



Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 02:31 am BST

PDB ID : 6K2M
Title : Crystal structure of the complex of Proliferating Cell Nuclear Antigen from *Leishmania donovani* with arginine at 3.19 Å resolution.
Authors : Viswanathan, V.; Iqbal, N.; Sharma, S.; Singh, T.P.
Deposited on : 2019-05-15
Resolution : 3.19 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
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) : 2.11

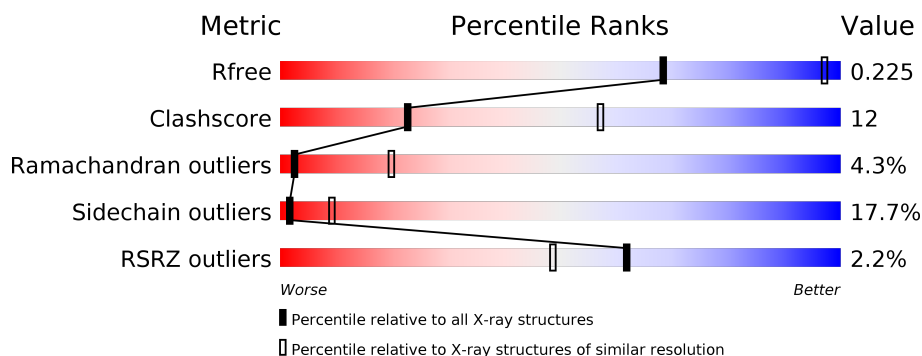
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.19 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}	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 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	302	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 1%, green 1%, green 59%, yellow 59%, yellow 77%, orange 77%, orange 78%, grey 78%, grey 100%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 59% 18% • • 18% </div> </div>
1	B	302	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 4%, green 4%, green 54%, yellow 54%, yellow 78%, orange 78%, orange 79%, grey 79%, grey 100%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 4% 54% 24% • 18% </div> </div>
1	C	302	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 1%, green 1%, green 46%, yellow 46%, yellow 76%, orange 76%, orange 77%, grey 77%, grey 100%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 46% 30% 5% • 18% </div> </div>
1	D	302	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 2%, green 2%, green 53%, yellow 53%, yellow 78%, orange 78%, orange 79%, grey 79%, grey 100%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 2% 53% 25% • • 17% </div> </div>
1	E	302	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 2%, green 2%, green 58%, yellow 58%, yellow 78%, orange 78%, orange 85%, grey 85%, grey 100%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 2% 58% 20% 7% 15% </div> </div>
1	F	302	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 1%, green 1%, green 50%, yellow 50%, yellow 76%, orange 76%, orange 77%, grey 77%, grey 100%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 50% 26% 5% • 18% </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11702 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 Proliferating cell nuclear antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	248	Total	C	N	O	S	0	0	0
			1919	1210	317	377	15			
1	D	251	Total	C	N	O	S	0	0	0
			1941	1222	320	384	15			
1	E	258	Total	C	N	O	S	0	0	0
			1988	1251	332	390	15			
1	B	248	Total	C	N	O	S	0	0	0
			1919	1210	317	377	15			
1	C	248	Total	C	N	O	S	0	0	0
			1919	1210	317	377	15			
1	F	248	Total	C	N	O	S	0	0	0
			1919	1210	317	377	15			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-9	HIS	-	expression tag	UNP B5TV91
A	-8	SER	-	expression tag	UNP B5TV91
A	-7	GLY	-	expression tag	UNP B5TV91
A	-6	ARG	-	expression tag	UNP B5TV91
A	-5	PRO	-	expression tag	UNP B5TV91
A	-4	VAL	-	expression tag	UNP B5TV91
A	-3	LEU	-	expression tag	UNP B5TV91
A	-2	GLY	-	expression tag	UNP B5TV91
A	-1	SER	-	expression tag	UNP B5TV91
A	0	SER	-	expression tag	UNP B5TV91
D	-9	HIS	-	expression tag	UNP B5TV91
D	-8	SER	-	expression tag	UNP B5TV91
D	-7	GLY	-	expression tag	UNP B5TV91
D	-6	ARG	-	expression tag	UNP B5TV91
D	-5	PRO	-	expression tag	UNP B5TV91
D	-4	VAL	-	expression tag	UNP B5TV91
D	-3	LEU	-	expression tag	UNP B5TV91

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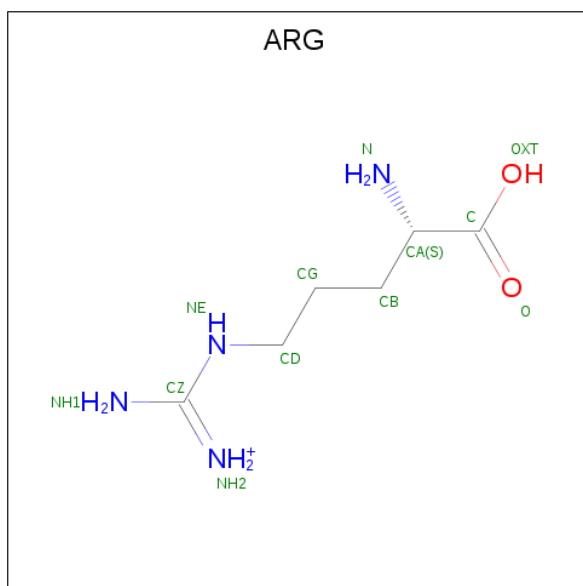
Chain	Residue	Modelled	Actual	Comment	Reference
D	-2	GLY	-	expression tag	UNP B5TV91
D	-1	SER	-	expression tag	UNP B5TV91
D	0	SER	-	expression tag	UNP B5TV91
E	-9	HIS	-	expression tag	UNP B5TV91
E	-8	SER	-	expression tag	UNP B5TV91
E	-7	GLY	-	expression tag	UNP B5TV91
E	-6	ARG	-	expression tag	UNP B5TV91
E	-5	PRO	-	expression tag	UNP B5TV91
E	-4	VAL	-	expression tag	UNP B5TV91
E	-3	LEU	-	expression tag	UNP B5TV91
E	-2	GLY	-	expression tag	UNP B5TV91
E	-1	SER	-	expression tag	UNP B5TV91
E	0	SER	-	expression tag	UNP B5TV91
B	-9	HIS	-	expression tag	UNP B5TV91
B	-8	SER	-	expression tag	UNP B5TV91
B	-7	GLY	-	expression tag	UNP B5TV91
B	-6	ARG	-	expression tag	UNP B5TV91
B	-5	PRO	-	expression tag	UNP B5TV91
B	-4	VAL	-	expression tag	UNP B5TV91
B	-3	LEU	-	expression tag	UNP B5TV91
B	-2	GLY	-	expression tag	UNP B5TV91
B	-1	SER	-	expression tag	UNP B5TV91
B	0	SER	-	expression tag	UNP B5TV91
C	-9	HIS	-	expression tag	UNP B5TV91
C	-8	SER	-	expression tag	UNP B5TV91
C	-7	GLY	-	expression tag	UNP B5TV91
C	-6	ARG	-	expression tag	UNP B5TV91
C	-5	PRO	-	expression tag	UNP B5TV91
C	-4	VAL	-	expression tag	UNP B5TV91
C	-3	LEU	-	expression tag	UNP B5TV91
C	-2	GLY	-	expression tag	UNP B5TV91
C	-1	SER	-	expression tag	UNP B5TV91
C	0	SER	-	expression tag	UNP B5TV91
F	-9	HIS	-	expression tag	UNP B5TV91
F	-8	SER	-	expression tag	UNP B5TV91
F	-7	GLY	-	expression tag	UNP B5TV91
F	-6	ARG	-	expression tag	UNP B5TV91
F	-5	PRO	-	expression tag	UNP B5TV91
F	-4	VAL	-	expression tag	UNP B5TV91
F	-3	LEU	-	expression tag	UNP B5TV91
F	-2	GLY	-	expression tag	UNP B5TV91
F	-1	SER	-	expression tag	UNP B5TV91

