W O R L D W I D E
wwPDB
P R O T E I N   D A T A   B A N K

wwPDB X-ray Structure Validation Summary Report (i)

Oct 12, 2021 – 12:28 PM EDT

PDB ID	:	2EX3
Title	:	Bacteriophage phi29 DNA polymerase bound to terminal protein
Authors	:	Kamtekar, S.; Berman, A.J.; Wang, J.; de Vega, M.; Blanco, L.; Salas, M.; Steitz, T.A.
Deposited on	:	2005-11-07
Resolution	:	3.00 Å(reported)

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

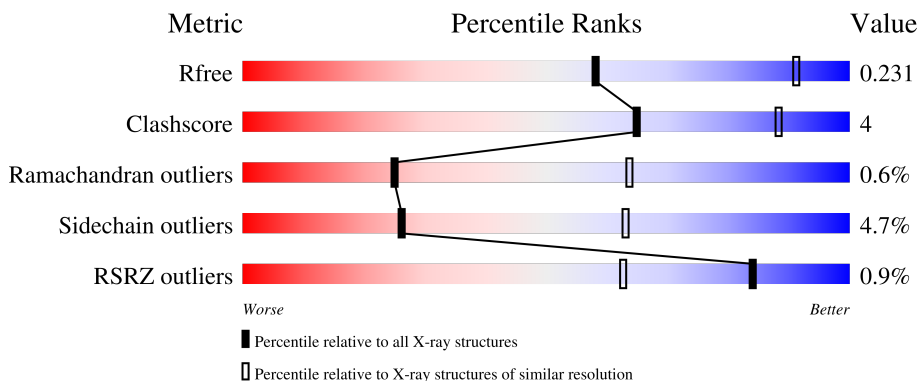|		
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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	Percentile Ranks	Value
Rfree		0.231
Clashscore		4
Ramachandran outliers		0.6%
Sidechain outliers		4.7%
RSRZ outliers		0.9%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (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 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 <=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	575	81% 18% ••
1	C	575	.% 82% 16% ••
1	E	575	.% 86% 12% ••
1	G	575	86% 11% ••
1	I	575	.% 87% 11% ••

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Mol	Chain	Length	Quality of chain
1	K	575	84% 14%
2	B	230	75% 10% 15%
2	D	230	77% 7% 15%
2	F	230	77% 7% 15%
2	H	230	73% 12% 15%
2	J	230	73% 12% 15%
2	L	230	76% 8% 15%

2 Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 37108 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 polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	570	Total	C	N	O	S	0	0	0
			4661	3036	753	851	21			
1	C	570	Total	C	N	O	S	0	0	0
			4661	3036	753	851	21			
1	E	570	Total	C	N	O	S	0	0	0
			4661	3036	753	851	21			
1	G	570	Total	C	N	O	S	0	0	0
			4661	3036	753	851	21			
1	I	570	Total	C	N	O	S	0	0	0
			4661	3036	753	851	21			
1	K	570	Total	C	N	O	S	0	0	0
			4661	3036	753	851	21			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	12	ALA	ASP	engineered mutation	UNP P03680
A	66	ALA	ASP	engineered mutation	UNP P03680
C	12	ALA	ASP	engineered mutation	UNP P03680
C	66	ALA	ASP	engineered mutation	UNP P03680
E	12	ALA	ASP	engineered mutation	UNP P03680
E	66	ALA	ASP	engineered mutation	UNP P03680
G	12	ALA	ASP	engineered mutation	UNP P03680
G	66	ALA	ASP	engineered mutation	UNP P03680
I	12	ALA	ASP	engineered mutation	UNP P03680
I	66	ALA	ASP	engineered mutation	UNP P03680
K	12	ALA	ASP	engineered mutation	UNP P03680
K	66	ALA	ASP	engineered mutation	UNP P03680

- Molecule 2 is a protein called DNA terminal protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	196	Total 1521	C 959	N 261	O 296	S 5	0	0	0
2	D	196	Total 1521	C 959	N 261	O 296	S 5	0	0	0
2	F	196	Total 1521	C 959	N 261	O 296	S 5	0	0	0
2	H	196	Total 1521	C 959	N 261	O 296	S 5	0	0	0
2	J	196	Total 1521	C 959	N 261	O 296	S 5	0	0	0
2	L	196	Total 1521	C 959	N 261	O 296	S 5	0	0	0

