



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 05:49 PM UTC

PDB ID : 4EFJ / pdb_00004efj
Title : Crystal structure of I-GzeII LAGLIDADG homing endonuclease in complex with DNA target site
Authors : Kulshina, N.
Deposited on : 2012-03-29
Resolution : 2.80 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 : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

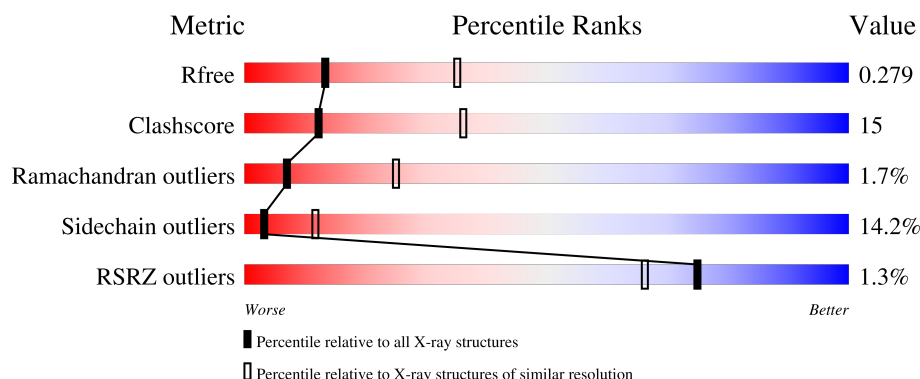
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	180053	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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 $\leq 5\%$. 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	C	27	41% 59%
1	E	27	56% 37% 7%
2	D	27	44% 41% 11% .
2	F	27	63% 26% 7% .
3	A	300	3% 59% 31% 8% .

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Mol	Chain	Length	Quality of chain
3	B	300	62% 27% 8%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6846 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 DNA chain called DNA target site top strand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	27	Total	C	N	O	P	0	0	0
			565	267	111	160	27			
1	E	27	Total	C	N	O	P	0	0	0
			562	267	111	158	26			

- Molecule 2 is a DNA chain called DNA target site bottom strand.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	26	Total	C	N	O	P	0	0	0
			523	251	88	158	26			
2	F	26	Total	C	N	O	P	0	0	0
			520	251	88	156	25			

- Molecule 3 is a protein called LAGLIDADG endonuclease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	291	Total	C	N	O	S	0	0	0
			2329	1496	390	434	9			
3	B	291	Total	C	N	O	S	0	0	0
			2314	1489	387	429	9			

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	1	Total	Ca	0	0
			1	1		
4	A	2	Total	Ca	0	0
			2	2		
4	B	1	Total	Ca	0	0
			1	1		

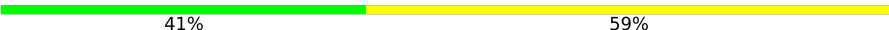
- Molecule 5 is water.

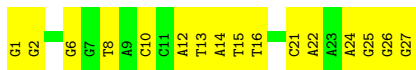
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	4	Total 4	O 4	0	0
5	D	3	Total 3	O 3	0	0
5	E	4	Total 4	O 4	0	0
5	F	6	Total 6	O 6	0	0
5	A	9	Total 9	O 9	0	0
5	B	3	Total 3	O 3	0	0

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: DNA target site top strand

Chain C: 

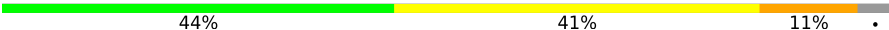


- Molecule 1: DNA target site top strand

Chain E: 



- Molecule 2: DNA target site bottom strand

Chain D: 



- Molecule 2: DNA target site bottom strand

Chain F: 



- Molecule 3: LAGLIDADG endonuclease

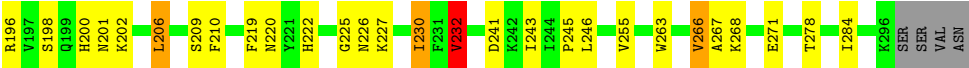
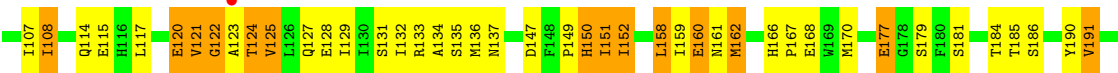
Chain A: 