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Chain	Residue	Modelled	Actual	Comment	Reference
F	0	SER	-	expression tag	UNP B5TV91

- Molecule 2 is ARGinine (three-letter code: ARG) (formula: $C_6H_{15}N_4O_2$) (labeled as "Ligand of Interest" by author).

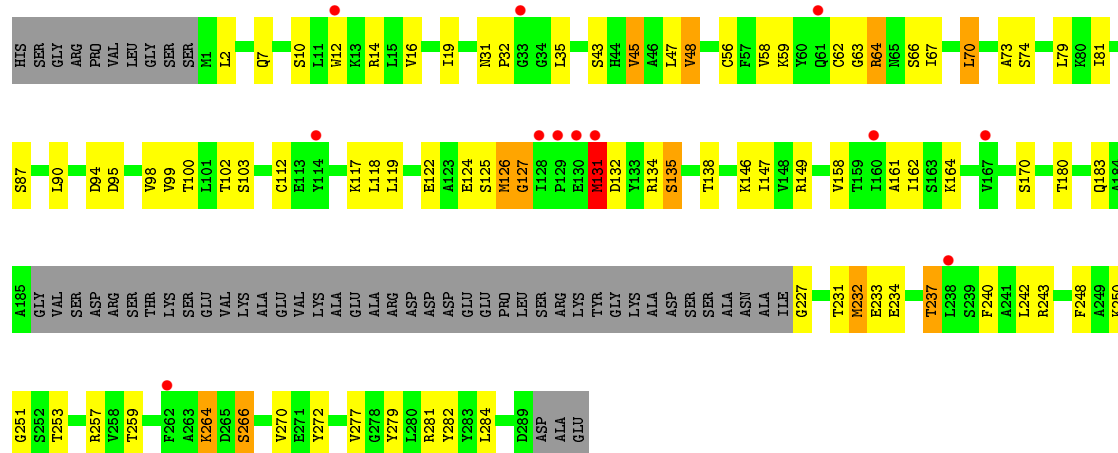


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			12	6	4	2		
2	E	1	Total	C	N	O	0	0
			12	6	4	2		

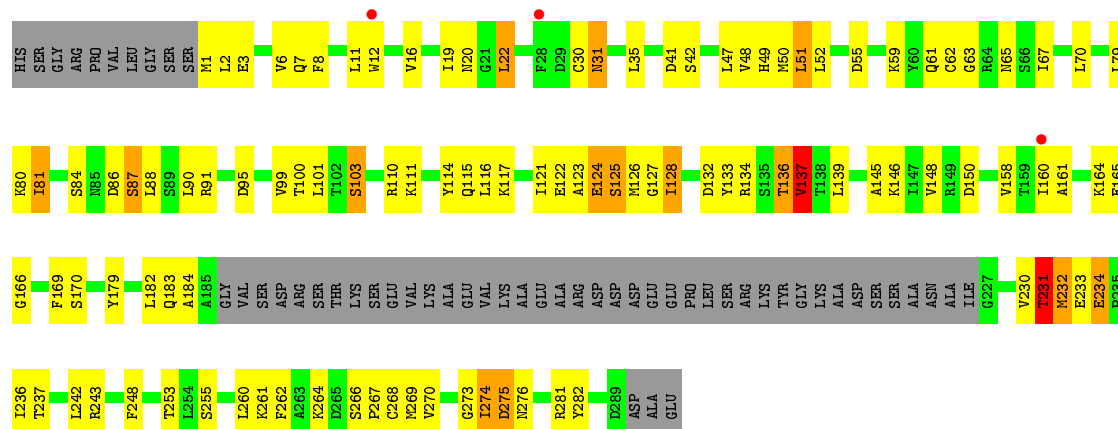
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	16	Total	O	0	0
			16	16		
3	D	22	Total	O	0	0
			22	22		
3	E	8	Total	O	0	0
			8	8		
3	B	8	Total	O	0	0
			8	8		
3	C	10	Total	O	0	0
			10	10		
3	F	9	Total	O	0	0
			9	9		

- Molecule 1: Proliferating cell nuclear antigen

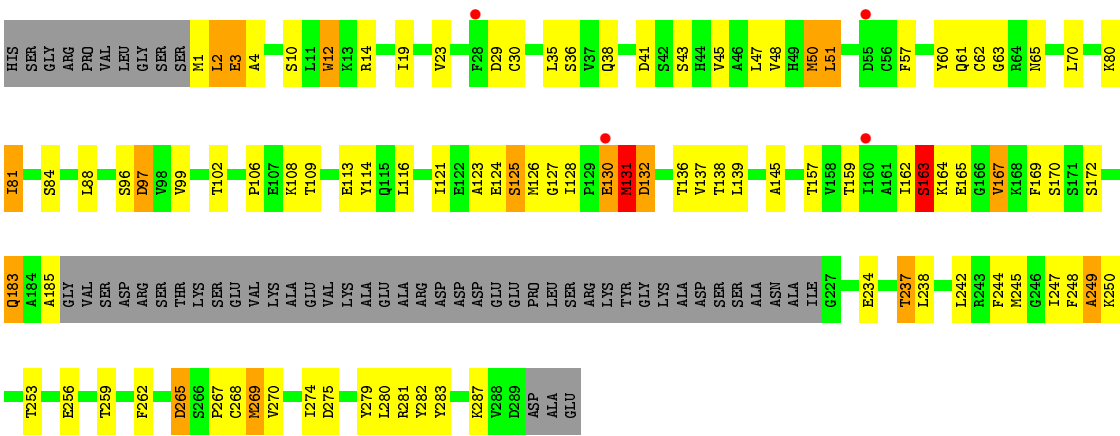


- Molecule 1: Proliferating cell nuclear antigen



- Molecule 1: Proliferating cell nuclear antigen





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	135.93Å 150.59Å 171.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	106.63 – 3.19 106.41 – 3.19	Depositor EDS
% Data completeness (in resolution range)	99.4 (106.63-3.19) 99.4 (106.41-3.19)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.45 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.167 , 0.227 0.173 , 0.225	Depositor DCC
R_{free} test set	3020 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å ²)	111.5	Xtriage
Anisotropy	0.356	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 80.6	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	11702	wwPDB-VP
Average B, all atoms (Å ²)	120.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.61% 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	0.69	0/1947	0.98	1/2627 (0.0%)
1	B	0.72	0/1947	0.92	0/2627
1	C	0.70	0/1947	0.94	0/2627
1	D	0.75	0/1969	0.95	0/2657
1	E	0.72	0/2018	0.98	0/2723
1	F	0.74	0/1947	0.92	0/2627
All	All	0.72	0/11775	0.95	1/15888 (0.0%)

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	A	0	1
1	B	0	2
1	C	0	2
1	D	0	3
1	E	0	1
1	F	0	3
All	All	0	12

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	95	ASP	CB-CA-C	-5.72	98.96	110.40

There are no chirality outliers.