- Molecule 3 is LEAD (II) ION (three-letter code: PB) (formula: Pb).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total 3	Pb 3	0	0
3	C	3	Total 3	Pb 3	0	0
3	E	3	Total 3	Pb 3	0	0
3	G	3	Total 3	Pb 3	0	0
3	I	2	Total 2	Pb 2	0	0
3	K	2	Total 2	Pb 2	0	0

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: DNA polymerase

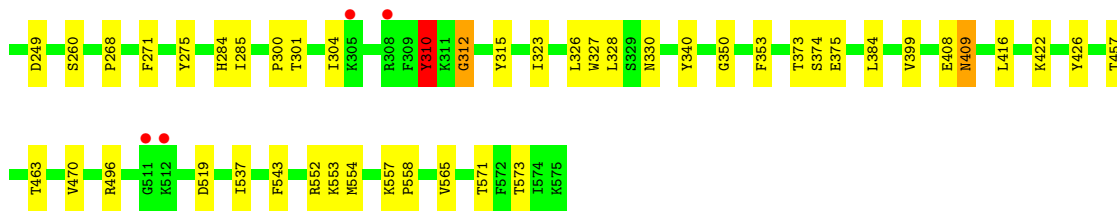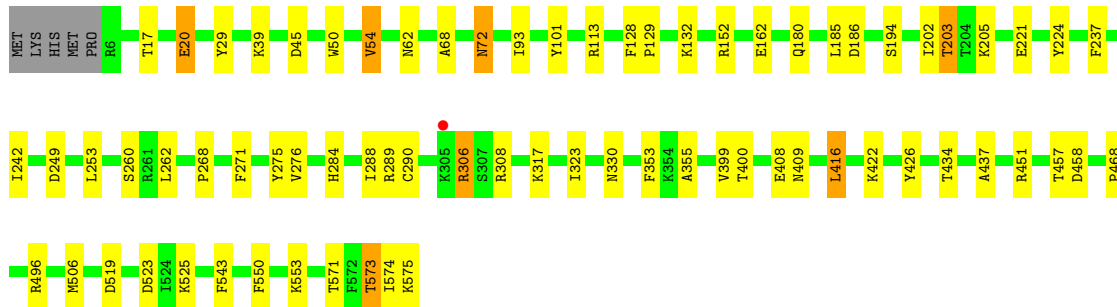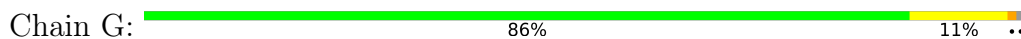Chain A:

• Molecule 1: DNA polymerase

Chain C:

• Molecule 1: DNA polymerase

Chain E:

