



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 12:08 am GMT

PDB ID : 2XUR
Title : THE G157C MUTATION IN THE ESCHERICHIA COLI SLIDING CLAMP SPECIFICALLY AFFECTS INITIATION OF REPLICATION
Authors : Johnsen, L.; Morigen; Dalhus, B.; Bjoras, M.; Flaatten, I.; Waldminghaus, T.; Skarstad, K.
Deposited on : 2010-10-20
Resolution : 1.90 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

<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
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

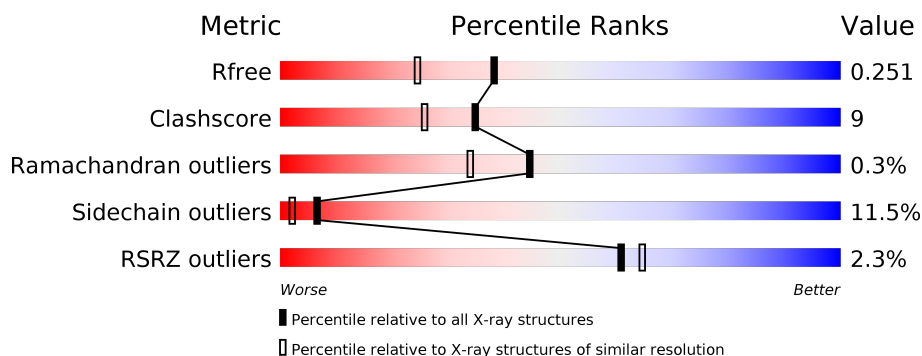
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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}	100719	5047 (1.90-1.90)
Clashscore	112137	5731 (1.90-1.90)
Ramachandran outliers	110173	5669 (1.90-1.90)
Sidechain outliers	110143	5670 (1.90-1.90)
RSRZ outliers	101464	5100 (1.90-1.90)

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	373	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="width: 80%; height: 10px; background-color: green;"></div> <div style="width: 14%; height: 10px; background-color: yellow;"></div> <div style="width: 6%; height: 10px; background-color: orange;"></div> <div style="width: 2%; height: 10px; background-color: grey;"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> % 80% 14% • • </div> </div>
1	B	373	<div> <div style="width: 3%; height: 10px; background-color: red;"></div> <div style="width: 73%; height: 10px; background-color: green;"></div> <div style="width: 19%; height: 10px; background-color: yellow;"></div> <div style="width: 5%; height: 10px; background-color: orange;"></div> <div style="width: 1%; height: 10px; background-color: grey;"></div> <div style="display: flex; justify-content: space-between; padding: 0 5px;"> 3% 73% 19% 5% • • </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6224 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 III SUBUNIT BETA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	366	Total	C	N	O	S	0	0	0
			2846	1787	498	541	20			
1	B	364	Total	C	N	O	S	0	0	0
			2826	1775	493	538	20			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	MET	-	EXPRESSION TAG	UNP P0A988
A	-5	HIS	-	EXPRESSION TAG	UNP P0A988
A	-4	HIS	-	EXPRESSION TAG	UNP P0A988
A	-3	HIS	-	EXPRESSION TAG	UNP P0A988
A	-2	HIS	-	EXPRESSION TAG	UNP P0A988
A	-1	HIS	-	EXPRESSION TAG	UNP P0A988
A	0	HIS	-	EXPRESSION TAG	UNP P0A988
A	157	CYS	GLY	ENGINEERED MUTATION	UNP P0A988
B	-6	MET	-	EXPRESSION TAG	UNP P0A988
B	-5	HIS	-	EXPRESSION TAG	UNP P0A988
B	-4	HIS	-	EXPRESSION TAG	UNP P0A988
B	-3	HIS	-	EXPRESSION TAG	UNP P0A988
B	-2	HIS	-	EXPRESSION TAG	UNP P0A988
B	-1	HIS	-	EXPRESSION TAG	UNP P0A988
B	0	HIS	-	EXPRESSION TAG	UNP P0A988
B	157	CYS	GLY	ENGINEERED MUTATION	UNP P0A988