VAL
ASN

● Molecule 3: LAGLIDADG endonuclease



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	125.83Å 61.18Å 128.88Å 90.00° 116.30° 90.00°	Depositor
Resolution (Å)	38.51 – 2.80 38.51 – 2.80	Depositor EDS
% Data completeness (in resolution range)	95.0 (38.51-2.80) 95.1 (38.51-2.80)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.51 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.183 , 0.278 0.182 , 0.279	Depositor DCC
R_{free} test set	1127 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å ²)	49.1	Xtriage
Anisotropy	0.385	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 35.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6846	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 34.52 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 6.7384e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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](#)

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	C	0.41	0/636	1.19	8/982 (0.8%)
1	E	0.49	0/633	1.21	5/978 (0.5%)
2	D	0.47	0/583	1.25	11/895 (1.2%)
2	F	0.45	0/580	1.26	7/891 (0.8%)
3	A	1.15	0/2383	1.21	8/3215 (0.2%)
3	B	1.12	2/2368 (0.1%)	1.13	8/3196 (0.3%)
All	All	0.96	2/7183 (0.0%)	1.19	47/10157 (0.5%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	263	TRP	NE1-CE2	-5.38	1.31	1.37
3	B	222	HIS	CG-CD2	5.14	1.41	1.35

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	3	DT	P-O3'-C3'	10.54	136.01	120.20
1	E	4	DT	O3'-P-O5'	-8.93	90.60	104.00
3	A	19	GLU	N-CA-C	-8.87	97.33	110.46
1	E	15	DT	O3'-P-O5'	7.58	115.38	104.00
2	D	23	DA	C2'-C3'-O3'	-7.10	100.85	111.50
1	C	13	DT	P-O3'-C3'	7.07	130.81	120.20
2	F	16	DG	O3'-P-O5'	-7.04	93.43	104.00
1	E	15	DT	OP1-P-O3'	-6.91	87.28	108.00
3	A	161	ASN	N-CA-C	-6.40	100.83	110.24
3	B	19	GLU	N-CA-C	-6.38	99.92	109.94
1	C	12	DA	O3'-P-O5'	-6.36	94.46	104.00
2	D	14	DA	O3'-P-O5'	-6.24	94.64	104.00
3	B	232	VAL	CB-CA-C	-6.13	100.11	110.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	266	VAL	N-CA-C	-6.12	104.78	110.53
1	C	10	DC	P-O3'-C3'	5.98	129.16	120.20
2	F	1	DC	C5'-C4'-O4'	5.95	118.33	109.40
3	B	243	ILE	CB-CA-C	-5.93	104.37	111.97
2	D	16	DG	O3'-P-O5'	-5.93	95.10	104.00
1	C	13	DT	C4'-C3'-O3'	-5.81	101.28	110.00
2	D	10	DC	O3'-P-O5'	-5.80	95.30	104.00
1	C	21	DC	P-O3'-C3'	5.74	128.81	120.20
2	D	13	DT	O3'-P-O5'	-5.73	95.40	104.00
3	B	268	LYS	N-CA-C	5.73	117.53	111.28
3	B	160	GLU	N-CA-C	-5.68	105.45	112.90
2	F	17	DG	OP1-P-O3'	-5.63	91.10	108.00
1	C	8	DT	P-O3'-C3'	5.62	128.62	120.20
3	A	166	HIS	CA-C-N	-5.60	113.12	119.28
3	A	166	HIS	C-N-CA	-5.60	113.12	119.28
2	D	6	DG	O3'-P-O5'	-5.53	95.71	104.00
2	D	17	DG	C2'-C3'-O3'	-5.48	103.28	111.50
3	B	57	TYR	N-CA-C	-5.47	104.71	111.33
2	F	20	DC	P-O3'-C3'	5.42	128.32	120.20
2	D	16	DG	P-O3'-C3'	5.41	128.31	120.20
1	E	23	DA	P-O3'-C3'	5.38	128.27	120.20
3	A	265	LYS	N-CA-C	-5.37	105.11	110.97
3	A	155	ASN	N-CA-C	-5.31	102.53	110.23
2	F	1	DC	C5'-C4'-C3'	5.31	122.86	114.90
2	F	5	DT	O3'-P-O5'	-5.28	96.08	104.00
3	A	21	SER	N-CA-C	5.21	116.99	108.76
2	D	16	DG	C4'-C3'-O3'	-5.16	102.25	110.00
1	C	22	DA	P-O3'-C3'	5.12	127.88	120.20
3	B	147	ASP	N-CA-C	5.11	119.36	113.18
1	E	12	DA	P-O3'-C3'	5.10	127.85	120.20
2	D	17	DG	C4'-C3'-O3'	5.08	117.61	110.00
2	D	15	DT	P-O3'-C3'	-5.06	112.61	120.20
1	C	14	DA	C4'-C3'-O3'	-5.02	102.47	110.00
3	A	92	ASN	N-CA-C	5.02	117.31	110.24

