Full wwPDB X-ray Structure Validation Report ⓘ

Mar 3, 2024 – 01:22 AM EST

PDB ID	:	6BCN
Title	:	I-LtrI E184D bound to cognate substrate (pre-cleavage complex)
Authors	:	Brown, C.; Zhang, K.; McMurrough, T.A.; Gloor, G.B.; Edgell, D.R.; Junop, M.
Deposited on	:	2017-10-20
Resolution	:	2.50 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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

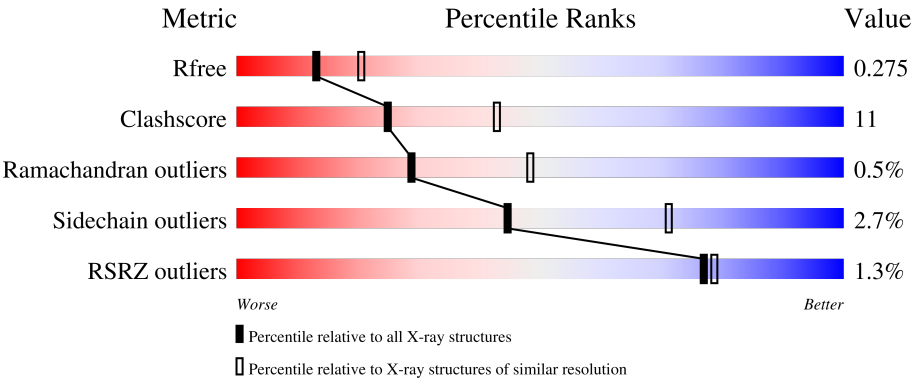
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	315	73% 19% 8%
1	C	315	70% 20% 8%
1	G	315	67% 23% 8%
1	J	315	70% 20% 8%
2	B	26	54% 46%

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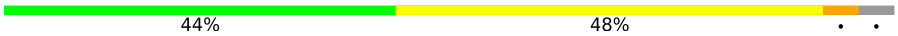
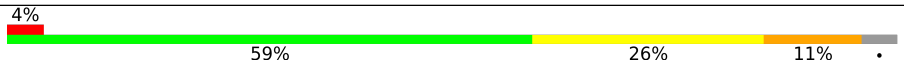
Mol	Chain	Length	Quality of chain
2	E	26	
2	H	26	
2	K	26	
3	D	27	
3	F	27	
3	I	27	
3	L	27	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 13491 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 Ribosomal protein 3/homing endonuclease-like fusion protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	291	Total	C	N	O	S	0	0	0
			2297	1467	403	421	6			
1	C	290	Total	C	N	O	S	0	0	0
			2281	1456	398	421	6			
1	G	290	Total	C	N	O	S	0	0	0
			2233	1429	385	413	6			
1	J	290	Total	C	N	O	S	0	0	0
			2243	1434	388	415	6			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	184	ASP	GLU	engineered mutation	UNP C7SWF3
C	184	ASP	GLU	engineered mutation	UNP C7SWF3
G	184	ASP	GLU	engineered mutation	UNP C7SWF3
J	184	ASP	GLU	engineered mutation	UNP C7SWF3

- Molecule 2 is a DNA chain called DNA (26-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	26	Total	C	N	O	P	0	0	0
			533	256	98	154	25			
2	E	26	Total	C	N	O	P	0	0	0
			533	256	98	154	25			
2	H	26	Total	C	N	O	P	0	0	0
			533	256	98	154	25			
2	K	26	Total	C	N	O	P	0	0	0
			533	256	98	154	25			

- Molecule 3 is a DNA chain called DNA (26-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	26	Total 528	C 252	N 95	O 155	P 26	0	0	0
3	F	26	Total 525	C 253	N 95	O 152	P 25	0	0	0
3	I	26	Total 525	C 253	N 95	O 152	P 25	0	0	0
3	L	26	Total 525	C 253	N 95	O 152	P 25	0	0	0

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total 3	Ca 3	0	0
4	C	3	Total 3	Ca 3	0	0
4	G	2	Total 2	Ca 2	0	0
4	J	3	Total 3	Ca 3	0	0
4	B	1	Total 1	Ca 1	0	0
4	E	1	Total 1	Ca 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	37	Total 37	O 37	0	0
5	C	38	Total 38	O 38	0	0
5	G	21	Total 21	O 21	0	0
5	J	21	Total 21	O 21	0	0
5	B	12	Total 12	O 12	0	0
5	D	7	Total 7	O 7	0	0
5	E	14	Total 14	O 14	0	0
5	F	12	Total 12	O 12	0	0

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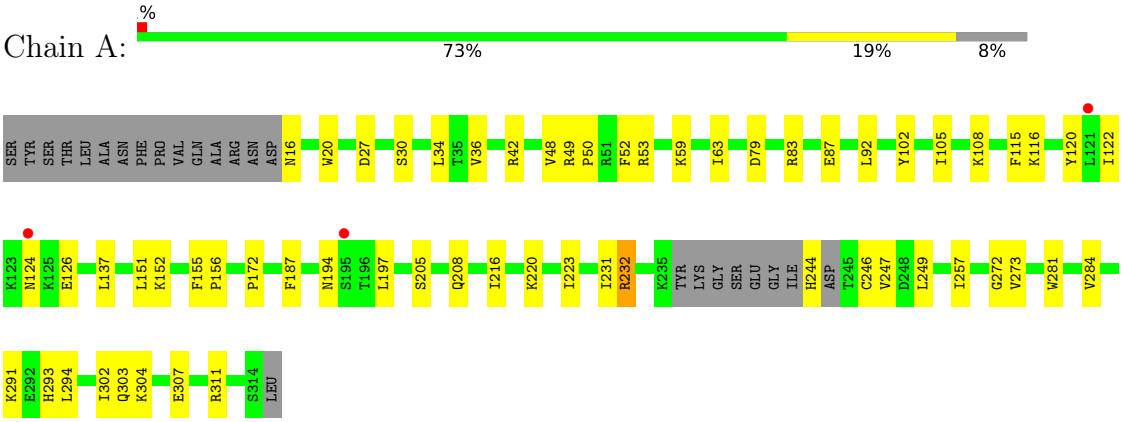
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	H	9	Total O 9 9	0	0
5	I	10	Total O 10 10	0	0
5	K	5	Total O 5 5	0	0
5	L	3	Total O 3 3	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