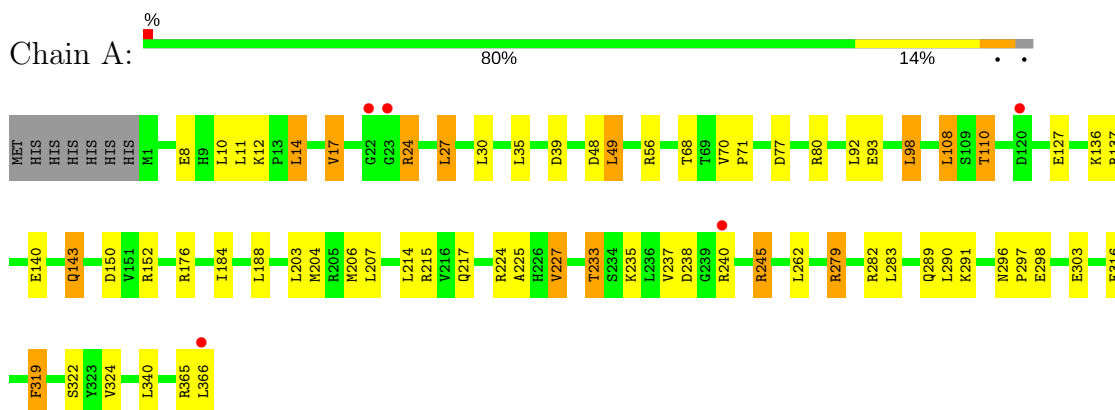
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	295	Total	O	0	0
			295	295		
2	B	257	Total	O	0	0
			257	257		

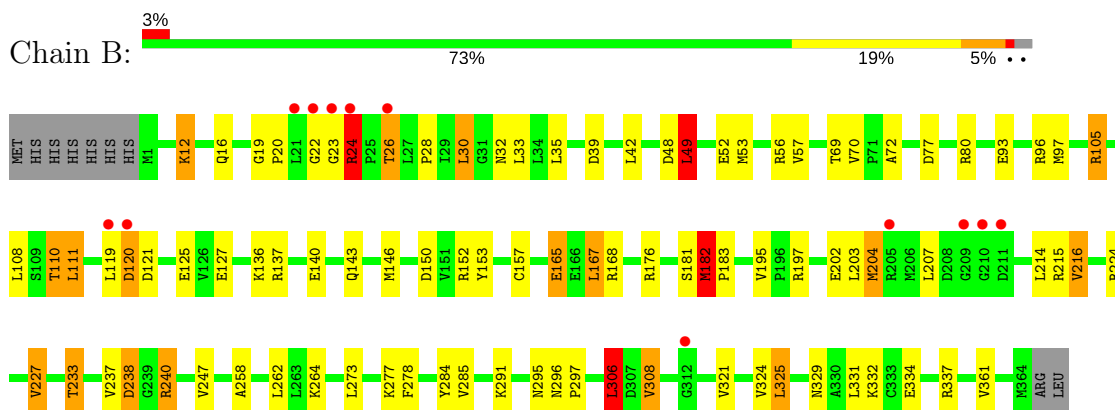
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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 III SUBUNIT BETA



• Molecule 1: DNA POLYMERASE III SUBUNIT BETA



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	79.98Å 66.49Å 81.70Å 90.00° 113.75° 90.00°	Depositor
Resolution (Å)	36.61 – 1.90 36.60 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.9 (36.61-1.90) 99.9 (36.60-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.00 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.194 , 0.252 0.193 , 0.251	Depositor DCC
R_{free} test set	3140 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	19.6	Xtriage
Anisotropy	0.067	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 57.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.019 for l,-k,h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6224	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.14% 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	0.91	0/2895	0.91	7/3918 (0.2%)
1	B	0.86	1/2875 (0.0%)	0.94	7/3893 (0.2%)
All	All	0.88	1/5770 (0.0%)	0.92	14/7811 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	165	GLU	CB-CG	-5.23	1.42	1.52

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	227	VAL	CB-CA-C	-6.91	98.27	111.40
1	B	168	ARG	NE-CZ-NH1	6.70	123.65	120.30
1	A	17	VAL	CG1-CB-CG2	6.37	121.09	110.90
1	B	168	ARG	NE-CZ-NH2	-6.35	117.13	120.30
1	A	245	ARG	NE-CZ-NH2	-6.33	117.14	120.30
1	A	279	ARG	NE-CZ-NH1	5.55	123.07	120.30
1	A	27	LEU	CA-CB-CG	5.53	128.02	115.30
1	B	306	LEU	CA-CB-CG	5.35	127.60	115.30
1	B	49	LEU	CA-CB-CG	5.29	127.46	115.30
1	B	182	MET	CG-SD-CE	5.23	108.56	100.20
1	B	216	VAL	CG1-CB-CG2	5.16	119.15	110.90
1	A	245	ARG	NE-CZ-NH1	5.15	122.87	120.30
1	A	108	LEU	CA-CB-CG	5.03	126.87	115.30
1	B	167	LEU	CA-CB-CG	5.02	126.85	115.30

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	2846	0	2863	44	1
1	B	2826	0	2839	64	1
2	A	295	0	0	18	1
2	B	257	0	0	12	1
All	All	6224	0	5702	107	2

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 9.