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	565	0	304	6	0
1	E	562	0	305	12	0
2	D	523	0	295	18	0
2	F	520	0	296	7	0
3	A	2329	0	2264	97	0
3	B	2314	0	2244	76	0
4	A	2	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
5	A	9	0	0	9	0
5	B	3	0	0	0	0
5	C	4	0	0	0	0
5	D	3	0	0	1	0
5	E	4	0	0	4	0
5	F	6	0	0	0	0
All	All	6846	0	5708	194	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 (194) 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)
3:A:196:ARG:HG2	3:A:232:VAL:HG13	1.40	1.02
3:B:196:ARG:HG2	3:B:232:VAL:HG13	1.50	0.94
2:D:17:DG:H3'	3:B:23:MET:CE	2.01	0.90
2:D:17:DG:H3'	3:B:23:MET:HE3	1.56	0.87
3:B:134:ALA:HB3	3:B:152:ILE:HG23	1.61	0.81
3:A:140:LEU:HD22	3:A:144:VAL:HG11	1.61	0.81
1:E:16:DT:OP2	5:E:104:HOH:O	1.98	0.81
3:A:150:HIS:HA	5:A:502:HOH:O	1.83	0.78
3:A:150:HIS:CB	5:A:502:HOH:O	2.32	0.77
3:A:96:GLN:HA	3:A:158:LEU:HD12	1.65	0.77
3:A:196:ARG:HG2	3:A:232:VAL:CG1	2.14	0.76
3:A:75:VAL:HG21	3:A:84:ILE:HD11	1.68	0.75
2:D:18:DT:H71	3:B:23:MET:HE1	1.69	0.74
3:A:151:ILE:HG22	3:A:152:ILE:H	1.53	0.74
3:A:162:MET:O	3:A:163:ASN:HB2	1.90	0.71
3:A:46:ARG:HD3	5:A:501:HOH:O	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:24:ILE:HD13	3:B:136:MET:HE1	1.73	0.70
2:D:17:DG:C3'	3:B:23:MET:CE	2.70	0.70
3:A:122:GLY:C	3:A:124:THR:H	2.00	0.69
3:A:134:ALA:HB3	3:A:152:ILE:HG23	1.75	0.69
3:B:225:GLY:O	3:B:227:LYS:N	2.25	0.69
3:A:150:HIS:CA	5:A:502:HOH:O	2.37	0.69
3:A:140:LEU:HD22	3:A:144:VAL:CG1	2.23	0.69
3:B:18:ALA:HB1	3:B:177:GLU:HG2	1.74	0.69
3:B:47:ASP:OD2	3:B:255:VAL:HG12	1.94	0.68
3:A:159:ILE:O	3:A:160:GLU:C	2.35	0.68
2:D:17:DG:H3'	3:B:23:MET:HE2	1.76	0.68
2:D:17:DG:C3'	3:B:23:MET:HE3	2.24	0.68
3:B:24:ILE:CD1	3:B:136:MET:HE1	2.25	0.68
1:E:27:DG:N3	5:E:101:HOH:O	2.27	0.67
3:A:216:CYS:SG	3:A:233:THR:HG21	2.36	0.66
3:B:59:ASN:HD22	3:B:83:ILE:HD13	1.60	0.66
3:A:56:ASN:ND2	5:A:505:HOH:O	2.29	0.65
3:A:121:VAL:HA	3:A:126:LEU:HD22	1.80	0.64
3:B:12:VAL:O	3:B:16:THR:HG23	1.98	0.64
3:A:130:ILE:HG23	3:A:140:LEU:HD21	1.78	0.64
3:B:134:ALA:CB	3:B:152:ILE:HG23	2.28	0.64
3:A:151:ILE:HG22	3:A:152:ILE:N	2.12	0.63
3:B:230:ILE:CG2	3:B:232:VAL:HG22	2.28	0.63
1:C:24:DA:H2'	1:C:25:DG:C8	2.33	0.62
3:B:160:GLU:O	3:B:162:MET:N	2.29	0.62