D249 S260 P268 F271 Y275 H284 I285 P300 T301 I304 K305 R308 F309 Y310 K311 G312 Y315 I323 L326 W327 L328 S329 N330 Y340 G350 F353 T373 S374 E375 L384 V399 E408 N409 L416 K422 Y426 T457
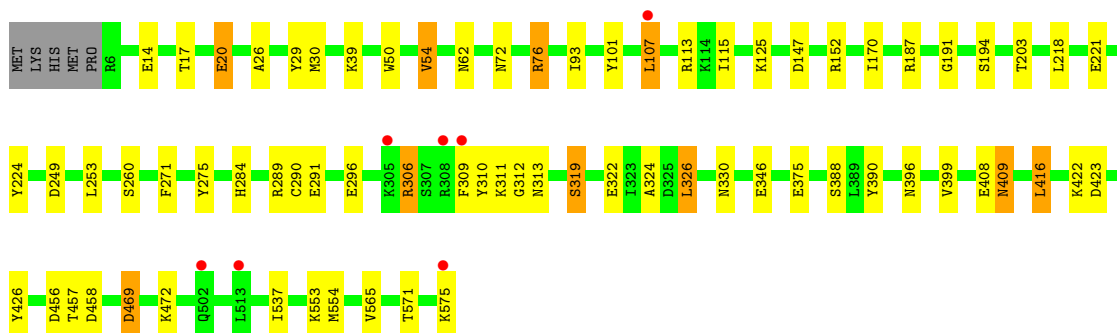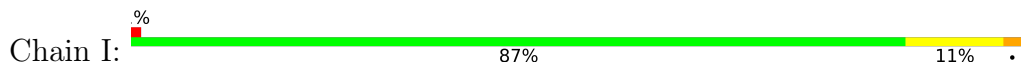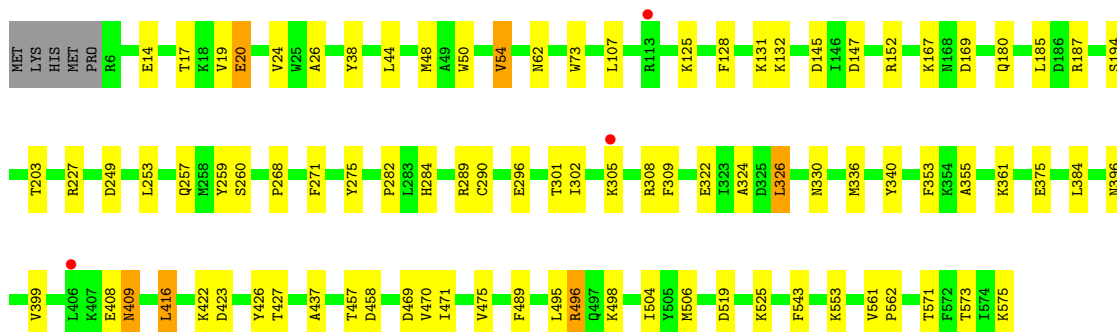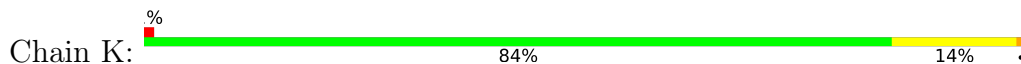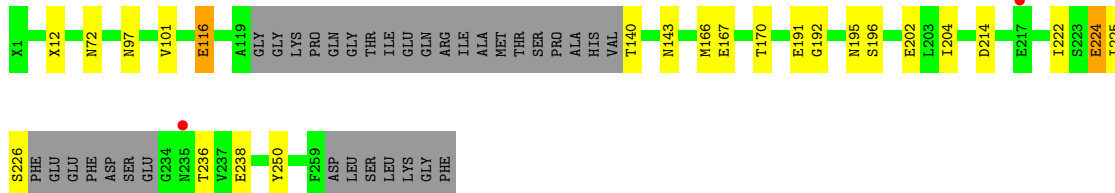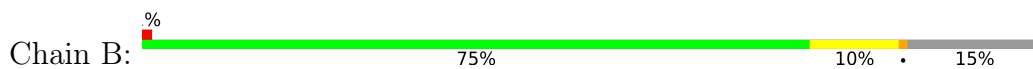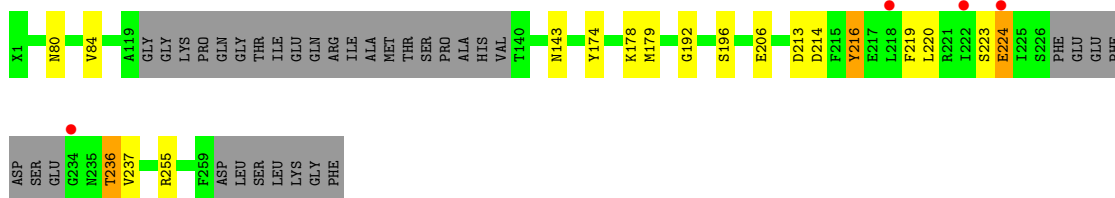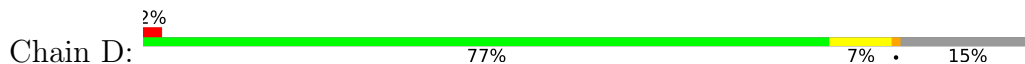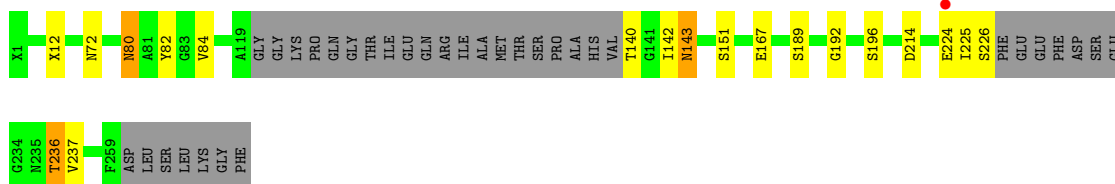
T463 V470 R496 G511 K512 D519 I537 F543 R552 K553 M554 K557 P558 V565 T571 F572 T573 I574 K575

• Molecule 1: DNA polymerase

Chain G: 86%   11%   ··

MET LYS HIS MET PRO R6 T17 E20 Y29 K39 D45 W50 V54 N62 A68 N72 I93 Y101 R113 F128 P129 K132 R152 E162 Q180 L185 D186 S194 I202 T203 T204 K205 E221 Y224 F237

