Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 08:22 PM GMT

PDB ID	:	1JRE
Title	:	DNA PROTECTION AND BINDING BY E. COLI DPS PROTEIN
Authors	:	Luo, J.; Liu, D.; White, M.A.; Fox, R.O.
Deposited on	:	2001-08-13
Resolution	:	2.65 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

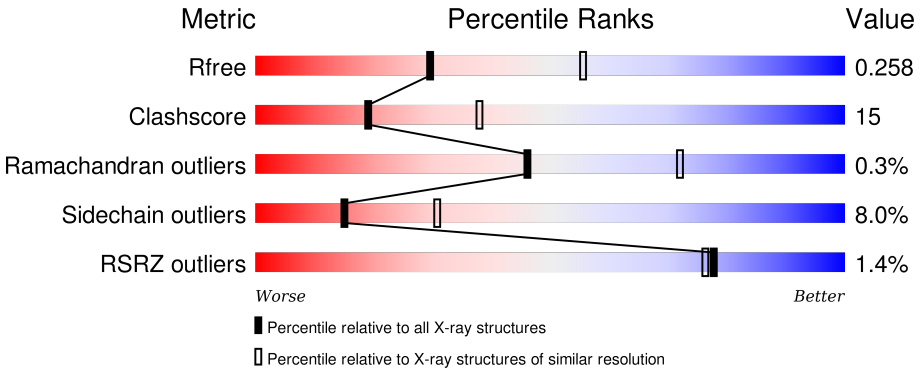
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	3152 (2.70-2.62)
Clashscore	102246	3524 (2.70-2.62)
Ramachandran outliers	100387	3469 (2.70-2.62)
Sidechain outliers	100360	3469 (2.70-2.62)
RSRZ outliers	91569	3161 (2.70-2.62)

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 <=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	167	62% 26% 6%
1	B	167	2% 62% 28% 6%
1	C	167	62% 26% 5% 7%
1	D	167	62% 29% 6%
1	E	167	66% 23% 7%

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Mol	Chain	Length	Quality of chain
1	F	167	4% 63% 26% 7%
1	G	167	63% 26% 7%
1	H	167	65% 25% 5% 6%
1	I	167	2% 62% 27% 7%
1	J	167	2% 62% 27% 7%
1	K	167	% 64% 25% 7%
1	L	167	% 64% 25% 7%

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
2	CD	B	201	-	-	-	X
3	TRS	A	301	-	-	-	X
3	TRS	B	304	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15083 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 PROTECTION DURING STARVATION PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	157	Total	C	N	O	S	0	0	0
			1236	777	217	238	4			
1	B	157	Total	C	N	O	S	0	0	0
			1236	777	217	238	4			
1	C	155	Total	C	N	O	S	0	0	0
			1224	770	215	235	4			
1	D	157	Total	C	N	O	S	0	0	0
			1236	777	217	238	4			
1	E	156	Total	C	N	O	S	0	0	0
			1231	774	216	237	4			
1	F	156	Total	C	N	O	S	0	0	0
			1231	774	216	237	4			
1	G	155	Total	C	N	O	S	0	0	0
			1224	770	215	235	4			
1	H	157	Total	C	N	O	S	0	0	0
			1236	777	217	238	4			
1	I	156	Total	C	N	O	S	0	0	0
			1231	774	216	237	4			
1	J	155	Total	C	N	O	S	0	0	0
			1224	770	215	235	4			
1	K	155	Total	C	N	O	S	0	0	0
			1224	770	215	235	4			
1	L	155	Total	C	N	O	S	0	0	0
			1224	770	215	235	4			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	75	CYS	ASP	ENGINEERED	UNP P0ABT2
A	78	ALA	ASP	ENGINEERED	UNP P0ABT2
B	75	CYS	ASP	ENGINEERED	UNP P0ABT2
B	78	ALA	ASP	ENGINEERED	UNP P0ABT2
C	75	CYS	ASP	ENGINEERED	UNP P0ABT2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	78	ALA	ASP	ENGINEERED	UNP P0ABT2
D	75	CYS	ASP	ENGINEERED	UNP P0ABT2
D	78	ALA	ASP	ENGINEERED	UNP P0ABT2
E	75	CYS	ASP	ENGINEERED	UNP P0ABT2
E	78	ALA	ASP	ENGINEERED	UNP P0ABT2
F	75	CYS	ASP	ENGINEERED	UNP P0ABT2
F	78	ALA	ASP	ENGINEERED	UNP P0ABT2
G	75	CYS	ASP	ENGINEERED	UNP P0ABT2
G	78	ALA	ASP	ENGINEERED	UNP P0ABT2
H	75	CYS	ASP	ENGINEERED	UNP P0ABT2
H	78	ALA	ASP	ENGINEERED	UNP P0ABT2
I	75	CYS	ASP	ENGINEERED	UNP P0ABT2
I	78	ALA	ASP	ENGINEERED	UNP P0ABT2
J	75	CYS	ASP	ENGINEERED	UNP P0ABT2
J	78	ALA	ASP	ENGINEERED	UNP P0ABT2
K	75	CYS	ASP	ENGINEERED	UNP P0ABT2
K	78	ALA	ASP	ENGINEERED	UNP P0ABT2
L	75	CYS	ASP	ENGINEERED	UNP P0ABT2
L	78	ALA	ASP	ENGINEERED	UNP P0ABT2

- Molecule 2 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	2	Total Cd 2 2	0	0
2	J	1	Total Cd 1 1	0	0
2	D	1	Total Cd 1 1	0	0
2	K	1	Total Cd 1 1	0	0
2	E	1	Total Cd 1 1	0	0
2	H	1	Total Cd 1 1	0	0
2	B	1	Total Cd 1 1	0	0
2	I	1	Total Cd 1 1	0	0
2	C	1	Total Cd 1 1	0	0
2	A	1	Total Cd 1 1	0	0

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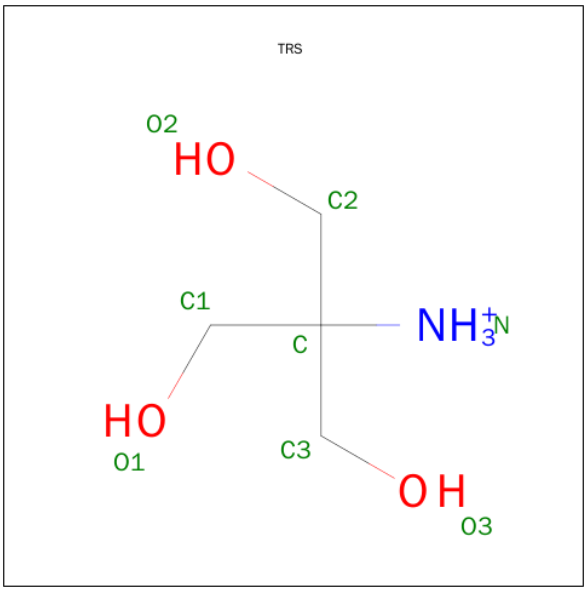
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	L	1	Total Cd 1 1	0	0
2	F	1	Total Cd 1 1	0	0

- Molecule 3 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 8 4 1 3	0	0
3	K	1	Total C N O 8 4 1 3	0	0
3	C	1	Total C N O 8 4 1 3	0	0
3	B	1	Total C N O 8 4 1 3	0	0
3	D	1	Total C N O 8 4 1 3	0	0
3	D	1	Total C N O 8 4 1 3	0	0
3	C	1	Total C N O 8 4 1 3	0	0
3	H	1	Total C N O 8 4 1 3	0	0
3	A	1	Total C N O 8 4 1 3	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	1	Total C N O 8 4 1 3	0	0
3	E	1	Total C N O 8 4 1 3	0	0
3	B	1	Total C N O 8 4 1 3	0	0

- Molecule 4 is water.

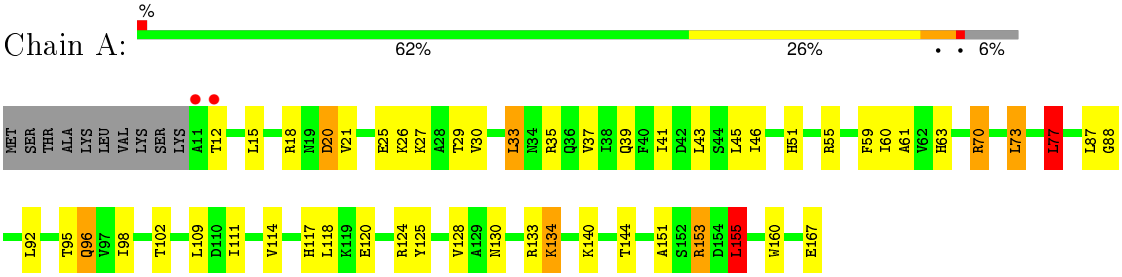
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	32	Total O 32 32	0	0
4	B	23	Total O 23 23	0	0
4	C	16	Total O 16 16	0	0
4	D	9	Total O 9 9	0	0
4	E	20	Total O 20 20	0	0
4	F	11	Total O 11 11	0	0
4	G	31	Total O 31 31	0	0
4	H	20	Total O 20 20	0	0
4	I	15	Total O 15 15	0	0
4	J	11	Total O 11 11	0	0
4	K	15	Total O 15 15	0	0
4	L	14	Total O 14 14	0	0

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 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.