2:F:17:DG:OP2	3:A:21:SER:CB	2.46	0.62
3:A:131:SER:O	3:A:153:PRO:HD2	2.00	0.62
3:A:7:ILE:CG2	3:A:7:ILE:O	2.48	0.62
2:D:1:DC:P	2:D:1:DC:C6	2.93	0.62
3:B:159:ILE:O	3:B:162:MET:SD	2.58	0.62
3:A:7:ILE:O	3:A:7:ILE:HG23	1.98	0.61
3:A:151:ILE:CG2	3:A:152:ILE:H	2.12	0.61
3:B:230:ILE:HG22	3:B:232:VAL:HG22	1.80	0.61
3:B:151:ILE:HG22	3:B:152:ILE:H	1.63	0.61
2:D:8:DA:OP2	3:B:220:ASN:ND2	2.26	0.61
3:B:158:LEU:HD12	3:B:158:LEU:O	2.00	0.61
3:A:207:LEU:HD12	3:A:229:VAL:HG23	1.82	0.61
3:A:122:GLY:O	3:A:124:THR:N	2.33	0.61
3:A:150:HIS:ND1	3:A:150:HIS:C	2.58	0.60
2:F:17:DG:OP2	3:A:21:SER:HB3	2.01	0.60
3:B:96:GLN:HA	3:B:158:LEU:HD11	1.81	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:15:DT:H2''	1:C:16:DT:H5'	1.83	0.59
3:A:192:SER:C	3:A:193:LEU:HD23	2.27	0.59
3:A:56:ASN:CB	5:A:505:HOH:O	2.51	0.59
3:B:55:LYS:NZ	3:B:60:ASN:HD22	2.01	0.58
3:B:7:ILE:CG2	3:B:53:GLU:OE2	2.52	0.58
3:A:46:ARG:CD	5:A:501:HOH:O	2.50	0.58
2:F:15:DT:C2'	2:F:16:DG:H5''	2.35	0.57
3:A:131:SER:O	3:A:153:PRO:CD	2.53	0.57
1:E:4:DT:OP2	3:A:118:SER:OG	2.23	0.57
2:D:26:DC:H3'	5:D:101:HOH:O	2.05	0.56
1:E:16:DT:P	5:E:104:HOH:O	2.60	0.56
3:B:266:VAL:O	3:B:267:ALA:C	2.49	0.56
3:B:107:ILE:HD13	3:B:129:ILE:HG23	1.88	0.54
3:B:7:ILE:HG22	3:B:53:GLU:OE2	2.07	0.54
2:F:15:DT:H2''	2:F:16:DG:H5''	1.89	0.54
1:C:24:DA:OP1	1:C:24:DA:H4'	2.07	0.54
3:A:184:THR:HG22	3:A:191:VAL:HG22	1.89	0.54
2:F:17:DG:OP2	3:A:21:SER:HB2	2.07	0.53
3:B:170:MET:HE1	3:B:210:PHE:CE2	2.43	0.53
3:A:121:VAL:HA	3:A:126:LEU:CD2	2.38	0.53
3:A:201:ASN:C	3:A:202:LYS:O	2.45	0.53
3:B:184:THR:HG22	3:B:191:VAL:HG23	1.91	0.53
3:A:122:GLY:C	3:A:124:THR:N	2.67	0.52
2:D:12:DA:H2''	2:D:13:DT:H72	1.90	0.52
1:E:4:DT:OP1	3:A:117:LEU:HG	2.10	0.52
3:B:120:GLU:O	3:B:122:GLY:N	2.42	0.52
3:B:241:ASP:O	3:B:245:PRO:HG3	2.10	0.52
3:B:162:MET:HE2	3:B:206:LEU:HB2	1.91	0.52
3:A:222:HIS:HD2	3:A:230:ILE:HD11	1.75	0.51
3:A:92:ASN:HD22	3:A:98:LYS:NZ	2.07	0.51
3:A:191:VAL:HG11	3:A:270:ILE:HD11	1.94	0.50
3:A:56:ASN:CG	5:A:505:HOH:O	2.53	0.50
3:A:151:ILE:CG2	3:A:152:ILE:N	2.72	0.50
3:A:196:ARG:CG	3:A:232:VAL:CG1	2.89	0.49
3:B:166:HIS:HD2	3:B:168:GLU:H	1.58	0.49
3:A:94:ILE:HD13	3:A:165:PRO:HD3	1.95	0.49
3:B:201:ASN:O	3:B:202:LYS:C	2.56	0.49