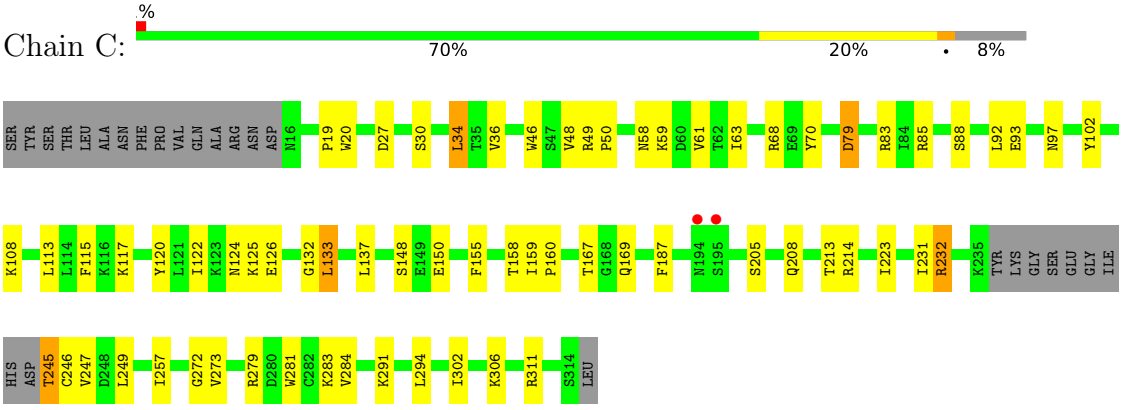
• Molecule 1: Ribosomal protein 3/homing endonuclease-like fusion protein

Chain A:



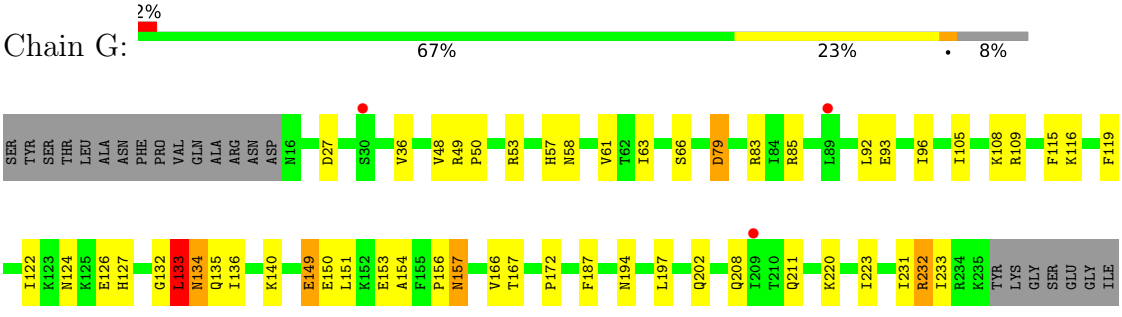
• Molecule 1: Ribosomal protein 3/homing endonuclease-like fusion protein

Chain C:



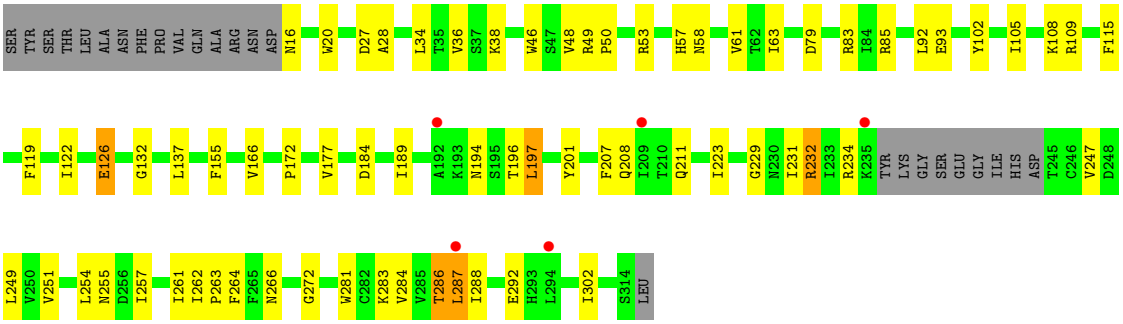
• Molecule 1: Ribosomal protein 3/homing endonuclease-like fusion protein

Chain G:



• Molecule 1: Ribosomal protein 3/homing endonuclease-like fusion protein

Chain J:



• Molecule 2: DNA (26-MER)

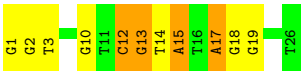
Chain B:

• Molecule 2: DNA (26-MER)

Chain E:

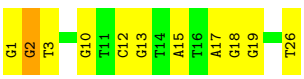
• Molecule 2: DNA (26-MER)

Chain H:



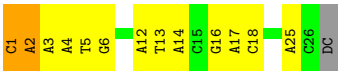
• Molecule 2: DNA (26-MER)

Chain K:

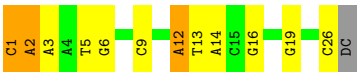


• Molecule 3: DNA (26-MER)

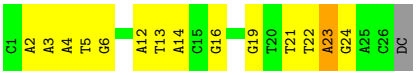
Chain D:



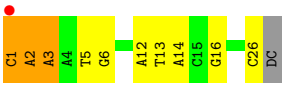
• Molecule 3: DNA (26-MER)



• Molecule 3: DNA (26-MER)



• Molecule 3: DNA (26-MER)



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	42.65Å 64.02Å 168.98Å 89.93° 90.19° 93.64°	Depositor
Resolution (Å)	35.71 – 2.50 84.49 – 2.50	Depositor EDS
% Data completeness (in resolution range)	94.3 (35.71-2.50) 94.1 (84.49-2.50)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.76 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.237 , 0.276 0.239 , 0.275	Depositor DCC
R_{free} test set	3240 reflections (5.36%)	wwPDB-VP
Wilson B-factor (Å^2)	36.1	Xtriage
Anisotropy	1.205	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 27.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.428 for -h,-k,l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	13491	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.74% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA

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	0.27	0/2336	0.56	0/3158
1	C	0.28	0/2320	0.59	0/3140
1	G	0.30	0/2272	0.61	1/3085 (0.0%)
1	J	0.28	0/2282	0.57	0/3097
2	B	0.67	0/598	1.14	2/923 (0.2%)
2	E	0.95	4/598 (0.7%)	1.34	5/923 (0.5%)
2	H	0.96	4/598 (0.7%)	1.10	1/923 (0.1%)
2	K	0.69	0/598	1.25	4/923 (0.4%)
3	D	0.71	0/589	2.07	8/903 (0.9%)
3	F	0.87	1/588 (0.2%)	2.04	7/905 (0.8%)
3	I	0.89	1/588 (0.2%)	2.02	10/905 (1.1%)
3	L	0.71	0/588	2.04	8/905 (0.9%)
All	All	0.53	10/13955 (0.1%)	1.12	46/19790 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	G	0	1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	12	DA	O3'-P	-9.56	1.49	1.61
2	E	15	DA	O3'-P	-9.54	1.49	1.61
2	H	14	DT	O3'-P	-8.36	1.51	1.61
2	H	15	DA	O3'-P	-6.71	1.53	1.61
2	H	12	DC	O3'-P	-6.56	1.53	1.61
3	I	2	DA	C3'-O3'	6.36	1.52	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	17	DA	O3'-P	-5.58	1.54	1.61
2	E	14	DT	O3'-P	-5.28	1.54	1.61
2	E	16	DT	O3'-P	-5.27	1.54	1.61
2	H	13	DG	O3'-P	-5.01	1.55	1.61

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	3	DA	O5'-P-OP2	-35.71	67.85	110.70
3	F	3	DA	O5'-P-OP2	-35.55	68.03	110.70
3	L	3	DA	O5'-P-OP2	-34.91	68.81	110.70
3	I	3	DA	O5'-P-OP2	-31.40	73.02	110.70
3	D	3	DA	OP1-P-OP2	-28.88	76.29	119.60
3	I	3	DA	OP1-P-OP2	-28.73	76.50	119.60
3	F	3	DA	OP1-P-OP2	-28.42	76.97	119.60
3	L	3	DA	OP1-P-OP2	-28.18	77.33	119.60
3	F	3	DA	O5'-P-OP1	16.67	130.71	110.70
3	D	3	DA	O5'-P-OP1	16.56	130.57	110.70
3	L	3	DA	O5'-P-OP1	16.29	130.25	110.70
3	I	3	DA	O5'-P-OP1	14.82	128.49	110.70
3	I	2	DA	OP2-P-O3'	14.65	137.42	105.20
3	L	2	DA	OP2-P-O3'	14.40	136.87	105.20
3	F	2	DA	OP2-P-O3'	13.70	135.35	105.20
3	D	2	DA	OP2-P-O3'	13.37	134.61	105.20
3	I	2	DA	OP1-P-O3'	-12.55	77.60	105.20
2	E	16	DT	OP2-P-O3'	12.05	131.72	105.20
2	E	17	DA	OP1-P-OP2	-11.89	101.77	119.60
2	E	1	DG	OP2-P-O3'	-10.31	82.53	105.20
3	L	2	DA	OP1-P-O3'	-10.21	82.73	105.20
2	K	1	DG	OP2-P-O3'	-10.17	82.83	105.20
2	E	1	DG	OP1-P-O3'	-9.87	83.48	105.20
3	D	2	DA	OP1-P-O3'	-9.70	83.85	105.20
3	F	2	DA	OP1-P-O3'	-9.65	83.98	105.20
2	K	1	DG	OP1-P-O3'	-9.46	84.38	105.20
2	B	17	DA	OP1-P-OP2	-8.20	107.30	119.60
2	B	16	DT	OP2-P-O3'	7.45	121.59	105.20
1	G	133	LEU	N-CA-C	-7.37	91.10	111.00
3	I	2	DA	C4'-C3'-C2'	-7.00	96.80	103.10
3	D	16	DG	OP1-P-OP2	-6.83	109.35	119.60
2	E	2	DG	OP1-P-OP2	6.74	129.71	119.60
2	K	2	DG	OP1-P-OP2	6.63	129.54	119.60
2	H	17	DA	OP1-P-OP2	-6.41	109.98	119.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	I	2	DA	O5'-P-OP1	-6.39	99.94	105.70
2	K	17	DA	OP1-P-OP2	-6.38	110.03	119.60
3	F	16	DG	OP1-P-OP2	-6.28	110.18	119.60
3	I	16	DG	OP1-P-OP2	-6.20	110.30	119.60
3	I	23	DA	P-O3'-C3'	5.74	126.59	119.70
3	I	5	DT	O4'-C1'-N1	5.73	112.01	108.00
3	L	5	DT	O4'-C1'-N1	5.70	111.99	108.00
3	L	16	DG	OP1-P-OP2	-5.58	111.23	119.60
3	D	5	DT	O4'-C1'-N1	5.52	111.86	108.00
3	L	1	DC	OP1-P-O3'	5.49	117.28	105.20
3	D	1	DC	OP1-P-O3'	5.43	117.16	105.20
3	F	1	DC	OP1-P-O3'	5.43	117.15	105.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	G	133	LEU	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	2297	0	2311	44	0
1	C	2281	0	2283	46	0
1	G	2233	0	2191	63	0
1	J	2243	0	2210	48	0
2	B	533	0	293	12	0
2	E	533	0	293	15	0
2	H	533	0	293	12	0
2	K	533	0	293	12	0
3	D	528	0	290	8	0
3	F	525	0	292	17	0
3	I	525	0	292	12	0
3	L	525	0	292	9	0
4	A	3	0	0	0	0
4	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	3	0	0	0	0
4	E	1	0	0	0	0
4	G	2	0	0	0	0
4	J	3	0	0	0	0
5	A	37	0	0	6	0
5	B	12	0	0	0	0
5	C	38	0	0	8	0
5	D	7	0	0	0	0
5	E	14	0	0	0	0
5	F	12	0	0	4	0
5	G	21	0	0	4	0
5	H	9	0	0	1	0
5	I	10	0	0	5	0
5	J	21	0	0	3	0
5	K	5	0	0	0	0
5	L	3	0	0	0	0
All	All	13491	0	11333	256	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 11.