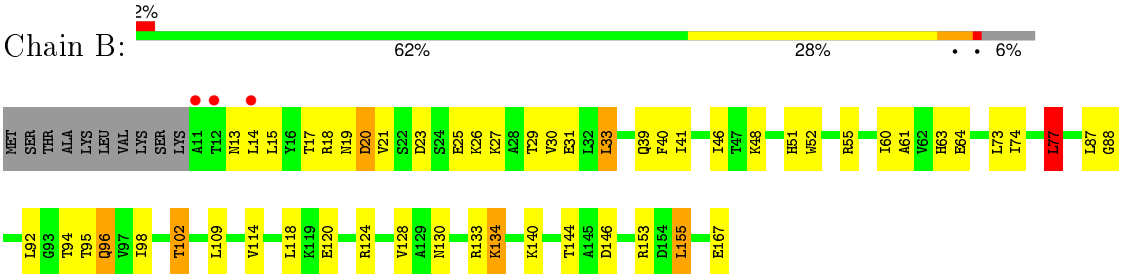
- Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

Chain A:



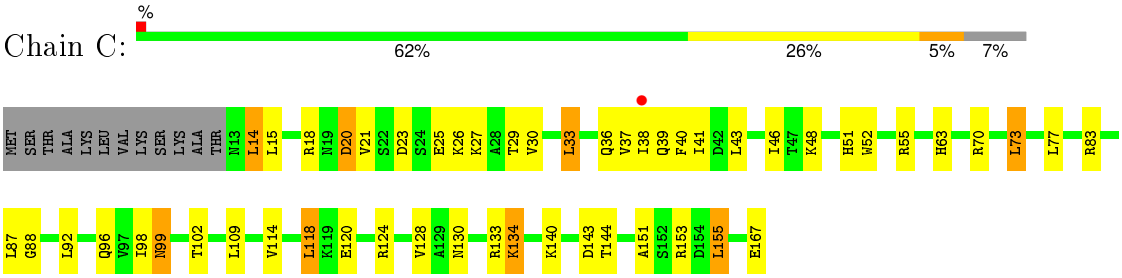
- Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

Chain B:



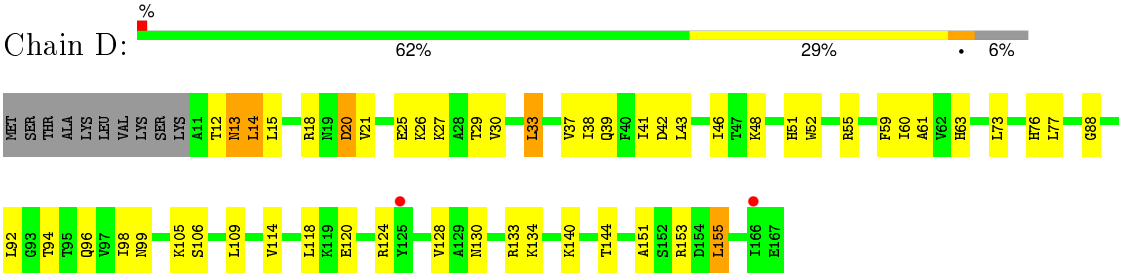
- Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

Chain C:



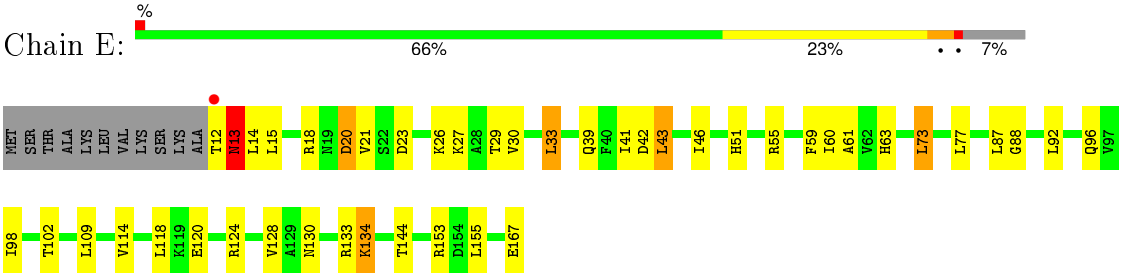
- Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

Chain D:



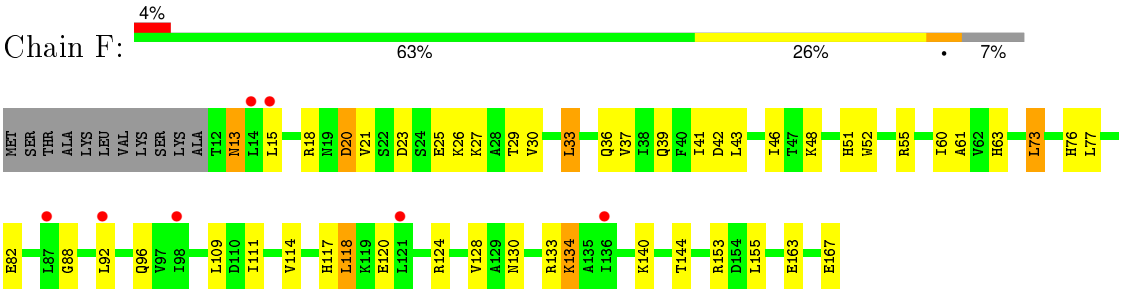
• Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

Chain E:



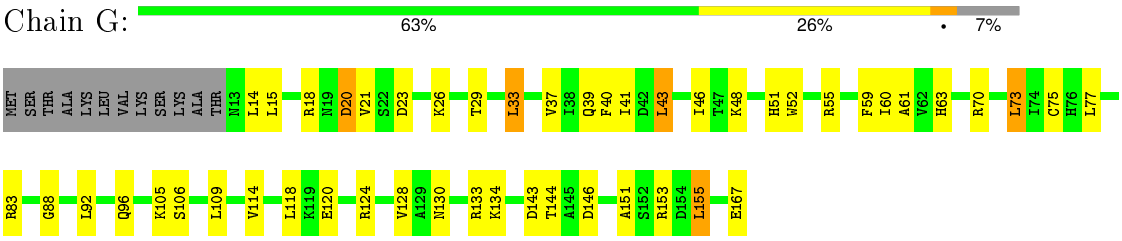
• Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

Chain F:



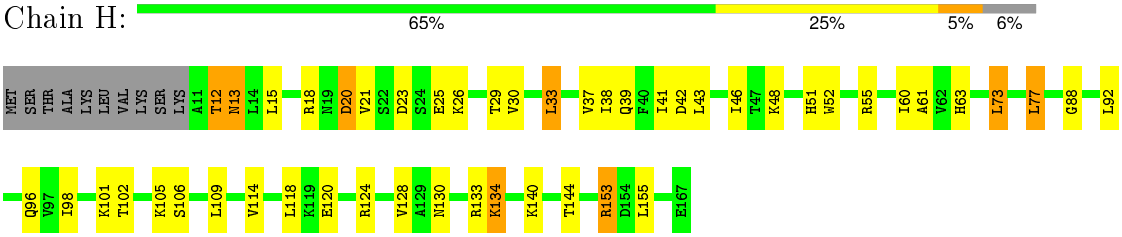
• Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

Chain G:



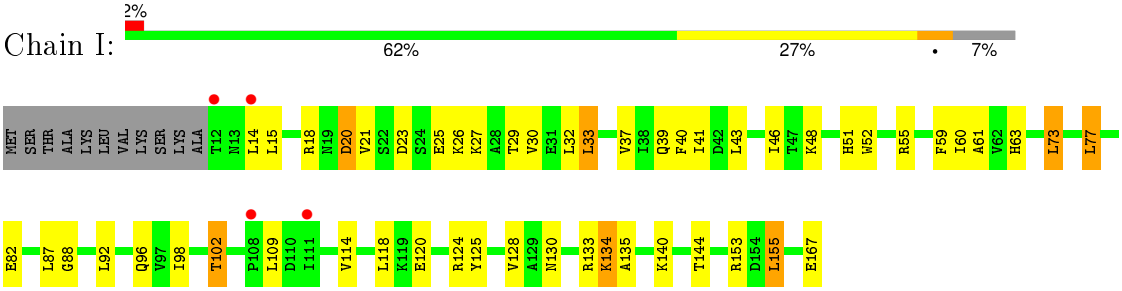
• Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

Chain H:



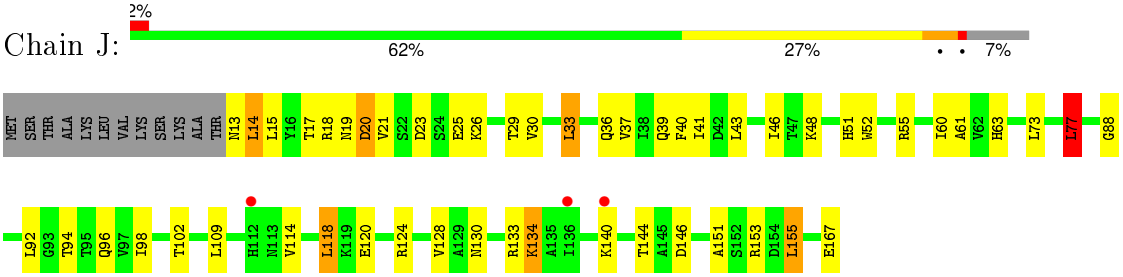
• Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

Chain I:



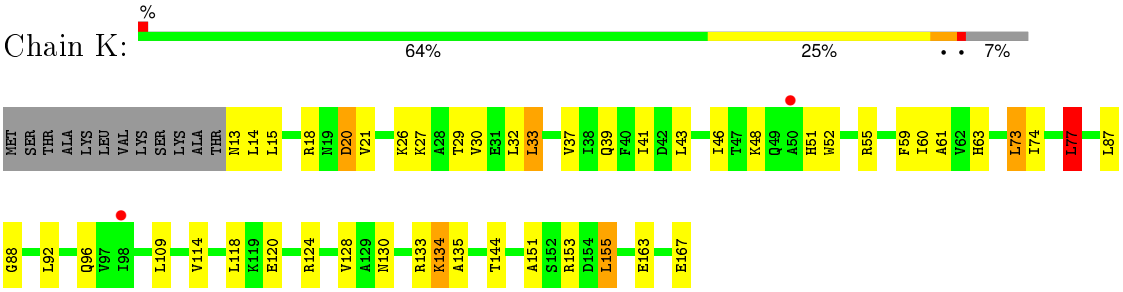
• Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