3:A:200:HIS:O	3:A:202:LYS:O	2.30	0.49
1:C:26:DG:H4'	1:C:27:DG:OP1	2.13	0.48
3:B:150:HIS:ND1	3:B:150:HIS:C	2.69	0.48
3:B:7:ILE:HG21	3:B:53:GLU:CG	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:121:VAL:O	3:B:121:VAL:HG12	2.14	0.48
3:A:23:MET:HE3	3:A:38:THR:HG23	1.95	0.48
3:B:101:PHE:O	3:B:104:PHE:HB3	2.13	0.48
2:D:16:DG:OP2	3:B:19:GLU:HA	2.13	0.48
3:A:55:LYS:HG3	3:A:73:TYR:CE1	2.47	0.48
3:B:58:PHE:O	3:B:59:ASN:C	2.57	0.48
3:A:116:HIS:CE1	3:A:119:TYR:CD1	3.01	0.48
2:F:17:DG:H2''	2:F:18:DT:H5'	1.94	0.48
3:A:46:ARG:HD3	3:A:255:VAL:HG11	1.96	0.48
3:B:170:MET:HE1	3:B:210:PHE:CZ	2.49	0.48
3:A:135:SER:OG	3:A:152:ILE:HG22	2.13	0.48
3:A:202:LYS:O	3:A:203:ASP:C	2.56	0.48
1:E:24:DA:H2''	1:E:25:DG:C8	2.49	0.47
3:A:7:ILE:HD11	3:A:11:PHE:CD2	2.49	0.47
3:A:131:SER:HB3	3:A:153:PRO:HD3	1.94	0.47
3:B:185:THR:CG2	3:B:190:TYR:HB2	2.44	0.47
3:B:8:ASN:CG	3:B:168:GLU:HG2	2.39	0.47
1:E:4:DT:OP2	3:A:117:LEU:HD12	2.13	0.47
3:A:217:GLY:N	3:A:233:THR:HG22	2.30	0.46
3:B:124:THR:O	3:B:125:VAL:C	2.58	0.46
3:B:196:ARG:CG	3:B:232:VAL:HG13	2.33	0.46
1:E:19:DT:H2''	1:E:20:DA:H5'	1.97	0.46
3:A:269:MET:HE1	3:A:283:GLU:HG2	1.96	0.46
3:B:55:LYS:HZ2	3:B:60:ASN:HD22	1.62	0.46
3:A:33:TRP:CH2	3:A:144:VAL:HG22	2.51	0.46
3:A:31:ASP:C	3:A:31:ASP:OD1	2.59	0.46
3:B:123:ALA:O	3:B:127:GLN:CB	2.63	0.46
3:B:56:ASN:O	3:B:57:TYR:C	2.52	0.46
3:B:241:ASP:O	3:B:245:PRO:CG	2.64	0.45
3:B:12:VAL:O	3:B:16:THR:CG2	2.64	0.45
3:A:24:ILE:HD13	3:A:37:PRO:HA	1.98	0.45
3:B:134:ALA:HB1	3:B:152:ILE:HD13	1.98	0.45
3:B:24:ILE:HG12	3:B:107:ILE:HG21	1.98	0.45
3:A:18:ALA:HB1	3:A:177:GLU:HG2	1.99	0.45
3:A:98:LYS:HB3	3:A:158:LEU:HD13	1.99	0.45
3:A:101:PHE:O	3:A:104:PHE:HB3	2.17	0.45
1:C:6:DG:O6	3:B:36:ARG:NH1	2.44	0.45
3:B:107:ILE:O	3:B:108:ILE:C	2.58	0.44
1:E:15:DT:H2''	1:E:16:DT:O5'	2.17	0.44
3:A:96:GLN:HG3	3:A:202:LYS:HB3	1.98	0.44
3:A:51:LEU:HD23	3:A:51:LEU:HA	1.68	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:191:VAL:HG21	3:B:284:ILE:HG21	1.99	0.44
3:B:58:PHE:C	3:B:59:ASN:O	2.57	0.44
3:A:56:ASN:HB2	5:A:505:HOH:O	2.16	0.43
3:A:193:LEU:HD23	3:A:193:LEU:N	2.32	0.43
3:A:210:PHE:O	3:A:211:VAL:C	2.60	0.43
3:B:7:ILE:HG21	3:B:53:GLU:OE2	2.17	0.43
3:A:103:LEU:HD22	3:A:132:ILE:HG23	2.01	0.43