All (256) 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:G:132:GLY:HA2	1:G:135:GLN:CB	1.76	1.14
1:G:132:GLY:HA2	1:G:135:GLN:HB3	1.18	1.11
1:G:132:GLY:CA	1:G:135:GLN:HB3	1.85	1.07
3:I:21:DT:H2"	5:I:202:HOH:O	1.60	1.00
2:E:15:DA:N1	3:F:13:DT:N3	2.12	0.96
5:J:504:HOH:O	3:L:3:DA:P	2.23	0.96
1:G:232:ARG:NH2	2:H:10:DG:N7	2.19	0.89
1:G:36:VAL:HG12	1:G:48:VAL:HG22	1.58	0.85
3:I:22:DT:H6	5:I:202:HOH:O	1.63	0.82
1:C:232:ARG:NH2	2:E:10:DG:N7	2.28	0.81
1:J:232:ARG:NH2	2:K:10:DG:N7	2.30	0.79
1:J:262:ILE:O	1:J:266:ASN:ND2	2.16	0.78
1:C:59:LYS:CE	5:C:502:HOH:O	2.33	0.76
1:A:232:ARG:NH2	2:B:10:DG:N7	2.34	0.76
1:G:202:GLN:HG3	5:H:101:HOH:O	1.85	0.75
1:G:132:GLY:O	1:G:136:ILE:N	2.20	0.75
1:J:286:THR:O	1:J:288:ILE:N	2.20	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:257:ILE:HD12	1:J:281:TRP:HH2	1.52	0.74
1:G:96:ILE:HD12	1:G:116:LYS:HG2	1.68	0.74
1:J:257:ILE:HD13	1:J:261:ILE:HD12	1.69	0.74
1:C:83:ARG:NH2	2:E:18:DG:O6	2.22	0.73
1:C:59:LYS:HD3	5:C:502:HOH:O	1.88	0.73
1:J:283:LYS:O	1:J:286:THR:OG1	2.06	0.72
1:C:284:VAL:HG13	1:C:302:ILE:HD12	1.71	0.71
1:A:284:VAL:HG13	1:A:302:ILE:HD12	1.70	0.71
1:C:306:LYS:NZ	3:F:19:DG:OP2	2.21	0.70
1:A:311:ARG:HE	3:D:17:DA:H4'	1.55	0.69
1:A:16:ASN:CB	5:A:502:HOH:O	2.40	0.69
1:J:92:LEU:HD22	1:J:115:PHE:HZ	1.57	0.69
1:G:220:LYS:HG2	1:G:231:ILE:HG13	1.73	0.69
3:I:22:DT:C6	5:I:202:HOH:O	2.41	0.68
1:G:284:VAL:HG13	1:G:302:ILE:HD12	1.75	0.67
1:C:245:THR:N	5:C:503:HOH:O	2.27	0.67
3:F:9:DC:H2'	5:F:102:HOH:O	1.95	0.67
1:C:245:THR:OG1	1:C:246:CYS:N	2.25	0.66
1:J:257:ILE:HD12	1:J:281:TRP:CH2	2.32	0.65
1:G:257:ILE:HD12	1:G:281:TRP:HH2	1.62	0.65
3:F:1:DC:H4'	3:F:2:DA:OP1	1.97	0.65
1:J:83:ARG:NH2	2:K:18:DG:O6	2.29	0.65
1:A:83:ARG:NH2	2:B:18:DG:O6	2.27	0.64
2:E:15:DA:N1	3:F:13:DT:C4	2.66	0.64
2:E:2:DG:H1	3:F:26:DC:H42	1.46	0.64
1:G:109:ARG:HB3	1:G:166:VAL:HG21	1.79	0.64
1:G:133:LEU:O	1:G:136:ILE:N	2.30	0.64
3:L:1:DC:H4'	3:L:2:DA:OP1	1.97	0.64
3:D:1:DC:H4'	3:D:2:DA:OP1	1.97	0.64
1:G:92:LEU:HD22	1:G:115:PHE:HZ	1.64	0.63
1:J:189:ILE:HG13	1:J:284:VAL:HG11	1.80	0.62
1:C:92:LEU:HD22	1:C:115:PHE:HZ	1.65	0.62
1:G:133:LEU:O	1:G:136:ILE:HB	1.99	0.62
1:C:232:ARG:NH1	5:C:504:HOH:O	2.32	0.62
1:J:284:VAL:HG13	1:J:302:ILE:HD12	1.83	0.60
1:G:79:ASP:N	1:G:79:ASP:OD1	2.36	0.59
1:G:310:ASN:HA	5:G:506:HOH:O	2.01	0.59
1:C:36:VAL:HG11	1:C:137:LEU:HD11	1.84	0.59
1:C:79:ASP:OD1	1:C:79:ASP:N	2.36	0.59
3:F:9:DC:H3'	5:F:102:HOH:O	2.01	0.59
1:G:258:LYS:N	5:G:501:HOH:O	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:306:LYS:NZ	3:I:19:DG:OP2	2.31	0.59
1:C:85:ARG:HH22	3:F:6:DG:H2'	1.68	0.59
1:G:283:LYS:O	1:G:286:THR:OG1	2.21	0.58
1:A:124:ASN:OD1	1:A:126:GLU:HG3	2.02	0.58
1:A:303:GLN:O	1:A:307:GLU:HG2	2.02	0.58
1:A:92:LEU:HD22	1:A:115:PHE:HZ	1.69	0.58