Chain J:



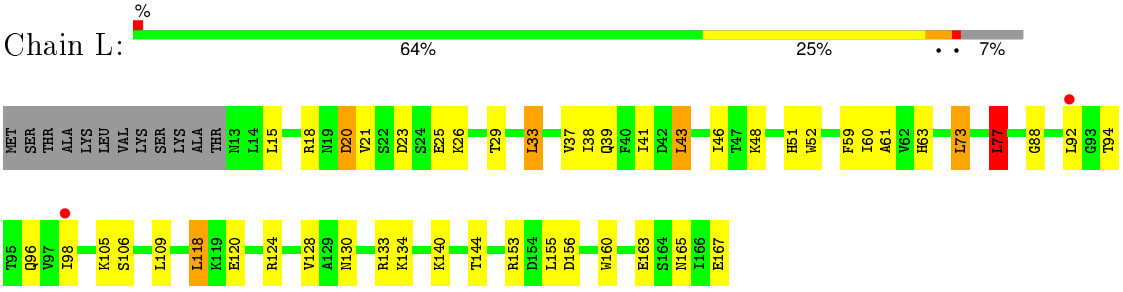
• Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

Chain K:



• Molecule 1: DNA PROTECTION DURING STARVATION PROTEIN

Chain L:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α, β, γ	90.58Å 90.58Å 226.51Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	45.92 – 2.65 54.40 – 2.62	Depositor EDS
% Data completeness (in resolution range)	97.1 (45.92-2.65) 96.2 (54.40-2.62)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.05 (at 2.61Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.229 , 0.264 0.225 , 0.258	Depositor DCC
R_{free} test set	2904 reflections (4.96%)	DCC
Wilson B-factor (Å^2)	60.5	Xtriage
Anisotropy	0.011	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 66.0	EDS
Estimated twinning fraction	0.008 for -h,-k,l 0.042 for h,-h-k,-l 0.025 for -k,-h,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 61793 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	15083	wwPDB-VP
Average B, all atoms (Å^2)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.83% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

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

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	0.43	0/1254	0.77	5/1698 (0.3%)
1	B	0.41	0/1254	0.63	1/1698 (0.1%)
1	C	0.39	0/1242	0.73	3/1681 (0.2%)
1	D	0.38	0/1254	0.61	0/1698
1	E	0.40	0/1249	0.62	0/1691
1	F	0.37	0/1249	0.60	0/1691
1	G	0.43	0/1242	0.63	0/1681
1	H	0.40	0/1254	0.62	0/1698
1	I	0.36	0/1249	0.60	1/1691 (0.1%)
1	J	0.37	0/1242	0.61	1/1681 (0.1%)
1	K	0.40	0/1242	0.61	1/1681 (0.1%)
1	L	0.40	0/1242	0.60	1/1681 (0.1%)
All	All	0.40	0/14973	0.64	13/20270 (0.1%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	70	ARG	NE-CZ-NH1	-11.85	114.38	120.30
1	C	70	ARG	NE-CZ-NH2	11.73	126.17	120.30
1	A	70	ARG	NE-CZ-NH2	11.44	126.02	120.30
1	A	70	ARG	NE-CZ-NH1	-10.96	114.82	120.30
1	K	77	LEU	CA-CB-CG	5.66	128.32	115.30
1	A	155	LEU	CA-CB-CG	-5.46	102.75	115.30
1	A	70	ARG	CD-NE-CZ	5.39	131.14	123.60
1	C	70	ARG	CD-NE-CZ	5.35	131.09	123.60
1	J	77	LEU	CA-CB-CG	5.34	127.58	115.30
1	B	77	LEU	CA-CB-CG	5.26	127.40	115.30
1	L	77	LEU	CA-CB-CG	5.26	127.39	115.30
1	A	77	LEU	CA-CB-CG	5.19	127.24	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	I	77	LEU	CA-CB-CG	5.19	127.24	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1236	0	1239	50	0
1	B	1236	0	1239	45	0
1	C	1224	0	1227	41	0
1	D	1236	0	1239	45	0
1	E	1231	0	1234	36	0
1	F	1231	0	1234	43	0
1	G	1224	0	1227	39	0
1	H	1236	0	1239	45	0
1	I	1231	0	1234	42	0
1	J	1224	0	1227	41	0
1	K	1224	0	1227	40	0
1	L	1224	0	1227	37	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	2	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
3	A	16	0	24	3	0
3	B	16	0	24	5	0
3	C	16	0	24	3	0
3	D	24	0	36	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	8	0	12	0	0
3	H	8	0	12	0	0
3	K	8	0	12	0	0
4	A	32	0	0	7	0
4	B	23	0	0	2	0
4	C	16	0	0	0	0
4	D	9	0	0	1	0
4	E	20	0	0	0	0
4	F	11	0	0	1	0
4	G	31	0	0	3	0
4	H	20	0	0	1	0
4	I	15	0	0	0	0
4	J	11	0	0	0	0
4	K	15	0	0	1	0
4	L	14	0	0	0	0
All	All	15083	0	14937	453	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 15.