All (107) 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:12:LYS:HE2	2:A:2013:HOH:O	1.60	1.00
1:A:24:ARG:CZ	2:A:2020:HOH:O	2.18	0.90
1:A:8:GLU:HB2	2:A:2009:HOH:O	1.70	0.89
1:A:12:LYS:HD2	2:A:2167:HOH:O	1.75	0.84
1:B:69:THR:HB	1:B:111:LEU:O	1.79	0.82
1:A:136:LYS:HD3	1:A:207:LEU:HB2	1.62	0.82
1:A:298:GLU:OE2	2:A:2239:HOH:O	1.96	0.81
1:B:140:GLU:HG3	1:B:204:MET:HE1	1.63	0.81
1:B:110:THR:HG23	2:B:2079:HOH:O	1.82	0.78
1:B:182:MET:HA	1:B:182:MET:HE3	1.66	0.77
1:A:143:GLN:HG3	2:A:2126:HOH:O	1.85	0.75
1:B:140:GLU:HG3	1:B:204:MET:CE	2.16	0.75
1:A:140:GLU:HG3	1:A:204:MET:HE1	1.69	0.75
1:B:182:MET:CE	1:B:182:MET:HA	2.18	0.74
1:B:119:LEU:HG	1:B:120:ASP:H	1.54	0.73
1:A:279:ARG:HD3	1:A:322:SER:OG	1.91	0.71
1:A:140:GLU:HG3	1:A:204:MET:CE	2.21	0.70
1:B:52:GLU:HB3	1:B:119:LEU:HD22	1.73	0.70
1:B:32:ASN:HD22	1:B:69:THR:HG22	1.56	0.69
1:A:365:ARG:HD3	2:A:2292:HOH:O	1.93	0.68
1:B:150:ASP:OD1	1:B:152:ARG:HD3	1.93	0.68
1:A:316:GLU:HG2	2:A:2224:HOH:O	1.95	0.67
1:A:215:ARG:NH2	2:A:2177:HOH:O	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:THR:HG21	1:A:92:LEU:HD11	1.77	0.67
1:B:240:ARG:HG2	1:B:240:ARG:O	1.95	0.66
1:B:26:THR:O	1:B:28:PRO:HD3	1.96	0.65
1:B:32:ASN:HD22	1:B:69:THR:CG2	2.10	0.64
1:B:48:ASP:O	1:B:49:LEU:HB2	1.97	0.64
1:B:77:ASP:OD1	1:B:80:ARG:NH2	2.30	0.64
1:B:182:MET:HE2	1:B:183:PRO:HD2	1.79	0.64
1:B:12:LYS:O	1:B:16:GLN:HG3	1.99	0.63
1:B:52:GLU:CB	1:B:119:LEU:HD22	2.28	0.62
1:B:224:ARG:HH21	1:B:233:THR:HG21	1.63	0.61
1:B:240:ARG:NH1	2:B:2164:HOH:O	2.32	0.61
1:B:119:LEU:HG	1:B:120:ASP:N	2.16	0.61
1:A:136:LYS:HD3	1:A:207:LEU:CB	2.32	0.60
1:B:42:LEU:HB3	1:B:57:VAL:HG22	1.85	0.58
1:A:233:THR:HG23	2:A:2044:HOH:O	2.04	0.57
1:B:165:GLU:OE2	2:B:2121:HOH:O	2.17	0.56
1:B:20:PRO:HB3	1:B:202:GLU:CD	2.25	0.56
1:B:23:GLY:O	1:B:24:ARG:HB3	2.05	0.55
1:A:203:LEU:O	1:A:206:MET:HG2	2.07	0.55
1:A:224:ARG:HH21	1:A:233:THR:HG21	1.71	0.55
1:A:289:GLN:HG3	2:A:2232:HOH:O	2.06	0.55
1:B:153:TYR:HE2	1:B:238:ASP:O	1.90	0.54
1:A:48:ASP:O	1:A:49:LEU:HB2	2.06	0.54
1:B:24:ARG:HG2	1:B:24:ARG:O	2.08	0.53
1:B:70:VAL:HG11	1:B:97:MET:SD	2.49	0.53
1:A:140:GLU:CG	1:A:204:MET:HE2	2.38	0.52
1:B:224:ARG:HE	1:B:233:THR:CG2	2.22	0.52
1:A:140:GLU:CG	1:A:204:MET:CE	2.87	0.52
1:B:197:ARG:NH2	2:B:2141:HOH:O	2.42	0.52
1:A:291:LYS:HE3	1:A:303:GLU:OE1	2.10	0.52
1:B:143:GLN:HG3	1:B:146:MET:CE	2.40	0.52