I242 D249 L253 S260 R261 L262 P268 F271 Y275 V276 H284 I288 R289 C290 K305 R306 S307 R308 K317 I323 N330 F353 K354 A355 V399 T400 E408 N409 L416 K422 Y426 T434 A437 R451 T457 D458 P468

R496 M506 D519 D523 I524 K525 F543 F550 K553 T571 F572 T573 I574 K575

• Molecule 1: DNA polymerase

Chain I: %   87%   11%   ··

MET LYS HIS MET PRO R6 E14 T17 E20 A26 Y29 M30 K39 W50 V54 N62 N72 R76 I93 Y101 L107 R113 K114 I115 K125 D147 R152 I170 R187 G191 S194 T203 L218 E221

Y224 D249 L253 S260 F271 Y275 H284 R289 C290 E291 E296 K305 R306 S307 R308 F309 Y310 K311 G312 N313 S319 E322 I323 A324 D325 L326 N330 E346 E375 S388 L389 Y390 N396 V399 E408 N409 L416 K422 D423

Y426 D456 T457 D458 D469 K472 Q502 L513 I537 K553 M554 V565 T571 K575

• Molecule 1: DNA polymerase

Chain K: %   84%   14%   ··

MET LYS HIS MET PRO R6 E14 T17 K18 V19 E20 V24 W25 A26 Y38 L44 M48 A49 W50 V54 N62 W73 L107 R113 K125 F128 K131 K132 D145 I146 D147 R152 K167 N168 D169 Q180 L185 D186 R187 S194

T203 R227 D249 L253 Q257 M258 Y259 S260 P268 F271 Y275 P282 L283 H284 R289 C290 E296 T301 I302 K305 R308 F309 E322 I323 A324 D325 L326 N330 M336 Y340 F353 K354 A355 K361 E375 L384 N396

V399 L406 K407 E408 N409 L416 K422 D423 Y426 T427 A437 T457 D458 D469 V470 I471 V475 F489 L495 R496 Q497 K498 I504 Y505 M506 D519 K525 F543 K553 V561 P562 T571 F572 T573 I574 K575
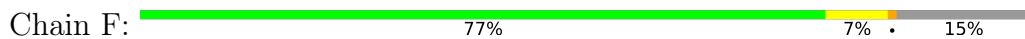
• Molecule 2: DNA terminal protein

Chain B:

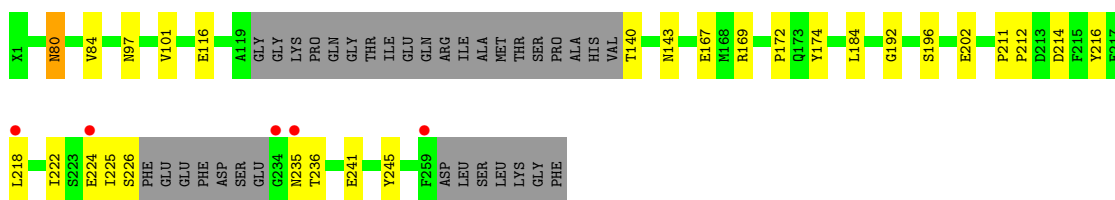• Molecule 2: DNA terminal protein

Chain D:

• Molecule 2: DNA terminal protein

Chain F:

• Molecule 2: DNA terminal protein

Chain H:

• Molecule 2: DNA terminal protein

Chain J:

F219 I222 S223 E224 I225 S226 PHE GLU GLU PHE ASP SER GLU G234 N235 T236 V237 E238 N239 F259 ASP LEU SER LEU LYS GLY PHE

• Molecule 2: DNA terminal protein

Chain L:

%

76%   8%   •   15%

X1 N80 A81 K88 E93 R96 R103 E107 A119 GLY GLY LYS PRO GLN GLY THR ILE GLU GLN ARG ILE ALA MET THR SER PRO ALA HIS VAL T140 G141 I142 N143 V153 L159 Y174 K178 L182 G192 S196 Y216 E217 L218 E224