All (453) 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)
4:A:550:HOH:O	1:B:95:THR:HB	1.68	0.94
1:B:98:ILE:O	1:B:102:THR:HG22	1.73	0.89
1:A:21:VAL:O	1:A:26:LYS:HE3	1.76	0.85
1:L:21:VAL:O	1:L:26:LYS:HE3	1.78	0.82
1:K:21:VAL:O	1:K:26:LYS:HE3	1.78	0.82
1:B:21:VAL:O	1:B:26:LYS:HE3	1.77	0.82
1:C:20:ASP:HB2	1:F:130:ASN:OD1	1.79	0.82
1:F:21:VAL:O	1:F:26:LYS:HE3	1.80	0.81
1:A:41:ILE:HG12	1:A:77:LEU:HD11	1.62	0.80
1:D:21:VAL:O	1:D:26:LYS:HE3	1.82	0.80
1:D:20:ASP:HB2	1:G:130:ASN:OD1	1.82	0.79
1:H:13:ASN:H	1:H:13:ASN:HD22	1.27	0.79
1:D:41:ILE:HG12	1:D:77:LEU:HD11	1.64	0.78
1:G:21:VAL:O	1:G:26:LYS:HE3	1.83	0.78
1:B:20:ASP:HB2	1:H:130:ASN:OD1	1.82	0.78
1:B:130:ASN:OD1	1:K:20:ASP:HB2	1.83	0.78
1:C:21:VAL:O	1:C:26:LYS:HE3	1.84	0.77
1:H:20:ASP:HB2	1:K:130:ASN:OD1	1.84	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:21:VAL:O	1:E:26:LYS:HE3	1.83	0.77
1:H:13:ASN:HD22	1:H:13:ASN:N	1.81	0.76
1:A:20:ASP:HB2	1:E:130:ASN:OD1	1.86	0.75
1:J:21:VAL:O	1:J:26:LYS:HE3	1.86	0.75
1:D:130:ASN:OD1	1:J:20:ASP:HB2	1.87	0.74
1:E:41:ILE:HG12	1:E:77:LEU:HD11	1.70	0.73
1:A:130:ASN:OD1	1:I:20:ASP:HB2	1.89	0.73
1:C:130:ASN:OD1	1:L:20:ASP:HB2	1.89	0.73
1:D:39:GLN:HG2	1:D:128:VAL:HG22	1.72	0.71
1:B:41:ILE:HG12	1:B:77:LEU:HD11	1.72	0.71
1:E:20:ASP:HB2	1:I:130:ASN:OD1	1.91	0.71
1:K:92:LEU:HD22	1:L:109:LEU:HD13	1.72	0.71
1:L:39:GLN:HG2	1:L:128:VAL:HG22	1.72	0.70
1:F:20:ASP:HB2	1:L:130:ASN:OD1	1.91	0.70
1:A:45:LEU:HD12	4:A:550:HOH:O	1.92	0.70
1:C:41:ILE:HG12	1:C:77:LEU:HD11	1.72	0.69
1:D:20:ASP:HB2	1:G:130:ASN:CG	2.13	0.69
1:I:21:VAL:O	1:I:26:LYS:HE3	1.92	0.69
1:J:41:ILE:HG12	1:J:77:LEU:HD11	1.75	0.68
1:G:39:GLN:HG2	1:G:128:VAL:HG22	1.76	0.68
1:A:109:LEU:HD13	1:B:92:LEU:HD22	1.74	0.68
1:C:109:LEU:HD13	1:D:92:LEU:HD22	1.75	0.68
1:I:39:GLN:HG2	1:I:128:VAL:HG22	1.74	0.68
1:D:130:ASN:CG	1:J:20:ASP:HB2	2.14	0.67
1:H:21:VAL:O	1:H:26:LYS:HE3	1.94	0.67
1:E:120:GLU:HG3	1:E:124:ARG:NH1	2.09	0.67
1:G:109:LEU:HD13	1:H:92:LEU:HD22	1.76	0.67
1:G:41:ILE:HG12	1:G:77:LEU:HD11	1.76	0.67
1:K:41:ILE:HG12	1:K:77:LEU:HD11	1.75	0.67
1:C:14:LEU:HD11	1:C:27:LYS:HG3	1.77	0.67
1:J:120:GLU:HG3	1:J:124:ARG:NH1	2.10	0.67
1:C:92:LEU:HD22	1:D:109:LEU:HD13	1.76	0.67
1:F:120:GLU:HG3	1:F:124:ARG:NH1	2.09	0.66
1:A:12:THR:O	1:A:12:THR:HG22	1.96	0.66
1:L:41:ILE:HG12	1:L:77:LEU:HD11	1.76	0.66
1:B:167:GLU:OE1	3:B:312:TRS:H31	1.93	0.66
1:D:14:LEU:HD22	1:D:26:LYS:HB3	1.79	0.65
1:B:130:ASN:CG	1:K:20:ASP:HB2	2.17	0.65
1:K:120:GLU:HG3	1:K:124:ARG:NH1	2.11	0.65
1:I:120:GLU:HG3	1:I:124:ARG:NH1	2.12	0.64
1:F:41:ILE:HG12	1:F:77:LEU:HD11	1.78	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:39:GLN:HG2	1:C:128:VAL:HG22	1.80	0.63
1:E:51:HIS:CE1	1:E:63:HIS:CE1	2.86	0.63
1:A:39:GLN:HG2	1:A:128:VAL:HG22	1.80	0.63
1:K:39:GLN:HG2	1:K:128:VAL:HG22	1.80	0.63
1:D:14:LEU:H	1:D:14:LEU:HD12	1.64	0.63
1:A:35:ARG:HD3	4:A:609:HOH:O	1.99	0.63
1:H:39:GLN:HG2	1:H:128:VAL:HG22	1.80	0.63
1:E:20:ASP:HB2	1:I:130:ASN:CG	2.20	0.62
1:A:120:GLU:HG3	1:A:124:ARG:NH1	2.14	0.62
1:K:109:LEU:HD13	1:L:92:LEU:HD22	1.80	0.62
1:H:51:HIS:CE1	1:H:63:HIS:CE1	2.88	0.62
1:A:167:GLU:OE1	3:A:309:TRS:H11	1.99	0.62
1:I:41:ILE:HG12	1:I:77:LEU:HD11	1.80	0.61
1:F:20:ASP:HB2	1:L:130:ASN:CG	2.21	0.61
1:G:20:ASP:OD2	1:J:134:LYS:NZ	2.30	0.61
1:H:13:ASN:H	1:H:13:ASN:ND2	1.96	0.61
1:G:33:LEU:HD11	1:G:144:THR:HG23	1.81	0.61
1:F:18:ARG:HG3	1:F:18:ARG:HH11	1.65	0.61
1:F:39:GLN:HG2	1:F:128:VAL:HG22	1.82	0.61
1:J:39:GLN:HG2	1:J:128:VAL:HG22	1.82	0.61
1:B:20:ASP:HB2	1:H:130:ASN:CG	2.20	0.61
1:A:20:ASP:HB2	1:E:130:ASN:CG	2.20	0.61
1:E:92:LEU:HD22	1:F:109:LEU:HD13	1.82	0.61
1:I:92:LEU:HD22	1:J:109:LEU:HD13	1.83	0.61
1:C:33:LEU:HD11	1:C:144:THR:HG23	1.82	0.61
1:E:14:LEU:HD11	1:E:27:LYS:HG3	1.83	0.61
1:A:130:ASN:CG	1:I:20:ASP:HB2	2.21	0.60
1:H:20:ASP:HB2	1:K:130:ASN:CG	2.22	0.60
1:H:41:ILE:HG12	1:H:77:LEU:HD11	1.83	0.60
1:C:20:ASP:HB2	1:F:130:ASN:CG	2.21	0.60
1:G:133:ARG:HB2	1:G:133:ARG:HH11	1.67	0.60
1:C:130:ASN:CG	1:L:20:ASP:HB2	2.21	0.60
1:C:133:ARG:HH11	1:C:133:ARG:HB2	1.67	0.60
1:F:33:LEU:HD11	1:F:144:THR:HG23	1.84	0.59
1:D:33:LEU:HD11	1:D:144:THR:HG23	1.82	0.59
1:G:75:CYS:HB2	4:G:635:HOH:O	2.01	0.59
1:G:20:ASP:HB2	1:J:130:ASN:OD1	2.02	0.59
1:L:120:GLU:HG3	1:L:124:ARG:NH1	2.18	0.59
1:H:120:GLU:HG3	1:H:124:ARG:NH1	2.17	0.59
1:H:46:ILE:HD13	1:H:124:ARG:HD3	1.84	0.59
1:C:51:HIS:CE1	1:C:63:HIS:CE1	2.90	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:29:THR:HG22	1:K:33:LEU:HD22	1.85	0.58
1:J:133:ARG:HH11	1:J:133:ARG:HB2	1.68	0.58
1:A:92:LEU:HD22	1:B:109:LEU:HD13	1.84	0.58
1:I:51:HIS:CE1	1:I:63:HIS:CE1	2.91	0.58
1:B:48:LYS:HG2	1:B:52:TRP:CZ2	2.39	0.58
1:I:18:ARG:HH11	1:I:18:ARG:HG3	1.67	0.58
1:L:33:LEU:HD11	1:L:144:THR:HG23	1.85	0.58
3:B:312:TRS:H11	1:E:167:GLU:OE1	2.03	0.58
1:J:133:ARG:NH1	1:J:133:ARG:HB2	2.19	0.58
1:B:133:ARG:HB2	1:B:133:ARG:HH11	1.69	0.58
1:C:167:GLU:OE1	3:C:303:TRS:H31	2.03	0.58
1:J:51:HIS:CE1	1:J:63:HIS:CE1	2.92	0.58
1:B:18:ARG:HH11	1:B:18:ARG:HG3	1.69	0.58
1:F:13:ASN:HA	1:F:27:LYS:HE2	1.86	0.58
1:I:33:LEU:HD11	1:I:144:THR:HG23	1.86	0.57
1:E:39:GLN:HG2	1:E:128:VAL:HG22	1.86	0.57
1:C:120:GLU:HG3	1:C:124:ARG:NH1	2.19	0.57
1:A:29:THR:HG22	1:A:33:LEU:HD22	1.85	0.57
1:F:133:ARG:HH11	1:F:133:ARG:HB2	1.68	0.57
1:C:15:LEU:HD23	1:C:88:GLY:O	2.03	0.57
1:K:33:LEU:HD11	1:K:144:THR:HG23	1.86	0.57
1:B:39:GLN:HG2	1:B:128:VAL:HG22	1.86	0.57
1:A:33:LEU:HD11	1:A:144:THR:HG23	1.87	0.56
1:D:13:ASN:CG	1:D:27:LYS:HZ1	2.08	0.56
1:G:18:ARG:HH11	1:G:18:ARG:HG3	1.70	0.56
1:G:133:ARG:HB2	1:G:133:ARG:NH1	2.20	0.56
1:D:13:ASN:HA	1:D:27:LYS:HE2	1.86	0.56
1:I:109:LEU:HD13	1:J:92:LEU:HD22	1.87	0.56
1:F:51:HIS:CE1	1:F:63:HIS:CE1	2.93	0.56
1:E:120:GLU:HG3	1:E:124:ARG:HH12	1.71	0.56
1:F:29:THR:HG22	1:F:33:LEU:HD22	1.87	0.56
1:G:92:LEU:HD22	1:H:109:LEU:HD13	1.86	0.56
1:C:133:ARG:HB2	1:C:133:ARG:NH1	2.21	0.56
1:D:46:ILE:HD13	1:D:124:ARG:HD3	1.86	0.56
1:F:48:LYS:HG2	1:F:52:TRP:CZ2	2.41	0.56
1:G:15:LEU:HD23	1:G:88:GLY:O	2.06	0.56
1:D:133:ARG:HH11	1:D:133:ARG:HB2	1.71	0.55
1:B:133:ARG:NH1	1:B:133:ARG:HB2	2.21	0.55
1:K:133:ARG:HH11	1:K:133:ARG:HB2	1.71	0.55
1:B:33:LEU:HD11	1:B:144:THR:HG23	1.88	0.55
1:E:98:ILE:O	1:E:102:THR:HG22	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:55:ARG:O	1:D:114:VAL:HG23	2.06	0.55
1:E:42:ASP:O	1:E:46:ILE:HG13	2.06	0.55
3:D:306:TRS:H31	1:F:167:GLU:OE1	2.07	0.55
1:A:55:ARG:O	1:A:114:VAL:HG23	2.06	0.55
1:A:39:GLN:NE2	4:A:604:HOH:O	2.39	0.55
1:D:29:THR:HG22	1:D:33:LEU:HD22	1.89	0.55
1:E:12:THR:HB	1:E:14:LEU:H	1.72	0.55
1:L:46:ILE:HD13	1:L:124:ARG:HD3	1.87	0.55
1:I:133:ARG:HH11	1:I:133:ARG:HB2	1.71	0.55
1:E:33:LEU:HD11	1:E:144:THR:HG23	1.88	0.55
1:L:29:THR:HG22	1:L:33:LEU:HD22	1.88	0.55
1:G:51:HIS:CE1	1:G:63:HIS:CE1	2.94	0.55
