23	Total	C	N	O	P	0	0	0
			467	223	80	141	23			

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).



- | Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|-----------------|---------|---------|
| 5 | I | 1 | Total Mg
1 1 | 0 | 0 |
| 5 | A | 2 | Total Mg
2 2 | 0 | 0 |
| 5 | D | 1 | Total Mg
1 1 | 0 | 0 |
| 5 | F | 2 | Total Mg
2 2 | 0 | 0 |

- | Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|------------------|---------|---------|
| 6 | A | 6 | Total O
6 6 | 0 | 0 |
| 6 | D | 28 | Total O
28 28 | 0 | 0 |
| 6 | F | 26 | Total O
26 26 | 0 | 0 |



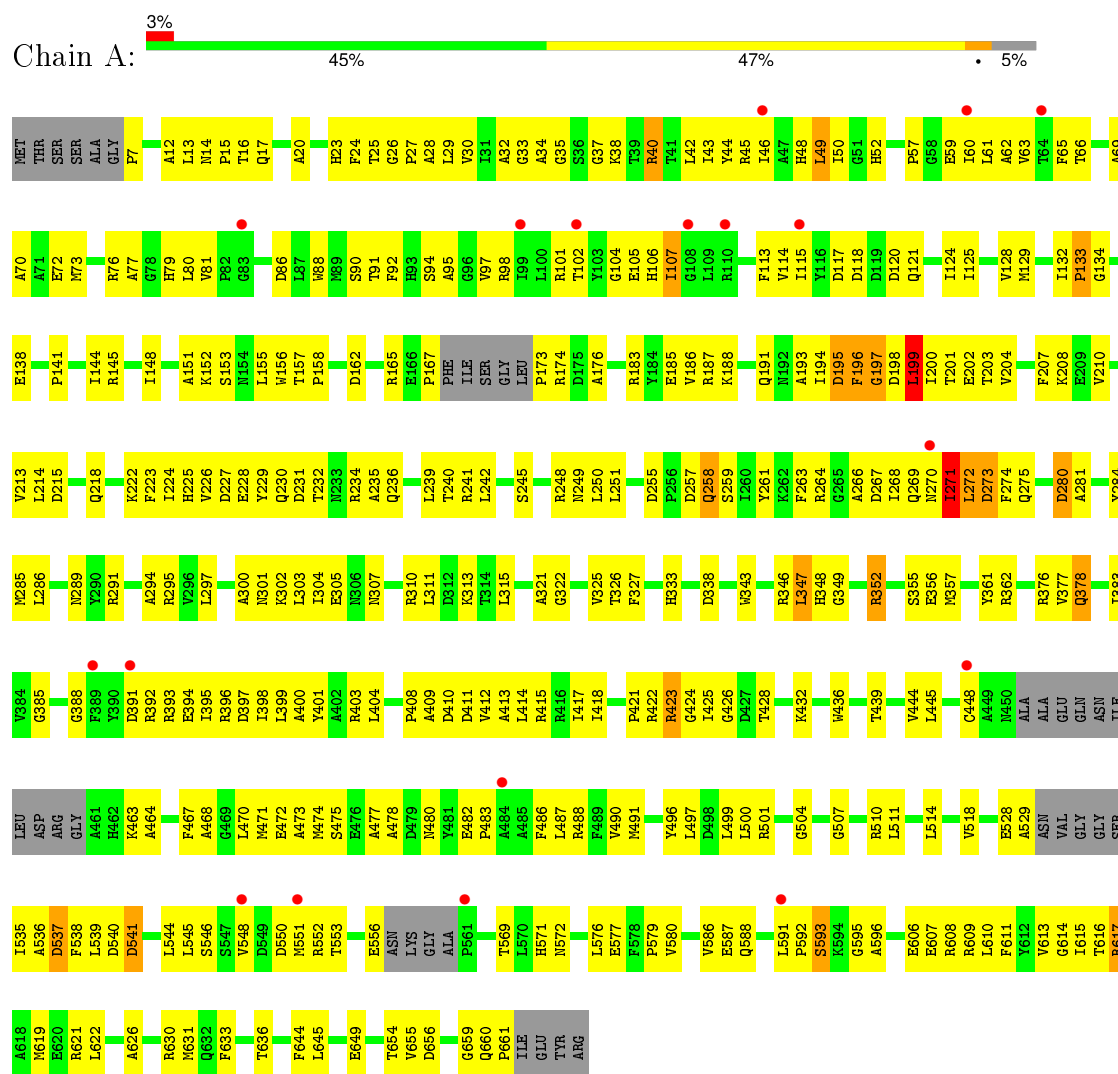
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	I	36	Total	O	0	0
			36	36		
6	Y	1	Total	O	0	0
			1	1		