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	104	GLU	Peptide
1	B	131	MET	Peptide
1	B	232	MET	Peptide
1	C	266	SER	Peptide
1	C	95	ASP	Peptide
1	D	1	MET	Peptide
1	D	119	LEU	Peptide
1	D	48	VAL	Peptide
1	E	38	GLN	Peptide
1	F	125	SER	Peptide
1	F	132	ASP	Peptide
1	F	62	CYS	Peptide

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	1919	0	1914	33	0
1	B	1919	0	1914	41	0
1	C	1919	0	1914	57	0
1	D	1941	0	1929	43	0
1	E	1988	0	1982	40	0
1	F	1919	0	1914	55	0
2	A	12	0	12	0	0
2	E	12	0	12	1	0
3	A	16	0	0	1	0
3	B	8	0	0	1	0
3	C	10	0	0	1	0
3	D	22	0	0	1	0
3	E	8	0	0	0	0
3	F	9	0	0	2	0
All	All	11702	0	11591	267	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 12.

All (267) 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:B:124:GLU:HB2	1:B:126:MET:SD	1.95	1.06
1:A:1:MET:N	1:A:94:ASP:OD2	2.00	0.93
1:A:22:LEU:HD12	1:A:48:VAL:HG22	1.61	0.82
1:C:2:LEU:HD23	1:C:3:GLU:N	1.94	0.81
1:A:1:MET:CA	1:A:94:ASP:OD2	2.30	0.79
1:D:56:CYS:HB2	1:D:277:VAL:HG13	1.64	0.79
1:F:130:GLU:O	1:F:131:MET:O	2.01	0.78
1:D:125:SER:O	1:D:127:GLY:N	2.20	0.74
1:A:95:ASP:OD1	1:A:96:SER:N	2.21	0.73
1:D:48:VAL:HG13	1:D:282:TYR:CE1	2.25	0.72
1:A:1:MET:HA	1:A:94:ASP:OD2	1.90	0.71
1:E:276:ASN:HD22	1:E:276:ASN:N	1.86	0.71
1:C:31:ASN:ND2	1:C:65:ASN:OD1	2.23	0.70
1:F:70:LEU:HD21	1:F:99:VAL:HG11	1.74	0.70
1:C:70:LEU:HD21	1:C:99:VAL:HG11	1.77	0.67
1:F:183:GLN:HG2	1:F:185:ALA:HB2	1.77	0.67
1:E:276:ASN:HD22	1:E:276:ASN:H	1.42	0.65
1:A:130:GLU:OE2	1:A:130:GLU:HA	1.97	0.64
1:D:49:HIS:ND1	1:D:128:ILE:HD11	2.13	0.63
1:C:22:LEU:HD12	1:C:48:VAL:CG2	2.28	0.63
1:F:116:LEU:N	1:F:116:LEU:HD23	2.13	0.63
1:A:105:ASN:HD22	1:A:106:PRO:HD2	1.64	0.63
1:D:56:CYS:HA	1:D:277:VAL:HG22	1.81	0.62
1:D:7:GLN:NE2	1:D:8:PHE:CE1	2.68	0.61
1:D:118:LEU:N	1:D:118:LEU:HD23	2.16	0.61
1:B:48:VAL:HG13	1:B:282:TYR:CE1	2.36	0.61
1:D:20:ASN:HB3	3:D:307:HOH:O	2.01	0.60
1:C:274:ILE:HG22	1:C:274:ILE:O	2.00	0.60
1:C:248:PHE:CD1	1:C:282:TYR:CG	2.89	0.60
1:A:18:CYS:HB3	1:A:282:TYR:OH	2.01	0.60
1:C:87:SER:O	1:C:103:SER:HA	2.00	0.60
1:E:126:MET:SD	2:E:301:ARG:HD2	2.41	0.60
1:C:116:LEU:N	1:C:116:LEU:HD12	2.17	0.59
1:C:81:ILE:HD11	1:C:114:TYR:CZ	2.38	0.59
1:F:96:SER:O	1:F:97:ASP:OD1	2.21	0.59
1:B:118:LEU:C	1:B:119:LEU:HD23	2.22	0.58
1:A:10:SER:HB3	1:A:14:ARG:NH1	2.19	0.58
1:E:276:ASN:H	1:E:276:ASN:ND2	2.00	0.58
1:F:248:PHE:CD1	1:F:282:TYR:CG	2.91	0.58
1:A:126:MET:HA	1:A:126:MET:CE	2.33	0.58
1:C:49:HIS:ND1	1:C:128:ILE:HD11	2.19	0.57
1:B:103:SER:HB3	1:B:112:CYS:HB2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:269:MET:HB2	1:F:283:TYR:CD1	2.39	0.57
1:B:149:ARG:HD2	3:B:308:HOH:O	2.04	0.57
1:F:2:LEU:HD23	1:F:3:GLU:N	2.19	0.57
1:D:37:VAL:HG23	1:D:50:MET:HE2	1.87	0.56
1:D:48:VAL:HG13	1:D:282:TYR:CD1	2.40	0.56
1:F:244:PHE:HA	1:F:247:ILE:HD12	1.87	0.56
1:E:242:LEU:O	1:E:243:ARG:C	2.43	0.56
1:D:249:ALA:HA	1:D:272:TYR:OH	2.05	0.56
1:D:266:SER:O	1:D:267:PRO:O	2.23	0.56
1:F:38:GLN:HA	1:F:48:VAL:O	2.06	0.56
1:A:48:VAL:HG13	1:A:282:TYR:CE1	2.41	0.56
1:A:158:VAL:H	1:A:242:LEU:HG	1.72	0.55
1:D:125:SER:O	1:D:126:MET:C	2.44	0.55
1:E:276:ASN:ND2	1:E:276:ASN:N	2.55	0.55
1:B:58:VAL:HG23	1:B:59:LYS:H	1.72	0.55
1:D:27:ASN:HD21	1:D:121:ILE:HG22	1.71	0.55
1:C:90:LEU:HD11	1:C:99:VAL:CG2	2.37	0.55
1:A:160:ILE:HG12	1:A:169:PHE:CD1	2.41	0.54
1:F:38:GLN:CD	1:F:128:ILE:HD11	2.28	0.54
1:F:162:ILE:HD11	1:F:262:PHE:CE2	2.42	0.54
1:B:270:VAL:HG22	1:B:282:TYR:HB2	1.89	0.54
1:C:30:CYS:SG	1:C:35:LEU:CD2	2.96	0.54
1:E:2:LEU:HD12	1:E:3:GLU:N	2.23	0.53
1:C:269:MET:HE1	1:C:281:ARG:HD2	1.91	0.53
1:F:81:ILE:HD11	1:F:114:TYR:CE1	2.44	0.53
1:D:53:ARG:O	1:D:56:CYS:HB3	2.08	0.52
1:E:51:LEU:HD12	1:E:51:LEU:C	2.29	0.52
1:B:227:GLY:O	1:B:257:ARG:NH2	2.42	0.52
1:C:243:ARG:HB2	3:C:302:HOH:O	2.09	0.52
1:F:51:LEU:HB2	1:F:279:TYR:CZ	2.44	0.52
1:D:118:LEU:CD2	1:D:118:LEU:N	2.73	0.52
1:A:98:VAL:CG1	1:A:99:VAL:N	2.73	0.52
1:D:25:GLU:HB2	1:D:121:ILE:HD11	1.92	0.52
1:D:31:ASN:ND2	1:D:65:ASN:OD1	2.40	0.52
1:F:2:LEU:HD23	1:F:3:GLU:H	1.74	0.52
1:A:264:LYS:HG3	3:A:407:HOH:O	2.11	0.51