1:I:39:GLN:CG	1:I:128:VAL:HG22	2.36	0.54
1:L:37:VAL:O	1:L:41:ILE:HG13	2.07	0.54
1:B:46:ILE:HD13	1:B:124:ARG:HD3	1.89	0.54
1:F:133:ARG:NH1	1:F:133:ARG:HB2	2.22	0.54
1:D:120:GLU:HG3	1:D:124:ARG:NH1	2.22	0.54
1:H:18:ARG:HH11	1:H:18:ARG:HG3	1.73	0.54
1:B:120:GLU:HG3	1:B:124:ARG:NH1	2.22	0.54
1:C:46:ILE:HD13	1:C:124:ARG:HD3	1.88	0.54
1:D:51:HIS:CE1	1:D:63:HIS:CE1	2.96	0.54
1:F:46:ILE:HD13	1:F:124:ARG:HD3	1.90	0.54
1:A:12:THR:H	1:A:27:LYS:NZ	2.05	0.54
1:J:55:ARG:O	1:J:114:VAL:HG23	2.08	0.54
1:G:120:GLU:HG3	1:G:124:ARG:NH1	2.22	0.54
1:K:26:LYS:O	1:K:30:VAL:HG23	2.08	0.53
1:A:37:VAL:O	1:A:41:ILE:HG13	2.09	0.53
1:E:133:ARG:HB2	1:E:133:ARG:NH1	2.24	0.53
1:B:14:LEU:HD11	1:B:27:LYS:HG3	1.90	0.53
1:E:46:ILE:HD13	1:E:124:ARG:HD3	1.91	0.53
1:E:29:THR:HG22	1:E:33:LEU:HD22	1.91	0.53
1:J:18:ARG:HH11	1:J:18:ARG:HG3	1.73	0.53
1:D:39:GLN:CG	1:D:128:VAL:HG22	2.38	0.53
1:D:12:THR:O	1:D:13:ASN:O	2.26	0.53
1:D:133:ARG:NH1	1:D:133:ARG:HB2	2.24	0.52
1:H:29:THR:HG22	1:H:33:LEU:HD22	1.90	0.52
1:J:33:LEU:HD11	1:J:144:THR:HG23	1.91	0.52
1:C:37:VAL:O	1:C:41:ILE:HG13	2.08	0.52
1:A:46:ILE:HD13	1:A:124:ARG:HD3	1.91	0.52
1:E:15:LEU:HD23	1:E:88:GLY:O	2.09	0.52
1:B:64:GLU:HB2	4:B:560:HOH:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:130:ASN:O	1:K:134:LYS:HE2	2.09	0.52
1:I:15:LEU:HD23	1:I:88:GLY:O	2.09	0.52
1:I:98:ILE:O	1:I:102:THR:HG22	2.10	0.52
1:I:120:GLU:HG3	1:I:124:ARG:HH12	1.75	0.52
1:A:134:LYS:NZ	1:I:20:ASP:OD2	2.41	0.52
1:E:109:LEU:HD13	1:F:92:LEU:HD22	1.90	0.52
1:B:51:HIS:CE1	1:B:63:HIS:CE1	2.98	0.52
1:C:55:ARG:O	1:C:114:VAL:HG23	2.10	0.52
1:K:133:ARG:HB2	1:K:133:ARG:NH1	2.25	0.51
1:K:120:GLU:HG3	1:K:124:ARG:HH12	1.76	0.51
1:B:20:ASP:OD2	1:H:134:LYS:NZ	2.40	0.51
1:A:130:ASN:O	1:A:134:LYS:HE2	2.10	0.51
1:J:15:LEU:HD23	1:J:88:GLY:O	2.10	0.51
1:A:133:ARG:NH1	1:A:133:ARG:HB2	2.25	0.51
1:F:120:GLU:HG3	1:F:124:ARG:HH12	1.73	0.51
1:D:15:LEU:HD23	1:D:88:GLY:O	2.09	0.51
1:K:51:HIS:CE1	1:K:63:HIS:CE1	2.98	0.51
3:B:312:TRS:H21	1:L:167:GLU:OE1	2.10	0.51
1:G:46:ILE:HD13	1:G:124:ARG:HD3	1.93	0.51
1:A:133:ARG:HB2	1:A:133:ARG:HH11	1.75	0.51
1:E:133:ARG:HB2	1:E:133:ARG:HH11	1.76	0.51
1:E:26:LYS:O	1:E:30:VAL:HG23	2.11	0.51
1:G:48:LYS:HG2	1:G:52:TRP:CZ2	2.46	0.51
1:J:120:GLU:HG3	1:J:124:ARG:HH12	1.75	0.51
1:J:46:ILE:HD13	1:J:124:ARG:HD3	1.92	0.51
1:J:130:ASN:O	1:J:134:LYS:HE2	2.11	0.50
1:C:98:ILE:O	1:C:102:THR:HG22	2.11	0.50
1:H:15:LEU:HD23	1:H:88:GLY:O	2.11	0.50
1:E:18:ARG:HG3	1:E:18:ARG:HH11	1.76	0.50
1:J:48:LYS:HG2	1:J:52:TRP:CZ2	2.47	0.50
1:K:46:ILE:HD13	1:K:124:ARG:HD3	1.92	0.50
1:H:37:VAL:O	1:H:41:ILE:HG13	2.11	0.50
1:I:133:ARG:NH1	1:I:133:ARG:HB2	2.25	0.50
1:G:151:ALA:O	1:G:155:LEU:HD12	2.10	0.50
1:K:15:LEU:HD23	1:K:88:GLY:O	2.11	0.50
1:D:26:LYS:O	1:D:30:VAL:HG23	2.12	0.50
1:G:20:ASP:HB2	1:J:130:ASN:CG	2.32	0.50
1:L:48:LYS:HG2	1:L:52:TRP:CZ2	2.47	0.50
1:E:55:ARG:O	1:E:114:VAL:HG23	2.11	0.50
1:I:26:LYS:O	1:I:30:VAL:HG23	2.12	0.50
1:G:20:ASP:HB3	1:J:134:LYS:NZ	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:ASP:OD2	1:E:134:LYS:NZ	2.37	0.49
1:F:18:ARG:HG3	1:L:163:GLU:OE1	2.11	0.49
1:G:29:THR:HG22	1:G:33:LEU:HD22	1.94	0.49
1:L:133:ARG:HB2	1:L:133:ARG:NH1	2.28	0.49
1:I:29:THR:HG22	1:I:33:LEU:HD22	1.95	0.49
1:F:76:HIS:ND1	4:F:645:HOH:O	2.35	0.49
1:L:133:ARG:HH11	1:L:133:ARG:HB2	1.77	0.49
1:I:46:ILE:HD13	1:I:124:ARG:HD3	1.94	0.49
1:I:37:VAL:O	1:I:41:ILE:HG13	2.12	0.49
1:H:33:LEU:HD11	1:H:144:THR:HG23	1.94	0.49
1:J:29:THR:HG22	1:J:33:LEU:HD22	1.95	0.49
1:L:39:GLN:CG	1:L:128:VAL:HG22	2.42	0.49
1:F:130:ASN:O	1:F:134:LYS:HE2	2.13	0.48
1:H:133:ARG:NH1	1:H:133:ARG:HB2	2.28	0.48
1:D:140:LYS:HE3	4:D:700:HOH:O	2.12	0.48
1:G:105:LYS:O	1:G:106:SER:C	2.50	0.48
1:H:133:ARG:HH11	1:H:133:ARG:HB2	1.77	0.48
1:H:12:THR:HG23	1:H:12:THR:O	2.12	0.48
1:I:48:LYS:HG2	1:I:52:TRP:CZ2	2.49	0.48
1:F:15:LEU:HD23	1:F:88:GLY:O	2.13	0.48
1:D:60:ILE:HG23	1:D:61:ALA:N	2.28	0.48
1:B:124:ARG:HG3	1:B:124:ARG:HH11	1.78	0.48
1:L:51:HIS:CE1	1:L:63:HIS:CE1	3.02	0.48
1:I:55:ARG:O	1:I:114:VAL:HG23	2.13	0.48
1:H:130:ASN:O	1:H:134:LYS:HE2	2.14	0.48
1:A:95:THR:HG23	1:A:96:GLN:N	2.29	0.48
1:L:38:ILE:HG23	1:L:98:ILE:HD13	1.95	0.48
1:A:18:ARG:HG3	1:A:18:ARG:HH11	1.78	0.48
1:K:37:VAL:O	1:K:41:ILE:HG13	2.14	0.48
1:K:39:GLN:CG	1:K:128:VAL:HG22	2.43	0.48
1:K:26:LYS:HD3	1:K:87:LEU:O	2.14	0.48
1:C:43:LEU:CD1	1:C:73:LEU:HD21	2.43	0.47
1:J:25:GLU:OE1	1:J:140:LYS:HD2	2.14	0.47
1:B:60:ILE:HG23	1:B:61:ALA:N	2.29	0.47
1:I:43:LEU:CD1	1:I:73:LEU:HD21	2.44	0.47
1:G:21:VAL:HG12	1:G:26:LYS:HG3	1.97	0.47
1:D:124:ARG:HG3	1:D:124:ARG:HH11	1.79	0.47
1:D:37:VAL:O	1:D:41:ILE:HG13	2.13	0.47
1:B:29:THR:HG22	1:B:33:LEU:HD22	1.97	0.47
1:K:60:ILE:HG23	1:K:61:ALA:N	2.29	0.47
1:A:26:LYS:O	1:A:30:VAL:HG23	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:26:LYS:O	1:H:30:VAL:HG23	2.14	0.47
1:F:36:GLN:NE2	1:F:36:GLN:HA	2.30	0.47
1:C:48:LYS:HG2	1:C:52:TRP:CZ2	2.49	0.47
1:C:130:ASN:O	1:C:134:LYS:HE2	2.15	0.46
1:I:124:ARG:HH11	1:I:124:ARG:HG3	1.80	0.46
1:C:29:THR:HG22	1:C:33:LEU:HD22	1.97	0.46
1:L:18:ARG:HH11	1:L:18:ARG:HG3	1.80	0.46
1:C:99:ASN:ND2	1:D:99:ASN:ND2	2.63	0.46
1:A:160:TRP:CH2	1:I:82:GLU:HG2	2.50	0.46
1:J:39:GLN:CG	1:J:128:VAL:HG22	2.46	0.46
1:J:151:ALA:O	1:J:155:LEU:HD12	2.15	0.46
1:K:18:ARG:HH11	1:K:18:ARG:HG3	1.80	0.46
1:H:13:ASN:ND2	1:H:13:ASN:N	2.54	0.46
1:F:55:ARG:O	1:F:114:VAL:HG23	2.15	0.46
1:K:14:LEU:HD11	1:K:27:LYS:HG3	1.97	0.46
1:K:48:LYS:HG2	1:K:52:TRP:CZ2	2.50	0.46
1:A:25:GLU:OE1	1:A:140:LYS:HD2	2.16	0.46
1:B:134:LYS:NZ	1:K:20:ASP:OD2	2.44	0.46
1:F:37:VAL:O	1:F:41:ILE:HG13	2.16	0.46
1:G:59:PHE:CD1	1:G:60:ILE:N	2.84	0.46
1:B:130:ASN:O	1:B:134:LYS:HE2	2.16	0.46
1:D:130:ASN:OD1	1:D:133:ARG:NH2	2.49	0.46
1:F:77:LEU:HD23	1:F:77:LEU:C	2.37	0.46
1:D:48:LYS:HG2	1:D:52:TRP:CZ2	2.50	0.46
1:B:55:ARG:O	1:B:114:VAL:HG23	2.16	0.46
1:C:18:ARG:HG3	1:C:18:ARG:HH11	1.81	0.45
1:C:26:LYS:O	1:C:30:VAL:HG23	2.16	0.45
1:B:77:LEU:HD23	1:B:77:LEU:C	2.37	0.45
1:H:39:GLN:CG	1:H:128:VAL:HG22	2.44	0.45
1:H:55:ARG:O	1:H:114:VAL:HG23	2.15	0.45
1:B:20:ASP:HB3	1:H:134:LYS:NZ	2.31	0.45
1:J:37:VAL:O	1:J:41:ILE:HG13	2.16	0.45
1:E:130:ASN:O	1:E:134:LYS:HE2	2.17	0.45
1:D:25:GLU:OE1	1:D:140:LYS:HD2	2.17	0.45
1:J:60:ILE:HG23	1:J:61:ALA:N	2.32	0.45
1:D:77:LEU:C	1:D:77:LEU:HD23	2.37	0.45
1:J:36:GLN:NE2	1:J:36:GLN:HA	2.32	0.45
1:E:60:ILE:HG23	1:E:61:ALA:N	2.32	0.45
1:L:60:ILE:HG23	1:L:61:ALA:N	2.32	0.45
1:H:98:ILE:O	1:H:102:THR:HG22	2.17	0.45
1:A:98:ILE:O	1:A:102:THR:HG22	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:60:ILE:HG23	1:G:61:ALA:N	2.33	0.44
1:D:76:HIS:CE1	1:D:151:ALA:HA	2.52	0.44
1:A:43:LEU:CD1	1:A:73:LEU:HD21	2.47	0.44
1:B:26:LYS:HD3	1:B:87:LEU:O	2.18	0.44
1:I:130:ASN:O	1:I:134:LYS:HE2	2.17	0.44
1:E:43:LEU:CD1	1:E:73:LEU:HD21	2.47	0.44