1:C:58:ASN:O	1:C:61:VAL:HG23	2.04	0.57
1:J:251:VAL:HG21	1:J:261:ILE:HD11	1.87	0.57
1:C:59:LYS:HD2	1:C:273:VAL:HG21	1.86	0.57
1:A:244:HIS:N	5:A:503:HOH:O	2.38	0.57
1:G:149:GLU:O	1:G:151:LEU:N	2.32	0.56
1:G:194:ASN:HB3	1:G:197:LEU:HD12	1.87	0.56
2:B:2:DG:H2"	2:B:3:DT:C5'	2.36	0.56
1:G:49:ARG:NH1	3:I:6:DG:O6	2.36	0.56
1:G:140:LYS:NZ	5:G:504:HOH:O	2.38	0.56
1:G:58:ASN:O	1:G:61:VAL:HG23	2.06	0.56
1:A:42:ARG:NH2	3:D:4:DA:N7	2.48	0.55
2:H:2:DG:H2"	2:H:3:DT:C5'	2.36	0.55
1:G:257:ILE:HD12	1:G:281:TRP:CH2	2.41	0.55
1:A:16:ASN:ND2	5:A:502:HOH:O	2.36	0.55
1:A:216:ILE:HD12	1:A:247:VAL:HG21	1.88	0.55
1:A:50:PRO:HD3	1:A:122:ILE:HD13	1.87	0.54
1:A:311:ARG:NH2	3:D:18:DC:H5'	2.22	0.54
1:G:57:HIS:HB2	2:H:15:DA:H3'	1.88	0.54
2:H:1:DG:C8	2:K:26:DT:H2"	2.42	0.54
1:G:83:ARG:NH2	2:H:18:DG:O6	2.35	0.54
2:H:1:DG:H1'	2:H:2:DG:C8	2.42	0.54
1:A:49:ARG:NH1	3:D:6:DG:O6	2.41	0.54
2:K:2:DG:H2"	2:K:3:DT:C5'	2.38	0.54
1:G:63:ILE:HD11	1:G:272:GLY:HA3	1.89	0.54
2:K:2:DG:N2	3:L:26:DC:O2	2.33	0.54
1:A:53:ARG:NH2	2:B:19:DG:N7	2.50	0.54
1:J:58:ASN:O	1:J:61:VAL:HG23	2.08	0.53
1:C:20:TRP:CE2	1:C:102:TYR:HD1	2.25	0.53
1:A:194:ASN:HB3	1:A:197:LEU:HD12	1.91	0.53
1:J:36:VAL:HG22	1:J:48:VAL:HG22	1.90	0.53
1:J:177:VAL:HG21	1:J:264:PHE:HZ	1.73	0.52
1:A:50:PRO:HG2	1:A:92:LEU:HD13	1.92	0.52
1:G:262:ILE:HD11	1:G:285:VAL:HG21	1.91	0.52
1:J:57:HIS:HB2	2:K:15:DA:H3'	1.90	0.52
1:J:63:ILE:HD11	1:J:272:GLY:HA3	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:150:GLU:O	1:G:154:ALA:N	2.41	0.52
1:G:255:ASN:C	5:G:501:HOH:O	2.47	0.52
1:J:177:VAL:HG21	1:J:264:PHE:CZ	2.44	0.52
1:C:208:GLN:HA	1:C:249:LEU:O	2.10	0.52
2:E:2:DG:H2"	2:E:3:DT:C5'	2.39	0.52
1:J:16:ASN:N	5:J:503:HOH:O	2.43	0.52
1:J:223:ILE:HD12	1:J:231:ILE:HG12	1.91	0.52
1:J:108:LYS:NZ	2:K:18:DG:OP2	2.43	0.51
1:A:50:PRO:HG2	1:A:92:LEU:CD1	2.40	0.51
1:G:85:ARG:HH22	3:I:6:DG:H2'	1.75	0.51
2:E:15:DA:C6	3:F:13:DT:O4	2.63	0.51
1:C:108:LYS:HE2	5:C:510:HOH:O	2.09	0.51
1:C:30:SER:O	1:C:108:LYS:NZ	2.33	0.51
1:C:155:PHE:O	1:C:158:THR:OG1	2.18	0.51
1:G:124:ASN:OD1	1:G:126:GLU:HG3	2.10	0.51
1:G:223:ILE:HD12	1:G:231:ILE:HG12	1.93	0.51
1:A:116:LYS:O	1:A:120:TYR:HD1	1.94	0.51
1:C:291:LYS:HB3	1:C:294:LEU:HD12	1.91	0.51
1:C:213:THR:HG22	1:C:247:VAL:HG13	1.93	0.51
1:C:148:SER:OG	1:C:150:GLU:OE2	2.28	0.50
1:G:132:GLY:H	1:G:134:ASN:CB	2.24	0.50
3:F:9:DC:C3'	5:F:102:HOH:O	2.56	0.50
1:G:108:LYS:NZ	2:H:18:DG:OP2	2.44	0.50
1:A:50:PRO:HD2	5:A:507:HOH:O	2.12	0.50
1:A:59:LYS:HD2	1:A:273:VAL:HG21	1.94	0.50
1:G:282:CYS:O	1:G:285:VAL:HG22	2.12	0.50
1:J:93:GLU:HG3	1:J:119:PHE:HZ	1.76	0.49
1:G:132:GLY:O	1:G:136:ILE:HG12	2.12	0.49
2:E:2:DG:H1	3:F:26:DC:N4	2.09	0.49
1:J:53:ARG:NH2	2:K:19:DG:N7	2.55	0.49
1:J:50:PRO:HD3	1:J:122:ILE:HD13	1.95	0.49
1:C:19:PRO:HB2	1:C:102:TYR:CE2	2.48	0.48