1:B:131:MET:SD	1:B:266:SER:HB3	2.51	0.51
1:D:119:LEU:HA	1:D:120:GLU:HG3	1.91	0.51
1:E:95:ASP:O	1:E:97:ASP:N	2.43	0.51
1:B:48:VAL:HG13	1:B:282:TYR:CD1	2.46	0.51
1:C:166:GLY:HA3	1:C:182:LEU:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:248:PHE:O	1:F:250:LYS:N	2.44	0.51
1:C:30:CYS:SG	1:C:35:LEU:HD23	2.51	0.51
1:F:81:ILE:HD11	1:F:114:TYR:CZ	2.46	0.51
1:E:179:TYR:CE2	1:F:113:GLU:HB3	2.45	0.51
1:D:158:VAL:HB	1:D:242:LEU:HD21	1.93	0.51
1:F:124:GLU:HG3	3:F:301:HOH:O	2.11	0.51
1:E:269:MET:HE3	1:E:271:GLU:HB2	1.93	0.50
1:C:90:LEU:HD11	1:C:99:VAL:HG21	1.92	0.50
1:C:30:CYS:O	1:C:62:CYS:SG	2.70	0.50
1:D:144:PHE:O	1:D:148:VAL:HG13	2.12	0.50
1:E:13:LYS:O	1:E:17:GLU:HG2	2.12	0.50
1:F:70:LEU:HD21	1:F:99:VAL:CG1	2.40	0.50
1:B:147:ILE:HG12	1:B:180:THR:HG21	1.93	0.50
1:B:279:TYR:CZ	1:B:281:ARG:NH2	2.80	0.50
1:C:233:GLU:O	1:C:234:GLU:CB	2.59	0.50
1:E:97:ASP:O	1:E:98:VAL:HG23	2.12	0.50
1:C:248:PHE:CE1	1:C:282:TYR:HB3	2.47	0.49
1:E:78:VAL:O	1:E:81:ILE:HG12	2.11	0.49
1:D:22:LEU:HD23	1:D:48:VAL:HG22	1.94	0.49
1:B:126:MET:CG	1:B:127:GLY:H	2.25	0.49
1:F:88:LEU:HD12	1:F:102:THR:O	2.12	0.49
1:D:99:VAL:HG12	1:D:118:LEU:HD21	1.94	0.49
1:E:78:VAL:HG21	1:E:116:LEU:HD11	1.93	0.49
1:C:116:LEU:CD1	1:C:116:LEU:N	2.74	0.49
1:F:237:THR:O	1:F:238:LEU:HG	2.13	0.49
1:B:119:LEU:HD23	1:B:119:LEU:N	2.26	0.49
1:C:133:TYR:HB3	1:C:261:LYS:HB3	1.93	0.49
1:E:156:ASP:N	1:E:156:ASP:OD1	2.45	0.49
1:B:16:VAL:HG21	1:B:79:LEU:CD1	2.43	0.49
1:D:135:SER:HA	1:D:232:MET:HA	1.95	0.49
1:F:30:CYS:SG	1:F:35:LEU:CD2	3.01	0.48
1:D:78:VAL:O	1:D:81:ILE:HG12	2.14	0.48
1:F:23:VAL:HG12	1:F:41:ASP:HA	1.94	0.48
1:C:22:LEU:HD12	1:C:48:VAL:HG22	1.94	0.48
1:D:71:ASN:ND2	1:D:74:SER:OG	2.46	0.48
1:C:158:VAL:HB	1:C:242:LEU:HD21	1.94	0.48
1:C:275:ASP:OD1	1:C:276:ASN:OD1	2.31	0.48
1:D:48:VAL:CG1	1:D:282:TYR:CE1	2.95	0.48
1:F:128:ILE:HG22	1:F:128:ILE:O	2.13	0.48
1:F:159:THR:O	1:F:159:THR:HG22	2.12	0.48
1:E:56:CYS:SG	1:E:56:CYS:O	2.72	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2:LEU:HD12	1:A:3:GLU:N	2.28	0.48
1:A:51:LEU:HD23	1:A:279:TYR:CE2	2.49	0.47
1:C:51:LEU:HD12	1:C:52:LEU:N	2.29	0.47
1:E:15:LEU:HD13	1:E:50:MET:HE2	1.97	0.47
1:C:230:VAL:HG12	1:C:231:THR:N	2.30	0.47
1:D:49:HIS:HB2	1:D:128:ILE:HD11	1.96	0.47
1:F:12:TRP:HA	1:F:12:TRP:CE3	2.49	0.47
1:B:43:SER:OG	1:B:45:VAL:CG2	2.62	0.47
1:B:31:ASN:HB3	1:B:32:PRO:HD2	1.97	0.47
1:E:260:LEU:HB2	1:E:262:PHE:HE1	1.79	0.47
1:B:248:PHE:CD1	1:B:282:TYR:CG	3.02	0.47
1:C:6:VAL:HG12	1:C:7:GLN:N	2.30	0.47
1:F:138:THR:OG1	1:F:259:THR:HG23	2.14	0.47
1:C:86:ASP:OD2	1:C:110:ARG:NH2	2.48	0.47
1:B:161:ALA:HA	1:B:237:THR:HB	1.98	0.46
1:C:115:GLN:C	1:C:116:LEU:HD12	2.35	0.46
1:C:165:GLU:OE1	1:C:165:GLU:N	2.45	0.46
1:C:160:ILE:HG12	1:C:169:PHE:CD1	2.51	0.46
1:C:260:LEU:HD22	1:C:270:VAL:HB	1.96	0.46
1:A:19:ILE:HG13	1:A:72:LEU:HD13	1.97	0.46
1:A:38:GLN:CG	1:A:38:GLN:O	2.64	0.46
1:A:71:ASN:OD1	1:A:73:ALA:HB3	2.16	0.46
1:C:132:ASP:CG	1:C:133:TYR:H	2.19	0.46
1:E:53:ARG:HB3	1:E:55:ASP:OD1	2.16	0.46
1:A:126:MET:N	1:A:126:MET:SD	2.89	0.46
1:B:232:MET:HG2	1:B:233:GLU:N	2.31	0.46
1:E:19:ILE:HD12	1:E:37:VAL:HG11	1.98	0.46
1:F:280:LEU:HD21	1:F:282:TYR:CZ	2.51	0.46
1:F:2:LEU:CD2	1:F:3:GLU:N	2.79	0.46
1:A:135:SER:HA	1:A:232:MET:HA	1.98	0.46
1:E:65:ASN:N	1:E:65:ASN:OD1	2.49	0.46
1:F:269:MET:SD	1:F:281:ARG:HG2	2.56	0.46
1:A:10:SER:HB3	1:A:14:ARG:HH12	1.80	0.45
1:B:125:SER:O	1:B:127:GLY:N	2.50	0.45
1:C:16:VAL:HG21	1:C:79:LEU:CD1	2.46	0.45
1:B:14:ARG:HD2	1:B:253:THR:O	2.16	0.45
1:C:124:GLU:OE1	1:C:126:MET:O	2.34	0.45
1:D:274:ILE:HG22	1:D:274:ILE:O	2.16	0.45
1:F:14:ARG:HD2	1:F:253:THR:O	2.16	0.45
1:C:233:GLU:O	1:C:234:GLU:HB2	2.16	0.45
1:E:136:THR:CG2	1:E:137:VAL:N	2.79	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:65:ASN:ND2	1:C:65:ASN:O	2.49	0.45
1:B:251:GLY:HA3	1:B:272:TYR:CE2	2.52	0.45
1:C:125:SER:OG	1:C:126:MET:N	2.49	0.45
1:F:125:SER:O	1:F:127:GLY:N	2.49	0.45
1:F:248:PHE:HA	1:F:282:TYR:CE2	2.52	0.45
1:A:134:ARG:H	1:A:134:ARG:HG2	1.64	0.44
1:C:145:ALA:O	1:C:148:VAL:HG22	2.18	0.44