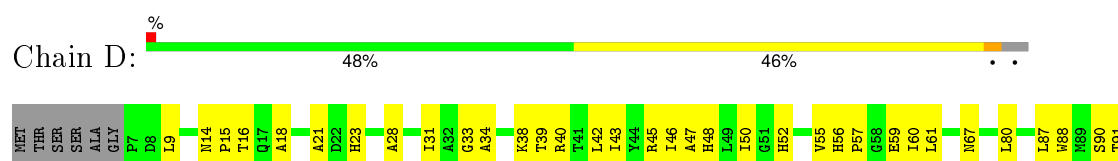
3 Residue-property plots

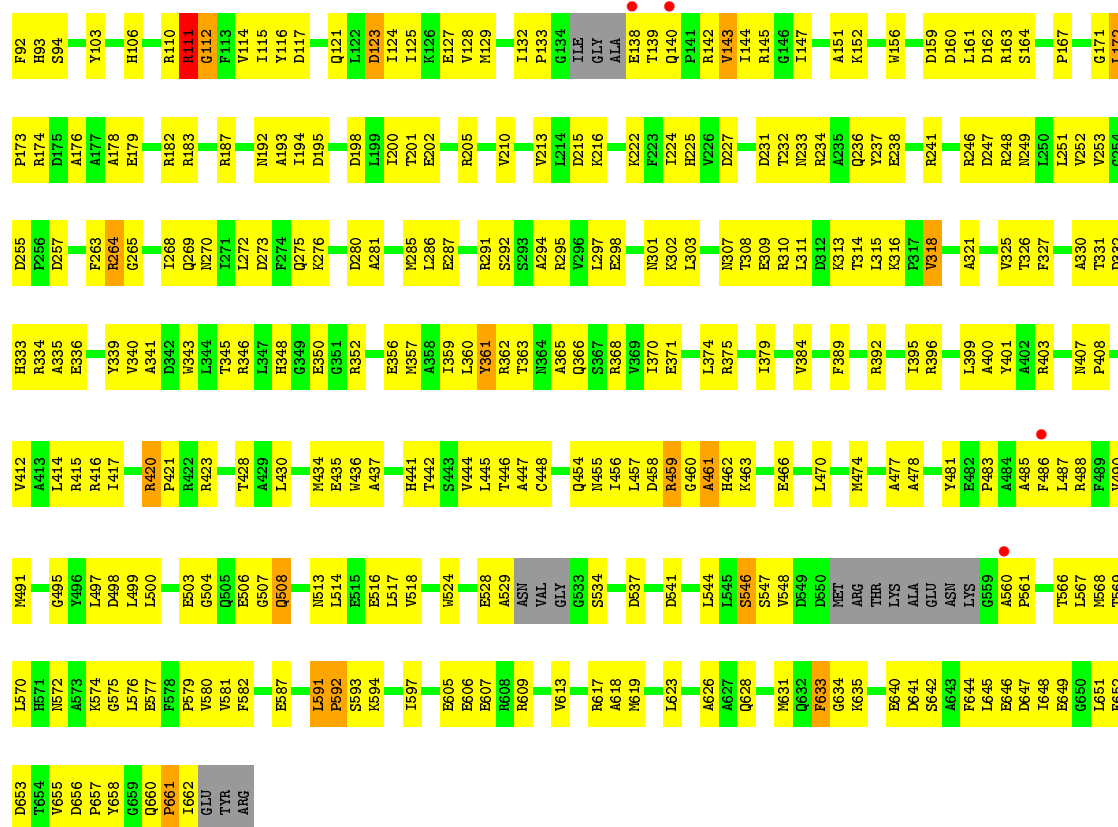
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: DNA HELICASE II