I225 S226 PHE GLU GLU PHE ASP SER GLU G234 N235 T236 V237 F259 ASP LEU SER LEU LYS GLY PHE

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	304.93Å　220.28Å　217.16Å 90.00°　45.40°　90.00°	Depositor
Resolution (Å)	48.85　–　3.00 48.83　–　3.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.85-3.00) 99.7 (48.83-3.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.43 (at 3.01Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.200　,　0.229 0.204　,　0.231	Depositor DCC
R_{free} test set	20161 reflections (9.97%)	wwPDB-VP
Wilson B-factor (Å^2)	91.1	Xtriage
Anisotropy	0.010	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 96.6	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.006 for -h+2*l,k,-h+l 0.011 for -h-k+l,-l,-k 0.006 for -h+k+l,l,k 0.008 for -k-l,-h+l,-l 0.008 for k-l,h-l,-l 0.039 for k+l,h-l,k 0.044 for h+k-l,l,h-l 0.038 for -k+l,-h+l,-k 0.036 for h-k-l,-l,h-l 0.010 for h,-k,h-l 0.023 for h-2*l,-k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	37108	wwPDB-VP
Average B, all atoms (Å^2)	99.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.97% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: PB

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	0.38	0/4780	0.53	0/6448
1	C	0.37	0/4780	0.52	0/6448
1	E	0.37	0/4780	0.52	0/6448
1	G	0.37	0/4780	0.53	0/6448
1	I	0.37	0/4780	0.51	0/6448
1	K	0.37	0/4780	0.51	0/6448
2	B	0.36	0/1373	0.50	0/1837
2	D	0.38	0/1373	0.50	0/1837
2	F	0.36	0/1373	0.50	0/1837
2	H	0.35	0/1373	0.50	0/1837
2	J	0.38	0/1373	0.49	0/1837
2	L	0.37	0/1373	0.48	0/1837
All	All	0.37	0/36918	0.51	0/49710

There are no bond length outliers.

There are no bond angle outliers.

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	4661	0	4668	53	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	4661	0	4668	51	0
1	E	4661	0	4668	35	0
1	G	4661	0	4668	35	0
1	I	4661	0	4668	36	0
1	K	4661	0	4668	43	0
2	B	1521	0	1366	13	0
2	D	1521	0	1365	13	0
2	F	1521	0	1366	11	0
2	H	1521	0	1365	15	0
2	J	1521	0	1366	14	0
2	L	1521	0	1366	14	0
3	A	3	0	0	0	0
3	C	3	0	0	0	0
3	E	3	0	0	0	0
3	G	3	0	0	0	0
3	I	2	0	0	0	0
3	K	2	0	0	0	0
All	All	37108	0	36202	303	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.

The worst 5 of 303 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)
2:L:80:ASN:HD22	2:L:81:ALA:H	1.28	0.81
1:E:310:TYR:CE1	1:E:312:GLY:HA2	2.20	0.76
1:E:399:VAL:HG21	1:E:422:LYS:HB2	1.69	0.75
1:I:309:PHE:CE1	1:I:322:GLU:HG2	2.24	0.72
1:A:370:ILE:O	1:A:374:SER:HB2	1.89	0.72

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	568/575 (99%)	547 (96%)	17 (3%)	4 (1%)	22	60
1	C	568/575 (99%)	543 (96%)	21 (4%)	4 (1%)	22	60
1	E	568/575 (99%)	540 (95%)	23 (4%)	5 (1%)	17	55
1	G	568/575 (99%)	549 (97%)	15 (3%)	4 (1%)	22	60
1	I	568/575 (99%)	543 (96%)	20 (4%)	5 (1%)	17	55
1	K	568/575 (99%)	543 (96%)	19 (3%)	6 (1%)	14	50
2	B	156/230 (68%)	149 (96%)	7 (4%)	0	100	100
2	D	156/230 (68%)	148 (95%)	8 (5%)	0	100	100
2	F	156/230 (68%)	149 (96%)	7 (4%)	0	100	100
2	H	156/230 (68%)	149 (96%)	7 (4%)	0	100	100
2	J	156/230 (68%)	148 (95%)	8 (5%)	0	100	100
2	L	156/230 (68%)	148 (95%)	8 (5%)	0	100	100
All	All	4344/4830 (90%)	4156 (96%)	160 (4%)	28 (1%)	25	64

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	310	TYR
1	A	426	TYR
1	C	312	GLY
1	C	511	GLY
1	E	312	GLY