1:C:255:SER:HB2	1:C:273:GLY:O	2.17	0.44
1:E:150:ASP:HB3	1:F:81:ILE:HD12	1.98	0.44
1:D:101:LEU:O	1:D:113:GLU:HA	2.16	0.44
1:D:147:ILE:O	1:D:151:MET:HG2	2.17	0.44
1:E:19:ILE:CD1	1:E:37:VAL:HG11	2.48	0.44
1:C:7:GLN:NE2	1:C:8:PHE:CE1	2.86	0.44
1:E:174:ASP:O	1:E:175:VAL:C	2.56	0.44
1:B:10:SER:CB	1:B:14:ARG:HH21	2.31	0.44
1:C:81:ILE:O	1:C:81:ILE:HG13	2.17	0.44
1:E:123:ALA:O	1:E:124:GLU:C	2.55	0.44
1:E:158:VAL:HB	1:E:242:LEU:HD21	2.00	0.44
1:E:268:CYS:SG	1:E:269:MET:N	2.91	0.44
1:F:60:TYR:CD2	1:F:61:GLN:N	2.85	0.44
1:D:46:ALA:HA	1:D:283:TYR:O	2.18	0.44
1:D:145:ALA:HA	1:D:249:ALA:HB1	2.00	0.43
1:A:154:PHE:O	1:A:173:GLY:HA3	2.18	0.43
1:B:248:PHE:CD1	1:B:282:TYR:CD1	3.06	0.43
1:A:48:VAL:HG13	1:A:282:TYR:CD1	2.54	0.43
1:B:12:TRP:HA	1:B:12:TRP:CE3	2.52	0.43
1:E:122:GLU:HG2	1:E:122:GLU:O	2.18	0.43
1:F:36:SER:HA	1:F:50:MET:O	2.18	0.43
1:F:45:VAL:CG1	1:F:45:VAL:O	2.66	0.43
1:F:265:ASP:OD1	1:F:265:ASP:N	2.51	0.43
1:B:248:PHE:CE1	1:B:282:TYR:HB3	2.53	0.43
1:D:38:GLN:HA	1:D:48:VAL:O	2.19	0.43
1:D:276:ASN:N	1:D:276:ASN:OD1	2.51	0.43
1:A:105:ASN:ND2	1:A:106:PRO:HD2	2.31	0.43
1:D:56:CYS:HB2	1:D:277:VAL:CG1	2.43	0.43
1:D:7:GLN:NE2	1:D:8:PHE:CZ	2.87	0.43
1:F:4:ALA:HB1	1:F:57:PHE:CE2	2.53	0.43
1:F:123:ALA:HB1	3:F:301:HOH:O	2.19	0.42
1:F:183:GLN:HG2	1:F:185:ALA:CB	2.48	0.42
1:A:129:PRO:O	1:A:130:GLU:C	2.56	0.42
1:C:70:LEU:CD2	1:C:99:VAL:HG11	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:150:ASP:O	1:D:153:VAL:HG13	2.19	0.42
1:D:90:LEU:HD11	1:D:99:VAL:HG21	2.00	0.42
1:E:0:SER:HB2	1:E:91:ARG:NH1	2.34	0.42
1:A:23:VAL:HG23	1:A:72:LEU:HD12	2.01	0.42
1:B:70:LEU:HD12	1:B:70:LEU:HA	1.82	0.42
1:C:232:MET:HG2	1:C:233:GLU:N	2.35	0.42
1:F:2:LEU:CD1	1:F:30:CYS:SG	3.08	0.42
1:A:5:GLN:HA	1:A:89:SER:HA	2.01	0.42
1:C:230:VAL:CG1	1:C:231:THR:N	2.82	0.42
1:E:240:PHE:CE1	1:E:268:CYS:HB3	2.54	0.42
1:F:242:LEU:HA	1:F:242:LEU:HD23	1.93	0.42
1:F:51:LEU:CB	1:F:279:TYR:CE2	3.03	0.42
1:B:90:LEU:CD1	1:B:99:VAL:HG13	2.49	0.42
1:E:136:THR:CG2	1:E:231:THR:HG22	2.50	0.42
1:A:136:THR:CG2	1:A:137:VAL:N	2.83	0.42
1:C:81:ILE:HD11	1:C:114:TYR:CE1	2.54	0.42
1:C:88:LEU:HD11	1:C:101:LEU:HB3	2.02	0.42
1:C:127:GLY:O	1:C:128:ILE:HB	2.20	0.42
1:E:48:VAL:HG13	1:E:282:TYR:CE1	2.55	0.42
1:F:137:VAL:HG21	1:F:167:VAL:HG11	2.01	0.42
1:B:48:VAL:CG1	1:B:282:TYR:CE1	3.03	0.41
1:F:14:ARG:HD2	1:F:253:THR:HB	2.01	0.41
1:B:233:GLU:C	1:B:234:GLU:HG2	2.39	0.41
1:C:12:TRP:HA	1:C:12:TRP:CE3	2.54	0.41
1:A:87:SER:O	1:A:103:SER:HA	2.20	0.41
1:B:242:LEU:O	1:B:243:ARG:C	2.58	0.41
1:B:43:SER:OG	1:B:45:VAL:HG22	2.20	0.41
1:D:264:LYS:O	1:D:266:SER:N	2.53	0.41
1:F:45:VAL:HG12	1:F:45:VAL:O	2.19	0.41
1:C:132:ASP:CG	1:C:133:TYR:N	2.74	0.41
1:E:45:VAL:O	1:E:45:VAL:HG22	2.20	0.41
1:E:70:LEU:HA	1:E:70:LEU:HD23	1.91	0.41
1:C:22:LEU:HD22	1:C:41:ASP:HB3	2.02	0.41
1:B:131:MET:SD	1:B:266:SER:CB	3.09	0.41
1:C:262:PHE:CD1	1:C:262:PHE:N	2.89	0.41
1:D:71:ASN:HD21	1:D:73:ALA:HB3	1.85	0.41
1:E:123:ALA:O	1:E:124:GLU:O	2.38	0.41
1:E:258:VAL:HG13	1:E:258:VAL:O	2.20	0.41
1:F:145:ALA:HA	1:F:249:ALA:HB1	2.02	0.41
1:F:70:LEU:HD23	1:F:70:LEU:HA	1.92	0.41
1:B:232:MET:HG2	1:B:234:GLU:H	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:232:MET:CG	1:C:233:GLU:N	2.82	0.41
1:C:161:ALA:HA	1:C:237:THR:HG22	2.02	0.41
1:D:279:TYR:CE2	1:D:281:ARG:NH2	2.89	0.41
1:F:57:PHE:N	1:F:57:PHE:CD1	2.89	0.41
1:C:79:LEU:HD21	1:C:88:LEU:HD21	2.03	0.41
1:D:49:HIS:HB2	1:D:128:ILE:CD1	2.51	0.41
1:F:163:SER:O	1:F:164:LYS:C	2.59	0.41
1:B:158:VAL:HG13	1:B:158:VAL:O	2.21	0.40
1:B:58:VAL:HG23	1:B:59:LYS:N	2.36	0.40
1:C:136:THR:CG2	1:C:137:VAL:N	2.84	0.40
1:E:87:SER:O	1:E:103:SER:HA	2.21	0.40
1:A:164:LYS:HE2	1:A:164:LYS:H	1.85	0.40
1:B:164:LYS:HE3	1:B:164:LYS:HB2	1.87	0.40
1:B:56:CYS:HB2	1:B:277:VAL:HB	2.03	0.40
1:F:248:PHE:CD1	1:F:282:TYR:CD2	3.09	0.40
1:F:60:TYR:O	1:F:61:GLN:HG3	2.21	0.40
1:B:87:SER:O	1:B:103:SER:HA	2.21	0.40
1:B:240:PHE:HD2	1:B:284:LEU:HD23	1.87	0.40
1:E:277:VAL:O	1:E:277:VAL:HG13	2.21	0.40
1:F:139:LEU:HD23	1:F:139:LEU:H	1.87	0.40