3:B:151:ILE:HG22	3:B:152:ILE:N	2.32	0.43
3:A:157:PRO:C	3:A:158:LEU:HD23	2.44	0.43
3:A:98:LYS:HB3	3:A:158:LEU:CD1	2.48	0.43
3:B:114:GLN:O	3:B:115:GLU:C	2.61	0.43
2:D:17:DG:C2'	3:B:23:MET:CE	2.97	0.43
3:A:10:TRP:O	3:A:169:TRP:HA	2.18	0.43
3:B:120:GLU:C	3:B:122:GLY:N	2.75	0.43
3:B:131:SER:O	3:B:134:ALA:HB3	2.18	0.43
3:A:75:VAL:HG21	3:A:84:ILE:CD1	2.44	0.42
3:B:136:MET:O	3:B:137:ASN:C	2.61	0.42
2:D:17:DG:N7	3:B:40:GLN:NE2	2.66	0.42
3:A:148:PHE:N	3:A:149:PRO:HD3	2.35	0.42
5:E:104:HOH:O	3:A:19:GLU:CD	2.62	0.42
3:A:134:ALA:CB	3:A:152:ILE:HG23	2.45	0.42
2:D:17:DG:C3'	3:B:23:MET:HE2	2.43	0.42
3:A:94:ILE:HB	3:A:162:MET:HB3	2.02	0.42
3:A:98:LYS:O	3:A:101:PHE:HB3	2.20	0.42
3:B:98:LYS:HB3	3:B:158:LEU:HD22	2.01	0.42
2:D:12:DA:H2''	2:D:13:DT:C7	2.50	0.42
3:B:162:MET:HB2	3:B:206:LEU:HD23	2.02	0.42
3:B:200:HIS:HD2	3:B:202:LYS:H	1.68	0.42
1:E:20:DA:OP2	3:A:183:TYR:OH	2.28	0.42
1:C:1:DG:H2'	1:C:2:DG:C8	2.55	0.41
2:D:1:DC:H1'	2:D:2:DC:H5'	2.01	0.41
3:A:99:ALA:H	3:A:158:LEU:HD11	1.85	0.41
3:A:142:SER:OG	3:A:143:SER:N	2.53	0.41
1:E:5:DG:C8	3:A:36:ARG:NH2	2.88	0.41
3:B:107:ILE:HG13	3:B:132:ILE:HG21	2.01	0.41
2:D:17:DG:H2'	3:B:23:MET:CE	2.51	0.41
3:A:75:VAL:HG11	3:A:84:ILE:HD12	2.02	0.41
3:A:247:PHE:CD1	3:A:252:ILE:HD11	2.55	0.41
3:B:121:VAL:O	3:B:121:VAL:CG1	2.68	0.41
3:A:61:THR:HG22	3:A:80:ASP:CG	2.45	0.41
3:A:120:GLU:O	3:A:121:VAL:HG13	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:200:HIS:ND1	3:A:201:ASN:N	2.68	0.41
3:B:94:ILE:HD11	3:B:206:LEU:HD11	2.02	0.41
3:A:63:SER:O	3:A:73:TYR:HA	2.21	0.41
1:E:9:DA:C2	2:F:19:DA:C2	3.09	0.41
3:A:170:MET:HE2	3:A:170:MET:HB2	1.95	0.41
3:A:217:GLY:CA	3:A:233:THR:HG22	2.51	0.41
3:B:55:LYS:O	3:B:59:ASN:O	2.39	0.41
3:B:266:VAL:HG13	3:B:284:ILE:HG12	2.03	0.41
3:A:95:THR:OG1	3:A:97:LYS:HB2	2.21	0.41
3:A:124:THR:HG22	3:A:124:THR:O	2.20	0.41
3:A:291:MET:HE3	3:A:291:MET:HB2	1.99	0.40
2:D:1:DC:H2''	2:D:2:DC:H5'	2.04	0.40
3:A:53:GLU:O	3:A:56:ASN:HB3	2.20	0.40
3:A:270:ILE:HD13	3:A:270:ILE:HG21	1.89	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	
3	A	289/300 (96%)	255 (88%)	29 (10%)	5 (2%)	7	25
3	B	289/300 (96%)	255 (88%)	29 (10%)	5 (2%)	7	25
All	All	578/600 (96%)	510 (88%)	58 (10%)	10 (2%)	7	25