1:B:32:ASN:HB3	1:B:69:THR:HG23	1.93	0.51
1:A:93:GLU:CD	1:A:98:LEU:HG	2.31	0.50
1:A:10:LEU:HG	1:A:14:LEU:HD22	1.94	0.50
1:B:110:THR:CG2	2:B:2079:HOH:O	2.48	0.50
1:B:284:TYR:HB2	1:B:291:LYS:HB3	1.92	0.50
1:B:215:ARG:CZ	2:B:2150:HOH:O	2.59	0.49
1:B:30:LEU:HD21	1:B:49:LEU:HD22	1.94	0.49
1:A:296:ASN:HB2	1:A:297:PRO:CD	2.42	0.49
1:B:127:GLU:HB3	1:B:215:ARG:HH21	1.77	0.48
1:A:110:THR:HG21	2:A:2075:HOH:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:214:LEU:HD11	1:A:225:ALA:HB1	1.96	0.48
1:B:224:ARG:HE	1:B:233:THR:HG21	1.78	0.48
1:B:306:LEU:HD23	1:B:306:LEU:N	2.29	0.48
1:A:319:PHE:CE1	1:A:324:VAL:HG21	2.48	0.47
1:B:127:GLU:OE1	1:B:215:ARG:NH2	2.47	0.47
1:B:140:GLU:HG3	1:B:204:MET:HE3	1.96	0.47
1:A:245:ARG:NH2	2:A:2193:HOH:O	2.48	0.47
1:B:119:LEU:HD13	2:B:2021:HOH:O	2.14	0.46
1:B:296:ASN:HB2	1:B:297:PRO:CD	2.45	0.46
1:B:19:GLY:N	1:B:20:PRO:HD2	2.29	0.46
1:B:157:CYS:HB3	1:B:195:VAL:O	2.15	0.46
1:B:143:GLN:HG3	1:B:146:MET:HE2	1.97	0.45
1:B:153:TYR:CE2	1:B:238:ASP:O	2.69	0.45
1:A:303:GLU:HB3	1:B:105:ARG:HG3	1.98	0.45
1:B:120:ASP:HB3	2:B:2156:HOH:O	2.16	0.45
1:B:42:LEU:HB3	1:B:57:VAL:CG2	2.47	0.45
1:A:150:ASP:OD1	1:A:152:ARG:HD3	2.16	0.45
1:A:24:ARG:NH2	2:A:2020:HOH:O	2.40	0.45
1:B:119:LEU:HD23	2:B:2089:HOH:O	2.17	0.45
1:B:119:LEU:CD1	2:B:2021:HOH:O	2.65	0.44
1:B:278:PHE:HB2	2:B:2202:HOH:O	2.17	0.44
1:A:233:THR:CG2	2:A:2044:HOH:O	2.63	0.44
1:A:184:ILE:HD11	1:A:188:LEU:HD11	2.00	0.43
1:B:264:LYS:HD2	1:B:329:ASN:ND2	2.33	0.43
1:A:110:THR:HG23	2:A:2094:HOH:O	2.17	0.43
1:A:24:ARG:HG3	1:A:24:ARG:O	2.19	0.43
1:A:77:ASP:OD1	1:A:80:ARG:NH2	2.51	0.43
1:B:214:LEU:HD12	1:B:227:VAL:HG13	2.01	0.43
1:B:33:LEU:HG	1:B:72:ALA:HB2	2.00	0.43
1:A:282:ARG:HD2	2:A:2238:HOH:O	2.18	0.43
1:A:283:LEU:HG	1:A:290:LEU:HD11	2.01	0.42
1:B:240:ARG:HH11	1:B:240:ARG:HB3	1.85	0.42
1:A:70:VAL:CG2	1:A:71:PRO:HD2	2.50	0.42
1:A:224:ARG:HE	1:A:233:THR:CG2	2.33	0.42
1:A:127:GLU:HG2	1:A:217:GLN:HG2	2.02	0.41
1:B:30:LEU:HD11	1:B:49:LEU:HD13	2.01	0.41
1:B:321:VAL:HG22	1:B:325:LEU:HD22	2.03	0.41
1:A:24:ARG:NH1	2:A:2020:HOH:O	2.45	0.41
1:B:33:LEU:O	1:B:69:THR:HA	2.21	0.40
1:B:240:ARG:O	1:B:240:ARG:CG	2.66	0.40
1:B:258:ALA:HB2	1:B:308:VAL:HG22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:337:ARG:NH1	2:B:2236:HOH:O	2.55	0.40
1:B:32:ASN:CB	1:B:69:THR:HG23	2.51	0.40