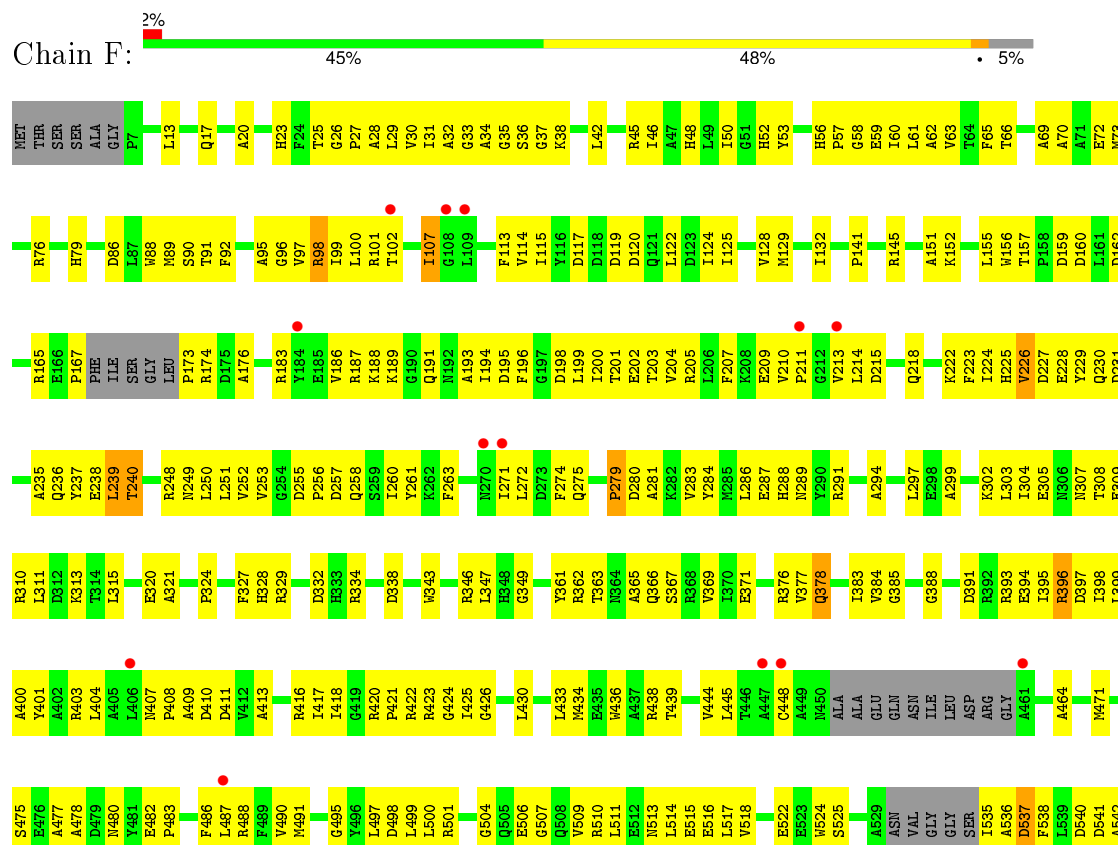


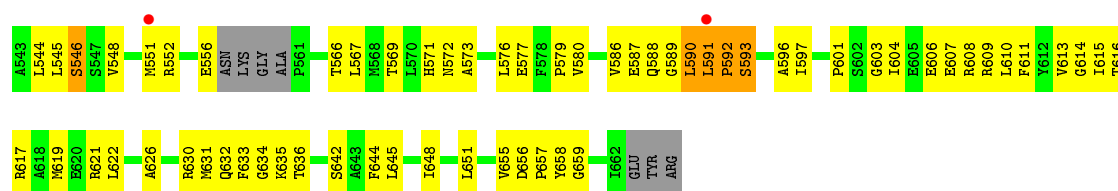
• Molecule 1: DNA HELICASE II



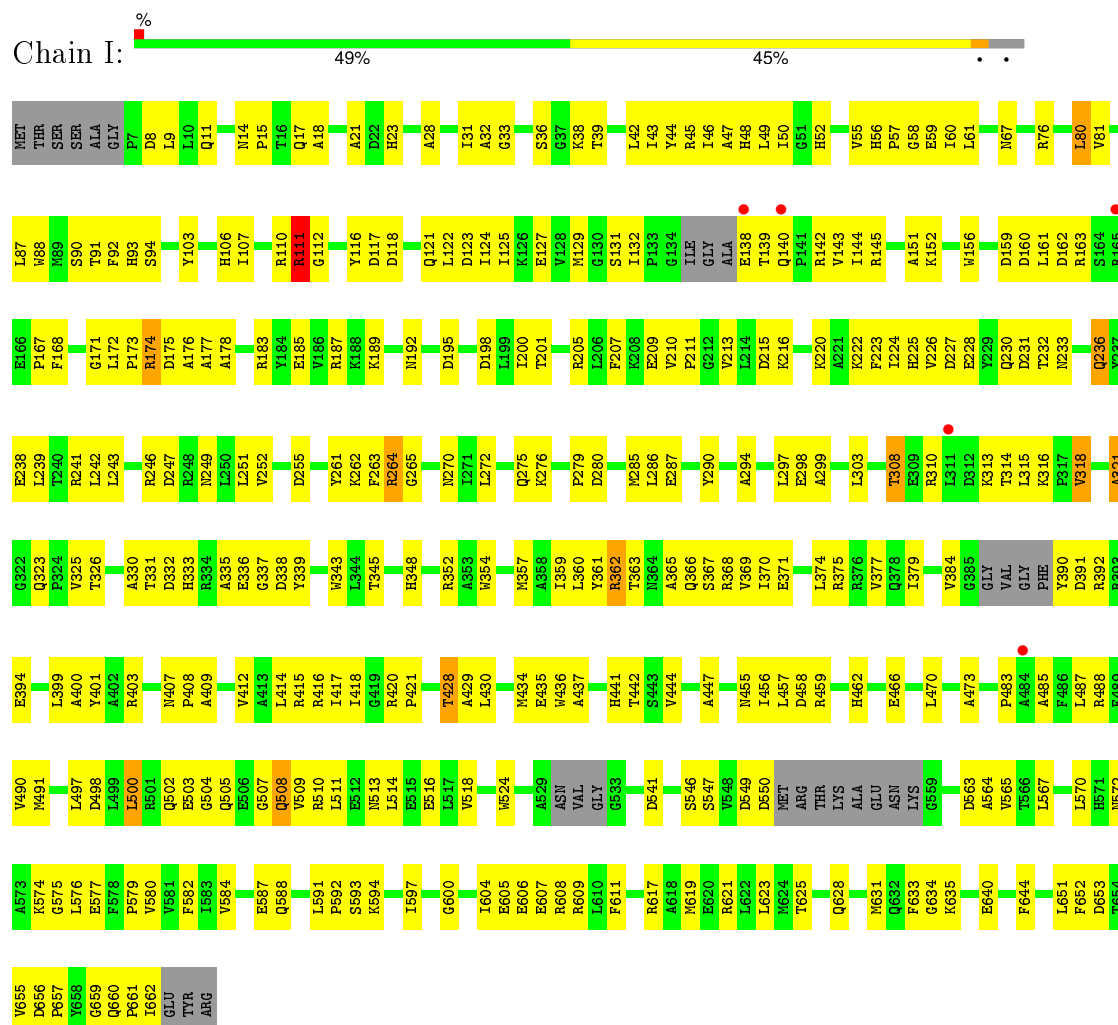


• Molecule 1: DNA HELICASE II





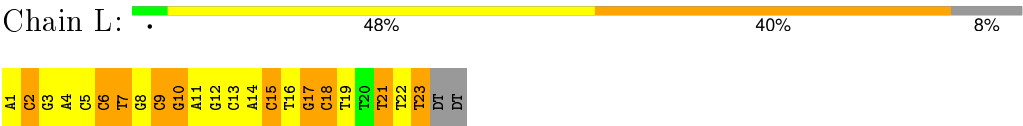
• Molecule 1: DNA HELICASE II



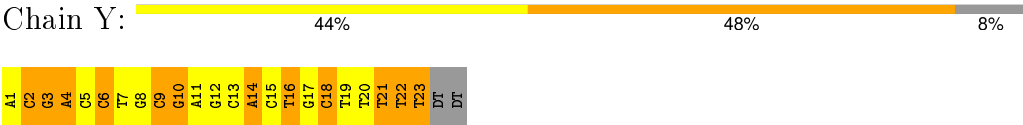
• Molecule 2: DNA STRAND FOR25



● Molecule 3: DNA STRAND REV25



● Molecule 3: DNA STRAND REV25



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	68.49 Å 89.78 Å 293.80 Å 90.00° 89.97° 90.00°	Depositor
Resolution (Å)	66.18 – 3.00 66.18 – 3.00	Depositor EDS
% Data completeness (in resolution range)	87.2 (66.18-3.00) 87.2 (66.18-3.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.91 (at 3.01 Å)	Xtriage
Refinement program	REFMAC 5.6.0085	Depositor
R, R_{free}	0.228 , 0.288 0.231 , 0.287	Depositor DCC
R_{free} test set	3128 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	71.2	Xtriage
Anisotropy	0.942	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 75.4	EDS
Estimated twinning fraction	0.439 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 62635 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	22073	wwPDB-VP