1:C:36:VAL:HG22	1:C:48:VAL:HG22	1.94	0.48
1:C:126:GLU:O	1:C:132:GLY:HA3	2.13	0.48
1:C:93:GLU:O	1:C:97:ASN:ND2	2.42	0.48
1:J:36:VAL:HG11	1:J:137:LEU:HD11	1.96	0.48
1:G:50:PRO:HD3	1:G:122:ILE:HD13	1.96	0.48
1:A:49:ARG:HH21	1:A:87:GLU:HB3	1.79	0.48
1:G:132:GLY:HA2	1:G:135:GLN:CA	2.42	0.48
1:A:208:GLN:HA	1:A:249:LEU:O	2.13	0.47
1:J:194:ASN:OD1	1:J:196:THR:OG1	2.22	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:17:DA:C2	3:I:12:DA:C2	3.02	0.47
1:A:152:LYS:O	1:A:156:PRO:HA	2.14	0.47
1:G:53:ARG:NH2	2:H:19:DG:N7	2.58	0.47
1:G:156:PRO:O	1:G:157:ASN:HB2	2.15	0.47
1:J:85:ARG:HH22	3:L:6:DG:H2'	1.78	0.47
1:A:223:ILE:HD12	1:A:231:ILE:HG12	1.97	0.47
2:E:15:DA:N1	3:F:13:DT:O4	2.48	0.47
1:C:59:LYS:CD	5:C:502:HOH:O	2.47	0.47
1:C:63:ILE:HD11	1:C:272:GLY:HA3	1.97	0.47
1:J:49:ARG:NH1	3:L:6:DG:O6	2.39	0.47
1:A:108:LYS:NZ	2:B:18:DG:OP2	2.48	0.47
1:C:49:ARG:NH1	3:F:6:DG:O6	2.43	0.46
3:I:4:DA:N3	5:I:204:HOH:O	2.36	0.46
1:A:20:TRP:CE2	1:A:102:TYR:HD1	2.34	0.46
1:G:150:GLU:HA	1:G:153:GLU:HB3	1.97	0.46
2:B:2:DG:H2"	2:B:3:DT:H5"	1.98	0.46
1:A:34:LEU:HD23	1:A:50:PRO:HA	1.98	0.46
1:G:105:ILE:HD13	1:G:172:PRO:HD3	1.97	0.46
1:G:208:GLN:HA	1:G:249:LEU:O	2.14	0.45
1:G:253:ASN:HB3	1:G:256:ASP:HB2	1.98	0.45
2:E:12:DC:H2"	2:E:13:DG:C8	2.51	0.45
1:A:244:HIS:HB2	1:A:246:CYS:N	2.32	0.45
1:C:34:LEU:HD12	1:C:50:PRO:HA	1.97	0.45
1:G:63:ILE:O	1:G:66:SER:OG	2.25	0.45
1:G:211:GLN:O	1:G:247:VAL:HG22	2.17	0.45
3:F:12:DA:H2"	3:F:13:DT:H72	1.99	0.45
1:G:132:GLY:HA2	1:G:135:GLN:N	2.31	0.45
1:A:16:ASN:HB3	5:A:502:HOH:O	2.11	0.45
1:A:137:LEU:HD22	1:A:155:PHE:CG	2.51	0.45
1:J:232:ARG:NE	1:J:234:ARG:HG2	2.31	0.45
1:J:254:LEU:O	1:J:255:ASN:HB2	2.16	0.45
1:A:30:SER:HB2	1:A:52:PHE:CE2	2.52	0.45
1:A:63:ILE:HD11	1:A:272:GLY:HA3	1.98	0.45
1:J:208:GLN:HA	1:J:249:LEU:O	2.17	0.45
3:I:21:DT:C2'	5:I:202:HOH:O	2.39	0.45
3:L:13:DT:H2"	3:L:14:DA:N7	2.32	0.45
1:J:257:ILE:CD1	1:J:261:ILE:HD12	2.43	0.44
2:B:3:DT:H3	3:D:25:DA:H61	1.65	0.44
1:C:50:PRO:HG2	1:C:92:LEU:CD1	2.47	0.44
2:E:3:DT:H6	2:E:3:DT:H5'	1.82	0.44
1:G:122:ILE:HG23	1:G:127:HIS:CE1	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:K:12:DC:H2"	2:K:13:DG:C8	2.52	0.44
1:J:38:LYS:HG2	1:J:46:TRP:CH2	2.52	0.44
2:H:2:DG:H2"	2:H:3:DT:H5'	2.00	0.44
1:C:137:LEU:HD22	1:C:155:PHE:CG	2.53	0.44
3:F:9:DC:C2'	5:F:102:HOH:O	2.59	0.44
1:C:245:THR:HG23	5:C:506:HOH:O	2.18	0.43
1:G:132:GLY:HA2	1:G:135:GLN:HB2	1.84	0.43
1:J:207:PHE:CD2	1:J:261:ILE:HD13	2.54	0.43
2:E:2:DG:H2"	2:E:3:DT:H5"	2.00	0.43
1:A:291:LYS:HA	1:A:293:HIS:CE1	2.53	0.43
1:J:126:GLU:O	1:J:132:GLY:HA3	2.19	0.43
1:J:229:GLY:CA	1:J:251:VAL:HG22	2.49	0.43
3:F:13:DT:H2"	3:F:14:DA:C8	2.54	0.43
1:A:36:VAL:HG22	1:A:48:VAL:HG22	2.00	0.43
1:C:50:PRO:HD3	1:C:122:ILE:HD13	2.00	0.43