1:F:13:ASN:HD22	1:F:13:ASN:N	2.14	0.44
1:L:15:LEU:HD23	1:L:88:GLY:O	2.16	0.44
1:A:60:ILE:HG23	1:A:61:ALA:N	2.33	0.44
4:A:563:HOH:O	1:B:74:ILE:HD13	2.16	0.44
1:F:42:ASP:O	1:F:46:ILE:HG13	2.17	0.44
3:A:309:TRS:H31	1:J:167:GLU:OE1	2.18	0.44
1:H:77:LEU:C	1:H:77:LEU:HD23	2.38	0.44
1:C:18:ARG:HG3	1:F:163:GLU:OE1	2.17	0.44
1:D:42:ASP:O	1:D:46:ILE:HG13	2.18	0.44
1:H:48:LYS:HG2	1:H:52:TRP:CZ2	2.53	0.44
1:C:134:LYS:NZ	1:L:20:ASP:OD2	2.45	0.44
1:J:14:LEU:H	1:J:14:LEU:HG	1.55	0.44
1:D:38:ILE:HG23	1:D:98:ILE:HD13	2.00	0.44
1:I:60:ILE:HG23	1:I:61:ALA:N	2.32	0.44
1:C:130:ASN:OD1	1:C:133:ARG:NH2	2.51	0.43
1:D:15:LEU:N	1:D:15:LEU:HD22	2.33	0.43
1:K:15:LEU:N	1:K:15:LEU:HD22	2.33	0.43
1:J:98:ILE:O	1:J:102:THR:HG22	2.17	0.43
1:C:25:GLU:OE1	1:C:140:LYS:HD2	2.19	0.43
1:B:95:THR:HG23	1:B:96:GLN:N	2.32	0.43
1:F:18:ARG:NH1	1:F:18:ARG:HG3	2.32	0.43
1:K:59:PHE:CD1	1:K:60:ILE:N	2.86	0.43
1:I:59:PHE:CD1	1:I:60:ILE:N	2.86	0.43
1:H:60:ILE:HG23	1:H:61:ALA:N	2.33	0.43
1:C:40:PHE:CE2	1:C:155:LEU:HD11	2.53	0.43
1:H:43:LEU:CD1	1:H:73:LEU:HD21	2.49	0.43
1:G:55:ARG:O	1:G:114:VAL:HG23	2.18	0.43
1:L:25:GLU:OE1	1:L:140:LYS:HD2	2.18	0.43
1:E:21:VAL:HG12	1:E:26:LYS:HG3	2.01	0.43
1:A:120:GLU:HG3	1:A:124:ARG:HH12	1.80	0.43
3:D:310:TRS:O3	1:G:146:ASP:OD2	2.36	0.43
1:A:134:LYS:NZ	1:I:20:ASP:HB3	2.34	0.43
1:K:43:LEU:CD1	1:K:73:LEU:HD21	2.48	0.43
1:F:60:ILE:HG23	1:F:61:ALA:N	2.33	0.43
1:F:111:ILE:HG13	1:F:117:HIS:CE1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:43:LEU:CD1	1:G:73:LEU:HD21	2.49	0.43
1:F:82:GLU:HG2	1:L:160:TRP:CH2	2.53	0.43
3:D:306:TRS:H11	1:I:167:GLU:OE1	2.19	0.43
1:A:151:ALA:O	1:A:155:LEU:HD12	2.19	0.43
3:C:303:TRS:H11	1:G:167:GLU:OE1	2.19	0.43
1:C:151:ALA:O	1:C:155:LEU:HD12	2.19	0.43
1:A:15:LEU:HD23	1:A:88:GLY:O	2.19	0.43
1:H:25:GLU:OE1	1:H:140:LYS:HD2	2.19	0.43
1:H:42:ASP:O	1:H:46:ILE:HG13	2.19	0.43
1:A:59:PHE:CD1	1:A:60:ILE:N	2.87	0.43
1:D:18:ARG:HG3	1:D:18:ARG:HH11	1.84	0.43
1:G:77:LEU:C	1:G:77:LEU:HD23	2.39	0.42
1:A:167:GLU:CD	3:A:309:TRS:H11	2.39	0.42
1:G:83:ARG:NH2	1:G:143:ASP:HB2	2.34	0.42
1:F:25:GLU:OE1	1:F:140:LYS:HD2	2.20	0.42
1:K:32:LEU:HD11	1:K:135:ALA:HB1	2.00	0.42
1:H:130:ASN:OD1	1:H:133:ARG:NH2	2.50	0.42
1:J:26:LYS:O	1:J:30:VAL:HG23	2.19	0.42
1:D:59:PHE:CD1	1:D:60:ILE:N	2.86	0.42
1:B:94:THR:O	1:B:98:ILE:HG12	2.18	0.42
1:A:12:THR:H	1:A:27:LYS:HZ1	1.65	0.42
1:G:18:ARG:NH1	1:G:18:ARG:HG3	2.34	0.42
1:E:59:PHE:CD1	1:E:60:ILE:N	2.86	0.42
1:K:55:ARG:O	1:K:114:VAL:HG23	2.20	0.42
1:B:15:LEU:HD23	1:B:88:GLY:O	2.20	0.42
1:B:31:GLU:HG2	4:B:511:HOH:O	2.20	0.42
1:E:26:LYS:HD3	1:E:87:LEU:O	2.19	0.42
1:I:26:LYS:HD3	1:I:87:LEU:O	2.19	0.42
1:L:130:ASN:OD1	1:L:133:ARG:NH2	2.53	0.42
1:G:55:ARG:NE	4:G:528:HOH:O	2.53	0.42
1:E:39:GLN:CG	1:E:128:VAL:HG22	2.50	0.42
1:H:38:ILE:HG23	1:H:98:ILE:HD13	2.02	0.42
1:A:111:ILE:HG13	1:A:117:HIS:CE1	2.55	0.42
1:A:77:LEU:C	1:A:77:LEU:HD23	2.40	0.42
1:I:18:ARG:HG3	1:I:18:ARG:NH1	2.32	0.42
1:C:120:GLU:HG3	1:C:124:ARG:HH12	1.85	0.42
1:J:25:GLU:OE2	1:J:140:LYS:HB2	2.20	0.42
1:A:43:LEU:HD11	1:A:125:TYR:CZ	2.55	0.42
1:B:40:PHE:CE2	1:B:155:LEU:HD11	2.54	0.42
1:C:39:GLN:CG	1:C:128:VAL:HG22	2.48	0.42
1:A:114:VAL:HB	4:A:613:HOH:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:101:LYS:O	1:H:102:THR:C	2.58	0.42
3:D:310:TRS:O2	1:J:146:ASP:OD2	2.38	0.42
1:B:26:LYS:O	1:B:30:VAL:HG23	2.20	0.41
1:G:39:GLN:CG	1:G:128:VAL:HG22	2.47	0.41
1:D:13:ASN:CG	1:D:27:LYS:NZ	2.73	0.41
1:B:39:GLN:CG	1:B:128:VAL:HG22	2.49	0.41
1:L:43:LEU:CD1	1:L:73:LEU:HD21	2.50	0.41
1:H:105:LYS:O	1:H:106:SER:C	2.58	0.41
1:A:26:LYS:HD3	1:A:87:LEU:O	2.20	0.41
3:C:303:TRS:H21	1:K:167:GLU:OE1	2.20	0.41
1:L:105:LYS:O	1:L:106:SER:C	2.58	0.41
1:A:153:ARG:HG2	1:A:153:ARG:NH1	2.36	0.41
1:C:36:GLN:NE2	1:C:36:GLN:HA	2.35	0.41
1:F:13:ASN:ND2	1:F:13:ASN:N	2.68	0.41
1:B:17:THR:C	1:B:19:ASN:H	2.23	0.41
1:J:118:LEU:HA	1:J:118:LEU:HD12	1.89	0.41
1:H:153:ARG:NH1	1:H:153:ARG:HG2	2.36	0.41
1:C:83:ARG:NH2	1:C:143:ASP:HB2	2.35	0.41
1:F:26:LYS:O	1:F:30:VAL:HG23	2.21	0.41
1:H:120:GLU:HG3	1:H:124:ARG:HH12	1.83	0.41
1:I:33:LEU:HA	1:I:33:LEU:HD12	1.87	0.41
1:K:15:LEU:H	1:K:15:LEU:HD22	1.85	0.41
1:L:59:PHE:CD1	1:L:60:ILE:N	2.88	0.41
1:K:74:ILE:HD12	4:K:547:HOH:O	2.21	0.41
1:B:25:GLU:OE1	1:B:140:LYS:HD2	2.21	0.41
1:B:146:ASP:OD2	3:B:304:TRS:O2	2.37	0.41
1:F:39:GLN:CG	1:F:128:VAL:HG22	2.48	0.41
1:D:94:THR:O	1:D:98:ILE:HG12	2.21	0.41
1:G:70:ARG:NH1	4:G:580:HOH:O	2.53	0.41
1:C:26:LYS:HD3	1:C:87:LEU:O	2.20	0.41
1:G:40:PHE:CE2	1:G:155:LEU:HD11	2.55	0.41
1:A:96:GLN:HE21	1:A:96:GLN:HB3	1.66	0.41
1:D:151:ALA:O	1:D:155:LEU:HD12	2.20	0.41
1:I:25:GLU:OE1	1:I:140:LYS:HD2	2.21	0.41
1:I:14:LEU:HD11	1:I:27:LYS:HG3	2.02	0.41
1:D:14:LEU:CD2	1:D:26:LYS:HB3	2.50	0.41
1:E:130:ASN:OD1	1:E:133:ARG:NH2	2.53	0.41
1:L:77:LEU:C	1:L:77:LEU:HD23	2.41	0.41
1:K:124:ARG:HH11	1:K:124:ARG:HG3	1.85	0.41
1:L:120:GLU:HG3	1:L:124:ARG:HH12	1.83	0.41
3:D:306:TRS:H31	1:F:167:GLU:CD	2.41	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:15:LEU:H	1:K:15:LEU:CD2	2.34	0.41
1:L:94:THR:O	1:L:98:ILE:HG12	2.21	0.41
1:L:133:ARG:NH1	1:L:156:ASP:OD2	2.54	0.41
1:A:51:HIS:CE1	1:A:63:HIS:CE1	3.09	0.41
1:K:151:ALA:O	1:K:155:LEU:HD12	2.20	0.41
1:F:118:LEU:HD12	1:F:118:LEU:HA	1.94	0.41
1:J:77:LEU:HD23	1:J:77:LEU:C	2.41	0.40
1:I:32:LEU:HD11	1:I:135:ALA:HB1	2.02	0.40
1:L:118:LEU:HD21	1:L:165:ASN:HB3	2.03	0.40
1:D:105:LYS:O	1:D:106:SER:C	2.60	0.40
1:B:167:GLU:CD	3:B:312:TRS:H31	2.42	0.40
1:H:18:ARG:HG3	1:K:163:GLU:OE1	2.21	0.40
1:C:38:ILE:HG23	1:C:98:ILE:HD13	2.02	0.40
1:J:94:THR:O	1:J:98:ILE:HG12	2.21	0.40
1:I:40:PHE:CE2	1:I:155:LEU:HD11	2.57	0.40
1:G:37:VAL:O	1:G:41:ILE:HG13	2.20	0.40
1:J:17:THR:C	1:J:19:ASN:H	2.24	0.40
1:B:96:GLN:HB3	1:B:96:GLN:HE21	1.66	0.40
1:E:12:THR:HB	1:E:13:ASN:H	1.68	0.40
1:F:43:LEU:CD1	1:F:73:LEU:HD21	2.50	0.40
1:H:63:HIS:NE2	4:H:643:HOH:O	2.33	0.40
1:I:43:LEU:HD11	1:I:125:TYR:CZ	2.57	0.40
1:J:40:PHE:CE2	1:J:155:LEU:HD11	2.57	0.40
1:A:70:ARG:HD3	4:A:563:HOH:O	2.22	0.40
1:C:118:LEU:HA	1:C:118:LEU:HD12	1.90	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	155/167 (93%)	149 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	155/167 (93%)	150 (97%)	5 (3%)	0	100	100
1	C	153/167 (92%)	148 (97%)	4 (3%)	1 (1%)	26	51
1	D	155/167 (93%)	147 (95%)	7 (4%)	1 (1%)	30	54
1	E	154/167 (92%)	148 (96%)	5 (3%)	1 (1%)	30	54
1	F	154/167 (92%)	147 (96%)	7 (4%)	0	100	100
1	G	153/167 (92%)	144 (94%)	8 (5%)	1 (1%)	26	51
1	H	155/167 (93%)	149 (96%)	5 (3%)	1 (1%)	30	54
1	I	154/167 (92%)	150 (97%)	4 (3%)	0	100	100
1	J	153/167 (92%)	147 (96%)	6 (4%)	0	100	100
1	K	153/167 (92%)	148 (97%)	5 (3%)	0	100	100
1	L	153/167 (92%)	147 (96%)	6 (4%)	0	100	100
All	All	1847/2004 (92%)	1774 (96%)	68 (4%)	5 (0%)	46	72