Average B, all atoms (Å ²)	104.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.90% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: MG, ANP

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	0.56	1/5059 (0.0%)	0.74	5/6838 (0.1%)
1	D	0.63	1/5156 (0.0%)	0.78	4/6972 (0.1%)
1	F	0.54	0/5067	0.72	3/6849 (0.0%)
1	I	0.63	0/5117	0.78	2/6919 (0.0%)
2	K	1.29	3/525 (0.6%)	1.76	17/809 (2.1%)
2	X	1.06	0/525	1.68	15/809 (1.9%)
3	L	1.09	0/521	1.62	14/801 (1.7%)
3	Y	1.24	1/521 (0.2%)	1.59	14/801 (1.7%)
All	All	0.67	6/22491 (0.0%)	0.89	74/30798 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	2
1	F	0	1
1	I	0	2
All	All	0	5

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	K	2	DC	O3'-P	-15.97	1.42	1.61
3	Y	16	DT	O3'-P	-7.85	1.51	1.61
2	K	12	DA	O3'-P	5.65	1.68	1.61
2	K	6	DG	C4'-O4'	5.29	1.50	1.45
1	D	661	PRO	N-CD	-5.17	1.40	1.47

The worst 5 of 74 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	K	9	DC	C1'-O4'-C4'	-10.43	99.67	110.10
2	K	9	DC	O4'-C1'-C2'	-9.11	98.61	105.90
3	Y	6	DC	P-O3'-C3'	8.78	130.24	119.70
1	D	112	GLY	N-CA-C	-8.77	91.19	113.10
2	X	9	DC	O4'-C1'-C2'	-8.59	99.03	105.90

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	111	ARG	Peptide