All (2) 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:A:215:ARG:NH2	1:B:39:ASP:OD2[1_455]	2.15	0.05
2:A:2116:HOH:O	2:B:2176:HOH:O[1_556]	2.19	0.01

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	364/373 (98%)	359 (99%)	5 (1%)	0	100	100
1	B	362/373 (97%)	348 (96%)	12 (3%)	2 (1%)	28	16
All	All	726/746 (97%)	707 (97%)	17 (2%)	2 (0%)	44	34

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	24	ARG
1	B	22	GLY

5.3.2 Protein sidechains [i](#)

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	314/321 (98%)	288 (92%)	26 (8%)	13	5
1	B	312/321 (97%)	266 (85%)	46 (15%)	3	1
All	All	626/642 (98%)	554 (88%)	72 (12%)	6	2

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	LEU
1	A	14	LEU
1	A	17	VAL
1	A	24	ARG
1	A	27	LEU
1	A	30	LEU
1	A	35	LEU
1	A	39	ASP
1	A	49	LEU
1	A	56	ARG
1	A	98	LEU
1	A	108	LEU
1	A	110	THR
1	A	137	ARG
1	A	143	GLN
1	A	176	ARG
1	A	227	VAL
1	A	233	THR
1	A	235	LYS
1	A	237	VAL
1	A	238	ASP
1	A	240	ARG
1	A	262	LEU
1	A	319	PHE
1	A	340	LEU
1	A	366	LEU
1	B	12	LYS
1	B	24	ARG
1	B	26	THR
1	B	30	LEU
1	B	35	LEU
1	B	49	LEU
1	B	53	MET
1	B	56	ARG

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Mol	Chain	Res	Type
1	B	93	GLU
1	B	96	ARG
1	B	105	ARG
1	B	108	LEU
1	B	110	THR
1	B	111	LEU
1	B	120	ASP
1	B	121	ASP
1	B	125	GLU
1	B	136	LYS
1	B	137	ARG
1	B	167	LEU
1	B	176	ARG
1	B	181	SER
1	B	182	MET
1	B	203	LEU
1	B	204	MET
1	B	207	LEU
1	B	216	VAL
1	B	227	VAL
1	B	233	THR
1	B	237	VAL
1	B	238	ASP
1	B	240	ARG
1	B	247	VAL
1	B	262	LEU
1	B	273	LEU
1	B	277	LYS
1	B	285	VAL
1	B	295	ASN
1	B	306	LEU
1	B	308	VAL
1	B	324	VAL
1	B	325	LEU
1	B	331	LEU
1	B	332	LYS
1	B	334	GLU
1	B	361	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	GLN
1	A	143	GLN
1	A	212	ASN
1	B	15	GLN
1	B	32	ASN
1	B	143	GLN
1	B	212	ASN
1	B	295	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 carbohydrates 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	366/373 (98%)	-0.31	5 (1%) 75 78	8, 18, 29, 42	0
1	B	364/373 (97%)	-0.14	12 (3%) 47 50	10, 19, 36, 56	0
All	All	730/746 (97%)	-0.23	17 (2%) 61 64	8, 18, 33, 56	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	22	GLY	9.1
1	B	23	GLY	6.5
1	B	209	GLY	5.4
1	B	24	ARG	5.2
1	B	21	LEU	4.3
1	B	119	LEU	3.8
1	A	240	ARG	3.3
1	B	26	THR	2.8
1	B	120	ASP	2.6
1	A	366	LEU	2.6
1	A	22	GLY	2.6
1	B	205	ARG	2.5
1	A	23	GLY	2.5
1	B	210	GLY	2.3
1	B	211	ASP	2.3
1	A	120	ASP	2.1
1	B	312	GLY	2.0

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 carbohydrates 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.