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	244/302 (81%)	209 (86%)	28 (12%)	7 (3%)	4	28
1	B	244/302 (81%)	214 (88%)	21 (9%)	9 (4%)	3	22
1	C	244/302 (81%)	195 (80%)	35 (14%)	14 (6%)	1	14
1	D	247/302 (82%)	215 (87%)	24 (10%)	8 (3%)	4	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	254/302 (84%)	210 (83%)	32 (13%)	12 (5%)	2	17
1	F	244/302 (81%)	203 (83%)	27 (11%)	14 (6%)	1	14
All	All	1477/1812 (82%)	1246 (84%)	167 (11%)	64 (4%)	2	20

All (64) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	10	SER
1	A	95	ASP
1	D	95	ASP
1	D	126	MET
1	D	231	THR
1	D	265	ASP
1	D	267	PRO
1	E	96	SER
1	E	98	VAL
1	E	124	GLU
1	E	125	SER
1	E	131	MET
1	B	94	ASP
1	B	126	MET
1	B	135	SER
1	C	84	SER
1	C	234	GLU
1	C	267	PRO
1	F	126	MET
1	F	130	GLU
1	F	131	MET
1	F	132	ASP
1	A	105	ASN
1	A	122	GLU
1	A	130	GLU
1	D	64	ARG
1	E	63	GLY
1	E	95	ASP
1	E	267	PRO
1	B	62	CYS
1	B	63	GLY
1	C	275	ASP
1	F	84	SER
1	F	165	GLU

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Mol	Chain	Res	Type
1	F	249	ALA
1	F	275	ASP
1	E	-1	SER
1	E	10	SER
1	B	64	ARG
1	C	59	LYS
1	C	91	ARG
1	C	231	THR
1	F	63	GLY
1	D	10	SER
1	E	-6	ARG
1	B	264	LYS
1	C	61	GLN
1	C	123	ALA
1	C	128	ILE
1	F	10	SER
1	A	164	LYS
1	D	132	ASP
1	B	127	GLY
1	C	137	VAL
1	C	184	ALA
1	F	163	SER
1	A	228	VAL
1	B	73	ALA
1	C	63	GLY
1	F	267	PRO
1	C	274	ILE
1	F	274	ILE
1	E	175	VAL
1	F	106	PRO

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	216/259 (83%)	180 (83%)	36 (17%)	2 10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	216/259 (83%)	182 (84%)	34 (16%)	2	12
1	C	216/259 (83%)	177 (82%)	39 (18%)	1	8
1	D	218/259 (84%)	176 (81%)	42 (19%)	1	8
1	E	224/259 (86%)	180 (80%)	44 (20%)	1	7
1	F	216/259 (83%)	181 (84%)	35 (16%)	2	11
All	All	1306/1554 (84%)	1076 (82%)	230 (18%)	2	9

All (230) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LEU
1	A	7	GLN
1	A	15	LEU
1	A	19	ILE
1	A	22	LEU
1	A	30	CYS
1	A	38	GLN
1	A	41	ASP
1	A	48	VAL
1	A	50	MET
1	A	54	ASP
1	A	80	LYS
1	A	81	ILE
1	A	90	LEU
1	A	96	SER
1	A	102	THR
1	A	103	SER
1	A	104	GLU
1	A	105	ASN
1	A	116	LEU
1	A	120	GLU
1	A	126	MET
1	A	131	MET
1	A	132	ASP
1	A	134	ARG
1	A	137	VAL
1	A	146	LYS
1	A	163	SER
1	A	164	LYS
1	A	167	VAL

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Mol	Chain	Res	Type
1	A	170	SER
1	A	171	SER
1	A	179	TYR
1	A	231	THR
1	A	234	GLU
1	A	265	ASP
1	D	1	MET
1	D	19	ILE
1	D	25	GLU
1	D	30	CYS
1	D	41	ASP
1	D	45	VAL
1	D	47	LEU
1	D	48	VAL
1	D	53	ARG
1	D	56	CYS
1	D	59	LYS
1	D	66	SER
1	D	80	LYS
1	D	84	SER
1	D	88	LEU
1	D	97	ASP
1	D	111	LYS
1	D	118	LEU
1	D	122	GLU
1	D	125	SER
1	D	128	ILE
1	D	130	GLU
1	D	134	ARG
1	D	136	THR
1	D	137	VAL
1	D	140	ASN
1	D	148	VAL
1	D	153	VAL
1	D	159	THR
1	D	163	SER
1	D	231	THR
1	D	234	GLU
1	D	237	THR
1	D	250	LYS
1	D	253	THR
1	D	256	GLU