1	D	420	ARG	Peptide
1	F	396	ARG	Sidechain
1	I	111	ARG	Peptide
1	I	362	ARG	Sidechain

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	4970	0	4901	444	0
1	D	5059	0	4993	368	0
1	F	4978	0	4912	433	0
1	I	5025	0	4955	354	0
2	K	471	0	263	121	0
2	X	471	0	263	88	0
3	L	467	0	261	98	0
3	Y	467	0	261	86	0
4	A	31	0	13	5	0
4	F	31	0	13	11	0
5	A	2	0	0	0	0
5	D	1	0	0	0	0
5	F	2	0	0	0	0
5	I	1	0	0	0	0
6	A	6	0	0	0	0
6	D	28	0	0	7	0
6	F	26	0	0	3	0
6	I	36	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	Y	1	0	0	0	0
All	All	22073	0	20835	1889	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 44.

The worst 5 of 1889 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:D:576:LEU:O	1:D:617:ARG:HD2	1.30	1.30
1:I:171:GLY:O	1:I:172:LEU:HG	1.29	1.26
1:A:401:TYR:OH	1:A:421:PRO:HG2	1.36	1.26
1:D:592:PRO:HD3	1:D:644:PHE:CE2	1.69	1.25
1:A:194:ILE:HD11	1:A:198:ASP:CB	1.65	1.25

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	621/665 (93%)	537 (86%)	71 (11%)	13 (2%)	9	40
1	D	636/665 (96%)	572 (90%)	56 (9%)	8 (1%)	15	53
1	F	622/665 (94%)	553 (89%)	60 (10%)	9 (1%)	14	51
1	I	629/665 (95%)	570 (91%)	54 (9%)	5 (1%)	24	66
All	All	2508/2660 (94%)	2232 (89%)	241 (10%)	35 (1%)	14	51