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	501/506 (99%)	478 (95%)	23 (5%)	27	64
1	C	501/506 (99%)	476 (95%)	25 (5%)	24	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles		
1	E	501/506 (99%)	479 (96%)	22 (4%)	28	65	
1	G	501/506 (99%)	480 (96%)	21 (4%)	30	66	
1	I	501/506 (99%)	477 (95%)	24 (5%)	25	62	
1	K	501/506 (99%)	477 (95%)	24 (5%)	25	62	
2	B	147/175 (84%)	139 (95%)	8 (5%)	22	57	
2	D	147/175 (84%)	143 (97%)	4 (3%)	44	77	
2	F	147/175 (84%)	140 (95%)	7 (5%)	25	62	
2	H	147/175 (84%)	138 (94%)	9 (6%)	18	53	
2	J	147/175 (84%)	139 (95%)	8 (5%)	22	57	
2	L	147/175 (84%)	139 (95%)	8 (5%)	22	57	
All	All	3888/4086 (95%)	3705 (95%)	183 (5%)	26	63	

5 of 183 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	202	GLU
2	J	80	ASN
1	I	17	THR
1	I	306	ARG
2	J	236	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	284	HIS
1	K	171	GLN
1	I	330	ASN
2	J	80	ASN
1	K	330	ASN

5.3.3   RNA (i)

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 monosaccharides in this entry.

5.6   Ligand geometry ⓘ

Of 16 ligands modelled in this entry, 16 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 ⓘ

There are no such residues in this entry.

5.8   Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	J	2
2	F	2
2	D	2
2	H	2
2	L	2
2	B	2

The worst 5 of 12 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	J	12:UNK	C	26:UNK	N	19.24
1	F	12:UNK	C	26:UNK	N	19.18

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	12:UNK	C	26:UNK	N	19.10
1	H	12:UNK	C	26:UNK	N	19.05
1	L	12:UNK	C	26:UNK	N	18.98

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(Å²)	Q<0.9
1	A	570/575 (99%)	0.21	1 (0%)	95	87	86, 99, 112, 132	0
1	C	570/575 (99%)	0.26	4 (0%)	87	69	84, 99, 112, 158	0
1	E	570/575 (99%)	0.24	5 (0%)	84	63	85, 99, 111, 143	0
1	G	570/575 (99%)	0.21	1 (0%)	95	87	85, 98, 111, 140	0
1	I	570/575 (99%)	0.20	7 (1%)	79	54	86, 99, 111, 148	0
1	K	570/575 (99%)	0.25	3 (0%)	91	75	86, 98, 112, 145	0
2	B	162/230 (70%)	0.26	2 (1%)	79	54	76, 99, 113, 124	0
2	D	162/230 (70%)	0.36	4 (2%)	57	29	83, 98, 114, 125	0
2	F	162/230 (70%)	0.34	1 (0%)	89	72	78, 99, 114, 125	0
2	H	162/230 (70%)	0.26	5 (3%)	49	21	80, 99, 114, 125	0
2	J	162/230 (70%)	0.28	3 (1%)	66	37	82, 98, 114, 125	0
2	L	162/230 (70%)	0.33	3 (1%)	66	37	82, 98, 115, 124	0
All	All	4392/4830 (90%)	0.24	39 (0%)	84	63	76, 99, 112, 158	0

The worst 5 of 39 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	J	224	GLU	4.2
1	E	308	ARG	3.6
2	D	234	GLY	3.6
1	E	512	LYS	3.5
1	E	305	LYS	3.5

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 (i)

There are no monosaccharides 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($\mathring{A}^2$)	Q<0.9
3	PB	C	706	1/1	0.56	0.16	191,191,191,191	1
3	PB	K	715	1/1	0.79	0.08	175,175,175,175	1
3	PB	E	707	1/1	0.81	0.09	174,174,174,174	1
3	PB	C	705	1/1	0.83	0.08	162,162,162,162	1
3	PB	E	709	1/1	0.85	0.07	182,182,182,182	1
3	PB	A	702	1/1	0.88	0.05	165,165,165,165	1
3	PB	I	714	1/1	0.89	0.09	180,180,180,180	1
3	PB	E	708	1/1	0.91	0.13	160,160,160,160	1
3	PB	G	710	1/1	0.93	0.12	158,158,158,158	1
3	PB	A	701	1/1	0.94	0.07	157,157,157,157	1
3	PB	I	713	1/1	0.94	0.13	155,155,155,155	1
3	PB	C	704	1/1	0.95	0.19	146,146,146,146	1
3	PB	K	716	1/1	0.96	0.13	160,160,160,160	1
3	PB	G	711	1/1	0.97	0.13	156,156,156,156	1
3	PB	A	703	1/1	0.98	0.19	103,103,103,103	1
3	PB	G	712	1/1	0.99	0.19	106,106,106,106	1

6.5 Other polymers (i)

There are no such residues in this entry.