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	13	ASN
1	E	13	ASN
1	G	14	LEU
1	H	12	THR
1	C	14	LEU

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	133/142 (94%)	124 (93%)	9 (7%)	20	40
1	B	133/142 (94%)	121 (91%)	12 (9%)	12	24
1	C	132/142 (93%)	122 (92%)	10 (8%)	16	34
1	D	133/142 (94%)	123 (92%)	10 (8%)	17	35

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	E	133/142 (94%)	122 (92%)	11 (8%)	14 28
1	F	133/142 (94%)	123 (92%)	10 (8%)	17 35
1	G	132/142 (93%)	122 (92%)	10 (8%)	16 34
1	H	133/142 (94%)	122 (92%)	11 (8%)	14 28
1	I	133/142 (94%)	123 (92%)	10 (8%)	17 35
1	J	132/142 (93%)	119 (90%)	13 (10%)	10 20
1	K	132/142 (93%)	122 (92%)	10 (8%)	16 34
1	L	132/142 (93%)	121 (92%)	11 (8%)	14 28
All	All	1591/1704 (93%)	1464 (92%)	127 (8%)	15 31

All (127) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	ASP
1	A	33	LEU
1	A	73	LEU
1	A	77	LEU
1	A	96	GLN
1	A	118	LEU
1	A	134	LYS
1	A	153	ARG
1	A	155	LEU
1	B	13	ASN
1	B	20	ASP
1	B	23	ASP
1	B	33	LEU
1	B	73	LEU
1	B	77	LEU
1	B	96	GLN
1	B	102	THR
1	B	118	LEU
1	B	134	LYS
1	B	153	ARG
1	B	155	LEU
1	C	20	ASP
1	C	23	ASP
1	C	33	LEU
1	C	73	LEU
1	C	96	GLN

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Mol	Chain	Res	Type
1	C	99	ASN
1	C	118	LEU
1	C	134	LYS
1	C	153	ARG
1	C	155	LEU
1	D	14	LEU
1	D	20	ASP
1	D	33	LEU
1	D	43	LEU
1	D	73	LEU
1	D	96	GLN
1	D	118	LEU
1	D	134	LYS
1	D	153	ARG
1	D	155	LEU
1	E	13	ASN
1	E	20	ASP
1	E	23	ASP
1	E	33	LEU
1	E	43	LEU
1	E	73	LEU
1	E	96	GLN
1	E	118	LEU
1	E	134	LYS
1	E	153	ARG
1	E	155	LEU
1	F	13	ASN
1	F	20	ASP
1	F	23	ASP
1	F	33	LEU
1	F	73	LEU
1	F	96	GLN
1	F	118	LEU
1	F	134	LYS
1	F	153	ARG
1	F	155	LEU
1	G	20	ASP
1	G	23	ASP
1	G	33	LEU
1	G	43	LEU
1	G	73	LEU
1	G	96	GLN

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Mol	Chain	Res	Type
1	G	118	LEU
1	G	134	LYS
1	G	153	ARG
1	G	155	LEU
1	H	13	ASN
1	H	20	ASP
1	H	23	ASP
1	H	33	LEU
1	H	73	LEU
1	H	77	LEU
1	H	96	GLN
1	H	118	LEU
1	H	134	LYS
1	H	153	ARG
1	H	155	LEU
1	I	20	ASP
1	I	23	ASP
1	I	33	LEU
1	I	73	LEU
1	I	96	GLN
1	I	102	THR
1	I	118	LEU
1	I	134	LYS
1	I	153	ARG
1	I	155	LEU
1	J	13	ASN
1	J	14	LEU
1	J	20	ASP
1	J	23	ASP
1	J	33	LEU
1	J	43	LEU
1	J	73	LEU
1	J	77	LEU
1	J	96	GLN
1	J	118	LEU
1	J	134	LYS
1	J	153	ARG
1	J	155	LEU
1	K	13	ASN
1	K	20	ASP
1	K	33	LEU
1	K	73	LEU