1:C:187:PHE:HB3	1:C:281:TRP:CG	2.53	0.43
1:A:216:ILE:O	1:A:220:LYS:HG3	2.19	0.43
1:J:286:THR:C	1:J:288:ILE:H	2.13	0.43
2:B:2:DG:H2"	2:B:3:DT:H5'	2.00	0.43
2:B:15:DA:N6	3:D:12:DA:C6	2.87	0.43
1:G:251:VAL:HG21	1:G:261:ILE:HD11	2.01	0.43
1:J:286:THR:C	1:J:288:ILE:N	2.73	0.43
1:A:49:ARG:HB2	5:A:507:HOH:O	2.18	0.42
1:G:92:LEU:O	1:G:96:ILE:HG12	2.19	0.42
1:A:151:LEU:HD23	1:A:151:LEU:HA	1.88	0.42
1:C:46:TRP:HB2	1:C:133:LEU:HD11	2.00	0.42
1:C:88:SER:HB3	3:F:5:DT:H3'	2.01	0.42
1:A:244:HIS:HB3	1:A:246:CYS:SG	2.59	0.42
1:G:132:GLY:C	1:G:136:ILE:H	2.17	0.42
2:B:3:DT:H5'	2:B:3:DT:H6	1.84	0.42
2:H:12:DC:H2"	2:H:13:DG:C8	2.54	0.42
2:K:15:DA:N6	3:L:12:DA:C6	2.88	0.42
1:C:205:SER:OG	1:C:257:ILE:HD13	2.20	0.42
3:D:13:DT:H2"	3:D:14:DA:N7	2.34	0.42
2:K:2:DG:H2"	2:K:3:DT:H5"	2.01	0.42
3:I:12:DA:H2"	3:I:13:DT:C7	2.50	0.42
1:J:137:LEU:HD22	1:J:155:PHE:CG	2.54	0.42
1:J:197:LEU:HD22	1:J:201:TYR:O	2.20	0.42
2:E:4:DC:H2"	2:E:5:DT:O5'	2.19	0.42
1:C:279:ARG:O	1:C:283:LYS:HG3	2.20	0.41
2:B:12:DC:H2"	2:B:13:DG:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:ILE:HD13	1:A:172:PRO:HD3	2.02	0.41
1:C:19:PRO:HB3	1:C:70:TYR:OH	2.21	0.41
1:G:262:ILE:CD1	1:G:285:VAL:HG21	2.49	0.41
1:J:38:LYS:HE2	1:J:38:LYS:HB3	1.75	0.41
1:A:187:PHE:HB3	1:A:281:TRP:CG	2.56	0.41
1:G:93:GLU:HG3	1:G:119:PHE:HZ	1.85	0.41
1:J:211:GLN:O	1:J:247:VAL:HG22	2.19	0.41
1:G:232:ARG:HG2	1:G:233:ILE:N	2.35	0.41
1:J:28:ALA:HB1	1:J:184:ASP:OD1	2.20	0.41
2:E:2:DG:H1'	2:E:3:DT:H5"	2.02	0.41
1:G:50:PRO:HG2	1:G:92:LEU:CD1	2.50	0.41
5:J:504:HOH:O	3:L:2:DA:H3'	2.21	0.41
1:C:59:LYS:NZ	5:C:502:HOH:O	2.24	0.41
1:C:223:ILE:HD12	1:C:231:ILE:HG12	2.03	0.41
1:C:311:ARG:HH22	2:E:13:DG:H4'	1.86	0.41
1:G:223:ILE:CD1	1:G:231:ILE:HG12	2.50	0.41
1:J:262:ILE:N	1:J:263:PRO:HD2	2.36	0.41
2:H:2:DG:H2"	2:H:3:DT:H5"	2.02	0.41
1:A:205:SER:OG	1:A:257:ILE:HD13	2.21	0.40
1:G:187:PHE:HB3	1:G:281:TRP:CG	2.56	0.40
1:G:276:GLN:HE22	1:G:279:ARG:NH1	2.20	0.40
1:C:159:ILE:HA	1:C:160:PRO:HD3	1.82	0.40
1:G:289:ASP:O	1:G:291:LYS:NZ	2.52	0.40
1:J:20:TRP:CE2	1:J:102:TYR:HD1	2.40	0.40
1:J:287:LEU:HD22	1:J:292:GLU:OE1	2.21	0.40
2:B:4:DC:H2"	2:B:5:DT:O5'	2.21	0.40
3:I:13:DT:H2"	3:I:14:DA:N7	2.36	0.40
2:K:2:DG:H2"	2:K:3:DT:H5'	2.04	0.40
1:A:291:LYS:HB3	1:A:294:LEU:HD12	2.03	0.40
1:J:109:ARG:HB3	1:J:166:VAL:HG21	2.04	0.40
1:C:124:ASN:O	1:C:125:LYS:HB2	2.21	0.40
1:J:105:ILE:HD13	1:J:172:PRO:HD3	2.03	0.40
3:I:23:DA:H4'	3:I:24:DG:OP1	2.22	0.40
3:L:2:DA:H2'	3:L:2:DA:O5'	2.21	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	286/315 (91%)	280 (98%)	6 (2%)	0	100	100
1	C	286/315 (91%)	278 (97%)	7 (2%)	1 (0%)	41	61
1	G	286/315 (91%)	274 (96%)	9 (3%)	3 (1%)	15	28
1	J	286/315 (91%)	277 (97%)	7 (2%)	2 (1%)	22	39
All	All	1144/1260 (91%)	1109 (97%)	29 (2%)	6 (0%)	29	48