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Mol	Chain	Res	Type
1	D	260	LEU
1	D	267	PRO
1	D	270	VAL
1	D	276	ASN
1	D	287	LYS
1	D	288	VAL
1	E	-8	SER
1	E	-6	ARG
1	E	-1	SER
1	E	7	GLN
1	E	18	CYS
1	E	19	ILE
1	E	22	LEU
1	E	25	GLU
1	E	31	ASN
1	E	48	VAL
1	E	50	MET
1	E	51	LEU
1	E	55	ASP
1	E	65	ASN
1	E	67	ILE
1	E	94	ASP
1	E	96	SER
1	E	100	THR
1	E	103	SER
1	E	108	LYS
1	E	116	LEU
1	E	117	LYS
1	E	120	GLU
1	E	124	GLU
1	E	130	GLU
1	E	134	ARG
1	E	136	THR
1	E	137	VAL
1	E	140	ASN
1	E	146	LYS
1	E	152	GLN
1	E	156	ASP
1	E	170	SER
1	E	179	TYR
1	E	232	MET
1	E	243	ARG

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Mol	Chain	Res	Type
1	E	268	CYS
1	E	270	VAL
1	E	275	ASP
1	E	276	ASN
1	E	277	VAL
1	E	281	ARG
1	E	287	LYS
1	E	288	VAL
1	B	2	LEU
1	B	7	GLN
1	B	19	ILE
1	B	35	LEU
1	B	45	VAL
1	B	47	LEU
1	B	48	VAL
1	B	64	ARG
1	B	66	SER
1	B	67	ILE
1	B	70	LEU
1	B	74	SER
1	B	81	ILE
1	B	95	ASP
1	B	98	VAL
1	B	100	THR
1	B	102	THR
1	B	117	LYS
1	B	122	GLU
1	B	131	MET
1	B	132	ASP
1	B	134	ARG
1	B	135	SER
1	B	138	THR
1	B	146	LYS
1	B	162	ILE
1	B	170	SER
1	B	183	GLN
1	B	231	THR
1	B	237	THR
1	B	250	LYS
1	B	259	THR
1	B	264	LYS
1	B	266	SER

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Mol	Chain	Res	Type
1	C	1	MET
1	C	11	LEU
1	C	19	ILE
1	C	20	ASN
1	C	22	LEU
1	C	31	ASN
1	C	42	SER
1	C	47	LEU
1	C	50	MET
1	C	51	LEU
1	C	55	ASP
1	C	67	ILE
1	C	80	LYS
1	C	81	ILE
1	C	87	SER
1	C	100	THR
1	C	103	SER
1	C	111	LYS
1	C	117	LYS
1	C	121	ILE
1	C	122	GLU
1	C	124	GLU
1	C	125	SER
1	C	134	ARG
1	C	136	THR
1	C	137	VAL
1	C	139	LEU
1	C	146	LYS
1	C	150	ASP
1	C	164	LYS
1	C	170	SER
1	C	179	TYR
1	C	183	GLN
1	C	231	THR
1	C	232	MET
1	C	236	ILE
1	C	253	THR
1	C	264	LYS
1	C	268	CYS
1	F	1	MET
1	F	2	LEU
1	F	3	GLU

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Mol	Chain	Res	Type
1	F	12	TRP
1	F	19	ILE
1	F	29	ASP
1	F	43	SER
1	F	47	LEU
1	F	50	MET
1	F	51	LEU
1	F	65	ASN
1	F	80	LYS
1	F	81	ILE
1	F	97	ASP
1	F	108	LYS
1	F	109	THR
1	F	121	ILE
1	F	131	MET
1	F	136	THR
1	F	157	THR
1	F	163	SER
1	F	167	VAL
1	F	169	PHE
1	F	170	SER
1	F	172	SER
1	F	183	GLN
1	F	234	GLU
1	F	237	THR
1	F	245	MET
1	F	256	GLU
1	F	265	ASP
1	F	268	CYS
1	F	269	MET
1	F	270	VAL
1	F	287	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	A	49	HIS
1	D	7	GLN
1	D	27	ASN
1	D	71	ASN
1	E	7	GLN

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Mol	Chain	Res	Type
1	E	183	GLN
1	E	276	ASN
1	F	20	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](#)

2 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	ARG	A	301	-	7,11,11	0.90	1 (14%)	6,13,13	1.41	1 (16%)
2	ARG	E	301	-	7,11,11	1.02	1 (14%)	6,13,13	1.30	1 (16%)

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
2	ARG	A	301	-	-	1/7/11/11	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ARG	E	301	-	-	1/7/11/11	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	301	ARG	CA-N	2.04	1.51	1.47
2	A	301	ARG	CA-N	2.02	1.51	1.47

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	ARG	CB-CG-CD	2.22	118.70	112.05
2	E	301	ARG	CG-CD-NE	2.03	118.01	112.21

There are no chirality outliers.

All (2) torsion outliers are listed below:

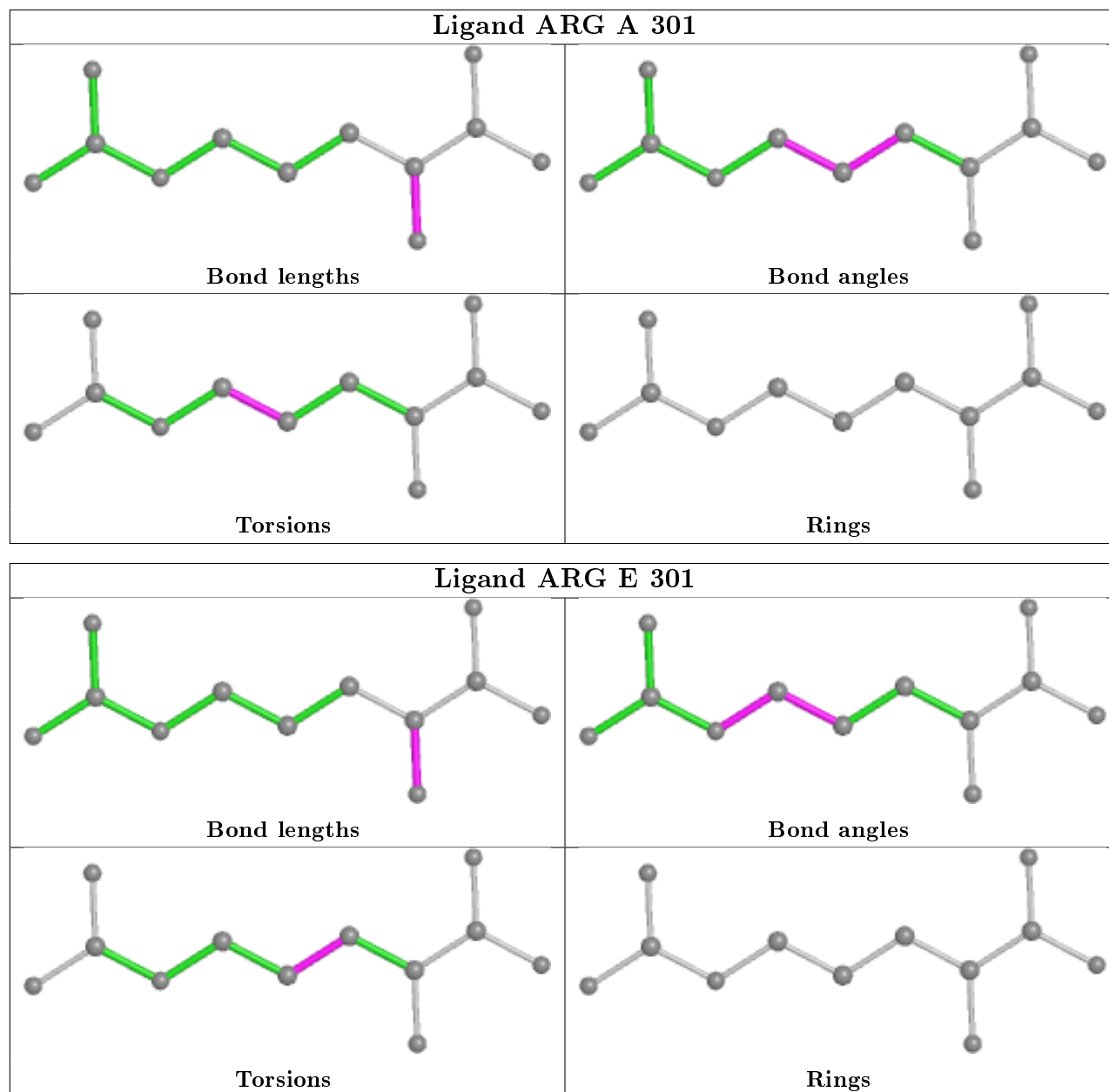
Mol	Chain	Res	Type	Atoms
2	E	301	ARG	CA-CB-CG-CD
2	A	301	ARG	NE-CD-CG-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	301	ARG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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	248/302 (82%)	0.31	2 (0%) 86 78	69, 103, 155, 205	0
1	B	248/302 (82%)	0.54	12 (4%) 30 18	82, 119, 168, 200	0
1	C	248/302 (82%)	0.23	3 (1%) 79 67	86, 118, 174, 201	0
1	D	251/302 (83%)	0.36	7 (2%) 53 37	75, 112, 163, 208	0
1	E	258/302 (85%)	0.41	5 (1%) 66 53	77, 108, 171, 203	0
1	F	248/302 (82%)	0.28	4 (1%) 72 59	91, 126, 181, 214	0
All	All	1501/1812 (82%)	0.35	33 (2%) 62 48	69, 115, 171, 214	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	289	ASP	7.0
1	D	185	ALA	5.7
1	E	185	ALA	3.4
1	B	131	MET	3.4
1	B	238	LEU	3.2
1	B	262	PHE	3.1
1	A	185	ALA	3.1
1	B	128	ILE	3.0
1	F	130	GLU	2.9
1	B	129	PRO	2.8
1	B	12	TRP	2.8
1	C	12	TRP	2.7
1	D	12	TRP	2.7
1	E	-3	LEU	2.7
1	D	130	GLU	2.7
1	E	-6	ARG	2.6
1	D	128	ILE	2.5
1	F	28	PHE	2.5
1	E	-4	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	160	ILE	2.4
1	B	130	GLU	2.3
1	C	160	ILE	2.3
1	D	28	PHE	2.3
1	B	61	GLN	2.3
1	F	160	ILE	2.2
1	D	230	VAL	2.2
1	C	28	PHE	2.1
1	B	33	GLY	2.1
1	E	-8	SER	2.1
1	B	167	VAL	2.1
1	D	162	ILE	2.1
1	F	55	ASP	2.1
1	B	114	TYR	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 carbohydrates in this entry.

6.4 Ligands [i](#)

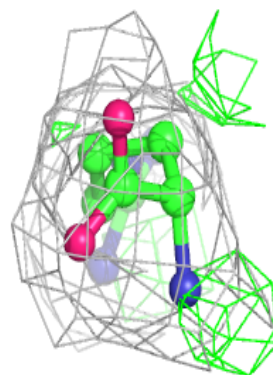
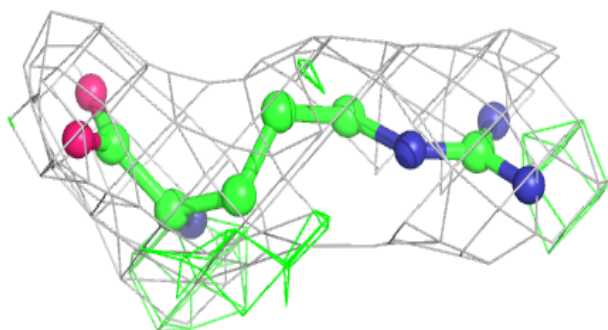
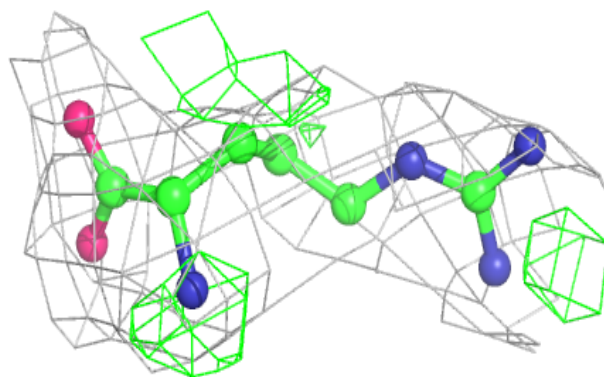
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	ARG	E	301	12/12	0.76	0.17	113,136,147,152	0
2	ARG	A	301	12/12	0.81	0.16	112,145,153,162	0

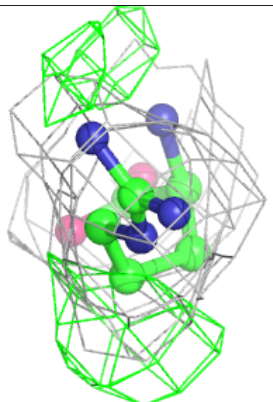
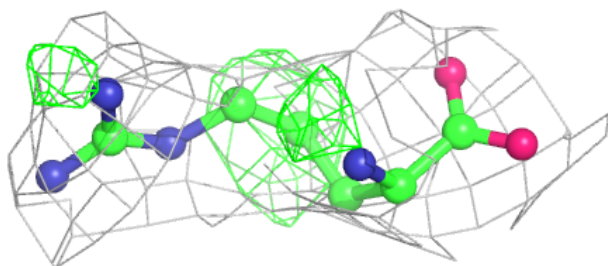
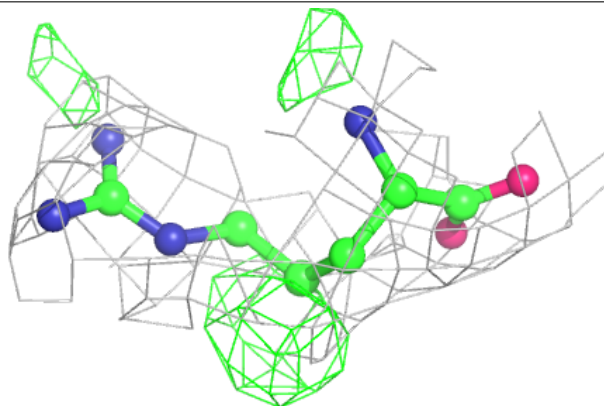
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around ARG E 301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around ARG A 301:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.