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Mol	Chain	Res	Type
1	K	77	LEU
1	K	96	GLN
1	K	118	LEU
1	K	134	LYS
1	K	153	ARG
1	K	155	LEU
1	L	20	ASP
1	L	23	ASP
1	L	33	LEU
1	L	43	LEU
1	L	73	LEU
1	L	77	LEU
1	L	96	GLN
1	L	118	LEU
1	L	134	LYS
1	L	153	ARG
1	L	155	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (48) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	GLN
1	A	39	GLN
1	A	96	GLN
1	A	99	ASN
1	B	13	ASN
1	B	36	GLN
1	B	96	GLN
1	B	99	ASN
1	B	112	HIS
1	C	13	ASN
1	C	36	GLN
1	C	96	GLN
1	C	99	ASN
1	D	36	GLN
1	D	96	GLN
1	D	99	ASN
1	D	112	HIS
1	E	13	ASN
1	E	36	GLN
1	E	96	GLN
1	F	13	ASN

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Mol	Chain	Res	Type
1	F	36	GLN
1	F	96	GLN
1	G	36	GLN
1	G	96	GLN
1	G	112	HIS
1	H	13	ASN
1	H	36	GLN
1	H	96	GLN
1	H	99	ASN
1	H	112	HIS
1	I	36	GLN
1	I	96	GLN
1	I	99	ASN
1	I	112	HIS
1	J	36	GLN
1	J	96	GLN
1	J	99	ASN
1	J	112	HIS
1	K	13	ASN
1	K	36	GLN
1	K	96	GLN
1	K	99	ASN
1	K	112	HIS
1	L	36	GLN
1	L	96	GLN
1	L	99	ASN
1	L	112	HIS

5.3.3 RNA

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 carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 25 ligands modelled in this entry, 13 are monoatomic - leaving 12 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	$\#\|Z\| > 2$
3	TRS	A	301	-	7,7,7	0.67	0	9,9,9	1.43	2 (22%)
3	TRS	A	309	-	7,7,7	0.43	0	9,9,9	1.45	2 (22%)
3	TRS	B	304	-	7,7,7	0.47	0	9,9,9	1.53	2 (22%)
3	TRS	B	312	-	7,7,7	0.26	0	9,9,9	1.52	2 (22%)
3	TRS	C	303	-	7,7,7	0.62	0	9,9,9	1.41	2 (22%)
3	TRS	C	307	-	7,7,7	0.54	0	9,9,9	1.56	2 (22%)
3	TRS	D	305	-	7,7,7	0.87	0	9,9,9	1.32	2 (22%)
3	TRS	D	306	-	7,7,7	0.61	0	9,9,9	1.47	2 (22%)
3	TRS	D	310	-	7,7,7	0.48	0	9,9,9	1.55	2 (22%)
3	TRS	E	311	-	7,7,7	0.66	0	9,9,9	1.47	2 (22%)
3	TRS	H	308	-	7,7,7	0.95	0	9,9,9	1.38	2 (22%)
3	TRS	K	302	-	7,7,7	0.86	0	9,9,9	1.36	2 (22%)

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
3	TRS	A	301	-	-	0/9/9/9	0/0/0/0
3	TRS	A	309	-	-	0/9/9/9	0/0/0/0
3	TRS	B	304	-	-	0/9/9/9	0/0/0/0
3	TRS	B	312	-	-	0/9/9/9	0/0/0/0
3	TRS	C	303	-	-	0/9/9/9	0/0/0/0
3	TRS	C	307	-	-	0/9/9/9	0/0/0/0
3	TRS	D	305	-	-	0/9/9/9	0/0/0/0
3	TRS	D	306	-	-	0/9/9/9	0/0/0/0
3	TRS	D	310	-	-	0/9/9/9	0/0/0/0
3	TRS	E	311	-	-	0/9/9/9	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	TRS	H	308	-	-	0/9/9/9	0/0/0/0
3	TRS	K	302	-	-	0/9/9/9	0/0/0/0

There are no bond length outliers.

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	306	TRS	C1-C-N	-2.80	102.98	108.09
3	E	311	TRS	C1-C-N	-2.78	103.03	108.09
3	B	312	TRS	C1-C-N	-2.77	103.05	108.09
3	D	310	TRS	C1-C-N	-2.75	103.07	108.09
3	B	304	TRS	C1-C-N	-2.73	103.11	108.09
3	C	307	TRS	C1-C-N	-2.65	103.27	108.09
3	H	308	TRS	C1-C-N	-2.62	103.32	108.09
3	C	303	TRS	C1-C-N	-2.62	103.32	108.09
3	K	302	TRS	C1-C-N	-2.62	103.33	108.09
3	A	301	TRS	C1-C-N	-2.58	103.39	108.09
3	A	309	TRS	C1-C-N	-2.52	103.51	108.09
3	D	305	TRS	C1-C-N	-2.46	103.60	108.09
3	D	305	TRS	C3-C-N	2.13	111.97	108.09
3	K	302	TRS	C3-C-N	2.17	112.04	108.09
3	H	308	TRS	C3-C-N	2.22	112.14	108.09
3	E	311	TRS	C3-C-N	2.37	112.39	108.09
3	C	303	TRS	C3-C-N	2.38	112.42	108.09
3	A	301	TRS	C3-C-N	2.45	112.54	108.09
3	A	309	TRS	C3-C-N	2.54	112.70	108.09
3	B	312	TRS	C3-C-N	2.68	112.96	108.09
3	D	306	TRS	C3-C-N	2.72	113.04	108.09
3	B	304	TRS	C3-C-N	2.74	113.08	108.09
3	D	310	TRS	C3-C-N	2.77	113.13	108.09
3	C	307	TRS	C3-C-N	2.90	113.37	108.09

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	309	TRS	3	0
3	B	304	TRS	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	312	TRS	4	0
3	C	303	TRS	3	0
3	D	306	TRS	3	0
3	D	310	TRS	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 95^{th} 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	157/167 (94%)	-0.08	2 (1%)	79	79	36, 54, 70, 97	0
1	B	157/167 (94%)	-0.05	3 (1%)	70	69	36, 54, 77, 105	0
1	C	155/167 (92%)	0.06	1 (0%)	90	91	45, 68, 89, 98	0
1	D	157/167 (94%)	0.29	2 (1%)	79	79	48, 70, 84, 99	0
1	E	156/167 (93%)	0.04	1 (0%)	90	91	42, 62, 89, 102	0
1	F	156/167 (93%)	0.26	7 (4%)	37	35	45, 74, 89, 104	0
1	G	155/167 (92%)	0.06	0	100	100	34, 54, 83, 95	0
1	H	157/167 (94%)	-0.14	0	100	100	42, 59, 79, 100	0
1	I	156/167 (93%)	0.30	4 (2%)	59	58	49, 71, 87, 100	0
1	J	155/167 (92%)	0.17	3 (1%)	70	69	48, 70, 87, 92	0
1	K	155/167 (92%)	-0.01	2 (1%)	79	79	42, 60, 78, 84	0
1	L	155/167 (92%)	0.12	2 (1%)	79	79	44, 64, 83, 91	0
All	All	1871/2004 (93%)	0.08	27 (1%)	78	76	34, 64, 85, 105	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	11	ALA	4.5
1	I	12	THR	4.0
1	C	38	ILE	3.6
1	B	11	ALA	3.5
1	F	98	ILE	3.3
1	J	136	ILE	3.0
1	J	112	HIS	2.9
1	E	12	THR	2.9
1	D	166	ILE	2.9
1	F	15	LEU	2.6
1	K	98	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
1	F	92	LEU	2.6
1	A	12	THR	2.5
1	F	87	LEU	2.5
1	L	92	LEU	2.5
1	L	98	ILE	2.4
1	K	50	ALA	2.4
1	F	14	LEU	2.3
1	B	14	LEU	2.2
1	I	111	ILE	2.2
1	B	12	THR	2.2
1	F	121	LEU	2.2
1	J	140	LYS	2.2
1	I	108	PRO	2.1
1	F	136	ILE	2.1
1	I	14	LEU	2.0
1	D	125	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. 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, 95^{th} 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
3	TRS	B	304	8/8	0.93	0.24	3.55	73,74,75,76	0
2	CD	B	201	1/1	1.00	0.18	3.28	61,61,61,61	0
3	TRS	A	301	8/8	0.90	0.21	2.40	70,71,73,73	0
2	CD	A	201	1/1	1.00	0.20	1.94	61,61,61,61	0
2	CD	H	201	1/1	0.99	0.19	1.88	57,57,57,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
3	TRS	D	310	8/8	0.95	0.20	1.80	50,52,53,55	0
2	CD	G	201	1/1	1.00	0.17	1.46	67,67,67,67	0
2	CD	K	201	1/1	0.99	0.18	1.11	67,67,67,67	0
2	CD	C	201	1/1	0.98	0.20	0.83	90,90,90,90	0
3	TRS	C	307	8/8	0.93	0.17	0.74	63,65,66,66	0
2	CD	I	201	1/1	0.99	0.18	0.63	72,72,72,72	0
2	CD	L	201	1/1	1.00	0.20	0.52	74,74,74,74	0
3	TRS	C	303	8/8	0.87	0.19	0.10	79,80,81,82	0
2	CD	J	201	1/1	0.99	0.16	0.00	75,75,75,75	0
2	CD	E	201	1/1	0.99	0.16	-0.19	73,73,73,73	0
3	TRS	A	309	8/8	0.87	0.17	-0.23	52,54,57,58	0
2	CD	F	201	1/1	1.00	0.15	-0.91	65,65,65,65	0
3	TRS	D	306	8/8	0.87	0.17	-2.85	72,75,75,76	0
3	TRS	B	312	8/8	0.97	0.11	-3.45	44,46,48,52	0
3	TRS	D	305	8/8	0.78	0.26	-	81,84,84,84	0
2	CD	G	202	1/1	0.98	0.15	-	87,87,87,87	0
3	TRS	E	311	8/8	0.81	0.29	-	86,87,88,91	0
2	CD	D	201	1/1	0.99	0.21	-	71,71,71,71	0
3	TRS	H	308	8/8	0.80	0.24	-	81,85,86,87	0
3	TRS	K	302	8/8	0.78	0.31	-	81,84,85,85	0

6.5 Other polymers

There are no such residues in this entry.