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	157	ASN
1	C	169	GLN
1	G	134	ASN
1	G	149	GLU
1	J	286	THR
1	J	287	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	249/282 (88%)	245 (98%)	4 (2%)	62	84
1	C	246/282 (87%)	234 (95%)	12 (5%)	25	47
1	G	234/282 (83%)	230 (98%)	4 (2%)	60	82
1	J	237/282 (84%)	231 (98%)	6 (2%)	47	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	966/1128 (86%)	940 (97%)	26 (3%)	44 71

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	ASP
1	A	79	ASP
1	A	232	ARG
1	A	304	LYS
1	C	27	ASP
1	C	34	LEU
1	C	68	ARG
1	C	79	ASP
1	C	113	LEU
1	C	117	LYS
1	C	120	TYR
1	C	133	LEU
1	C	167	THR
1	C	214	ARG
1	C	232	ARG
1	C	245	THR
1	G	27	ASP
1	G	79	ASP
1	G	167	THR
1	G	232	ARG
1	J	27	ASP
1	J	34	LEU
1	J	79	ASP
1	J	126	GLU
1	J	197	LEU
1	J	232	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	G	266	ASN
1	G	276	GLN
1	J	266	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry

Of 13 ligands modelled in this entry, 13 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	291/315 (92%)	0.07	3 (1%) 82 84	22, 39, 55, 67	0
1	C	290/315 (92%)	0.12	2 (0%) 87 89	22, 39, 57, 69	0
1	G	290/315 (92%)	0.15	7 (2%) 59 62	30, 50, 62, 76	0
1	J	290/315 (92%)	0.14	5 (1%) 70 72	32, 51, 64, 72	0
2	B	26/26 (100%)	-0.38	0 100 100	24, 34, 46, 50	0
2	E	26/26 (100%)	-0.28	0 100 100	28, 37, 50, 55	0
2	H	26/26 (100%)	-0.20	0 100 100	30, 49, 62, 65	0
2	K	26/26 (100%)	-0.13	0 100 100	31, 52, 60, 64	0
3	D	26/27 (96%)	-0.31	0 100 100	25, 37, 55, 71	0
3	F	26/27 (96%)	-0.28	0 100 100	27, 42, 59, 67	0
3	I	26/27 (96%)	-0.09	0 100 100	37, 48, 67, 72	0
3	L	26/27 (96%)	-0.07	1 (3%) 40 43	40, 48, 66, 68	0
All	All	1369/1472 (93%)	0.07	18 (1%) 77 79	22, 45, 62, 76	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	294	LEU	3.2
1	J	287	LEU	2.8
1	A	121	LEU	2.7
1	G	264	PHE	2.6
1	J	235	LYS	2.6
1	C	194	ASN	2.6
1	G	250	VAL	2.6
1	A	124	ASN	2.5
3	L	1	DC	2.3
1	G	302	ILE	2.3
1	G	209	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	195	SER	2.2
1	C	195	SER	2.2
1	G	30	SER	2.2
1	G	251	VAL	2.1
1	J	192	ALA	2.1
1	G	89	LEU	2.1
1	J	209	ILE	2.1

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 monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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	B-factors(Å^2)	Q<0.9
4	CA	G	402	1/1	0.91	0.05	58,58,58,58	0
4	CA	J	402	1/1	0.92	0.10	57,57,57,57	0
4	CA	J	403	1/1	0.92	0.16	47,47,47,47	0
4	CA	A	403	1/1	0.93	0.22	56,56,56,56	0
4	CA	A	401	1/1	0.95	0.20	46,46,46,46	0
4	CA	C	403	1/1	0.95	0.12	37,37,37,37	0
4	CA	G	401	1/1	0.95	0.18	51,51,51,51	0
4	CA	C	402	1/1	0.96	0.06	49,49,49,49	0
4	CA	C	401	1/1	0.96	0.18	43,43,43,43	0
4	CA	A	402	1/1	0.97	0.15	36,36,36,36	0
4	CA	J	401	1/1	0.97	0.12	42,42,42,42	0
4	CA	B	101	1/1	0.98	0.07	56,56,56,56	0
4	CA	E	101	1/1	0.99	0.05	59,59,59,59	0

6.5 Other polymers (i)

There are no such residues in this entry.