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	107	ILE

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Mol	Chain	Res	Type
1	D	143	VAL
1	D	172	LEU
1	D	592	PRO
1	F	107	ILE

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	512/536 (96%)	498 (97%)	14 (3%)	52	85
1	D	521/536 (97%)	513 (98%)	8 (2%)	72	92
1	F	513/536 (96%)	503 (98%)	10 (2%)	65	90
1	I	518/536 (97%)	511 (99%)	7 (1%)	74	93
All	All	2064/2144 (96%)	2025 (98%)	39 (2%)	66	90

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	361	TYR
1	D	633	PHE
1	I	428	THR
1	D	435	GLU
1	D	459	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	450	ASN
1	F	225	HIS
1	I	407	ASN
1	D	660	GLN
1	F	258	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 for Mogul analysis.

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	$\# Z > 2$
4	ANP	A	1662	5	27,33,33	1.90	8 (29%)	30,52,52	1.91	6 (20%)
4	ANP	F	1663	5	27,33,33	1.85	9 (33%)	30,52,52	2.19	7 (23%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ANP	A	1662	5	-	0/12/38/38	0/3/3/3
4	ANP	F	1663	5	-	1/12/38/38	0/3/3/3

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1662	ANP	PG-O3G	-2.97	1.48	1.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1662	ANP	PG-O2G	-2.76	1.49	1.56
4	F	1663	ANP	PG-O2G	-2.71	1.49	1.56
4	F	1663	ANP	PG-O3G	-2.45	1.49	1.56
4	A	1662	ANP	PB-O2B	-2.13	1.50	1.56

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	1663	ANP	N3-C2-N1	-6.57	123.86	128.89
4	A	1662	ANP	N3-C2-N1	-5.96	124.33	128.89
4	F	1663	ANP	O1G-PG-N3B	-5.03	104.19	111.90
4	F	1663	ANP	PA-O3A-PB	-4.24	118.46	132.67
4	A	1662	ANP	C4-C5-N7	-3.34	106.40	109.48

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	F	1663	ANP	O1G-PG-N3B-PB

There are no ring outliers.

2 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1662	ANP	5	0
4	F	1663	ANP	11	0

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	631/665 (94%)	0.13	18 (2%) 55 26	61, 115, 166, 194	0
1	D	642/665 (96%)	-0.06	4 (0%) 90 73	59, 83, 137, 200	0
1	F	632/665 (95%)	0.10	15 (2%) 62 32	36, 115, 166, 196	0
1	I	638/665 (95%)	-0.04	5 (0%) 87 67	59, 83, 137, 199	0
2	K	23/25 (92%)	-0.33	0 100 100	117, 131, 152, 202	0
2	X	23/25 (92%)	-0.32	0 100 100	110, 125, 145, 187	0
3	L	23/25 (92%)	-0.37	0 100 100	91, 132, 169, 194	0
3	Y	23/25 (92%)	-0.41	0 100 100	89, 130, 147, 165	0
All	All	2635/2760 (95%)	0.02	42 (1%) 74 47	36, 95, 161, 202	0

The worst 5 of 42 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	406	LEU	4.0
1	A	448	CYS	3.7
1	F	211	PRO	3.6
1	D	560	ALA	3.2
1	A	108	GLY	3.1

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
4	ANP	F	1663	31/31	0.94	0.17	-0.75	72,85,91,95	0
4	ANP	A	1662	31/31	0.96	0.18	-0.92	71,82,92,93	0
5	MG	I	1663	1/1	0.95	0.14	-0.96	45,45,45,45	0
5	MG	F	1665	1/1	0.84	0.20	-1.41	137,137,137,137	0
5	MG	A	1663	1/1	0.70	0.15	-1.78	190,190,190,190	0
5	MG	D	1663	1/1	0.95	0.07	-3.31	53,53,53,53	0
5	MG	A	1664	1/1	0.90	0.18	-	112,112,112,112	0
5	MG	F	1664	1/1	0.91	0.17	-	98,98,98,98	0

6.5 Other polymers [i](#)

There are no such residues in this entry.