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	120	GLU
3	A	123	ALA
3	B	122	GLY
3	B	161	ASN

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Mol	Chain	Res	Type
3	B	226	ASN
3	A	46	ARG
3	B	121	VAL
3	A	30	LYS
3	A	202	LYS
3	B	149	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	
3	A	256/279 (92%)	225 (88%)	31 (12%)	5	16
3	B	252/279 (90%)	211 (84%)	41 (16%)	2	8
All	All	508/558 (91%)	436 (86%)	72 (14%)	3	12

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

Mol	Chain	Res	Type
3	A	7	ILE
3	A	31	ASP
3	A	38	THR
3	A	51	LEU
3	A	63	SER
3	A	66	THR
3	A	72	VAL
3	A	76	ARG
3	A	86	SER
3	A	117	LEU
3	A	127	GLN
3	A	143	SER
3	A	144	VAL
3	A	152	ILE
3	A	155	ASN
3	A	160	GLU
3	A	177	GLU

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Mol	Chain	Res	Type
3	A	186	SER
3	A	193	LEU
3	A	206	LEU
3	A	209	SER
3	A	232	VAL
3	A	233	THR
3	A	234	ARG
3	A	241	ASP
3	A	246	LEU
3	A	252	ILE
3	A	265	LYS
3	A	271	GLU
3	A	279	ASN
3	A	296	LYS
3	B	7	ILE
3	B	16	THR
3	B	24	ILE
3	B	38	THR
3	B	43	LEU
3	B	45	ILE
3	B	60	ASN
3	B	61	THR
3	B	63	SER
3	B	72	VAL
3	B	76	ARG
3	B	84	ILE
3	B	93	LEU
3	B	108	ILE
3	B	117	LEU
3	B	120	GLU
3	B	124	THR
3	B	125	VAL
3	B	128	GLU
3	B	133	ARG
3	B	135	SER
3	B	150	HIS
3	B	151	ILE
3	B	152	ILE
3	B	158	LEU
3	B	162	MET
3	B	167	PRO
3	B	177	GLU

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Mol	Chain	Res	Type
3	B	179	SER
3	B	181	SER
3	B	186	SER
3	B	191	VAL
3	B	198	SER
3	B	206	LEU
3	B	209	SER
3	B	219	PHE
3	B	230	ILE
3	B	232	VAL
3	B	246	LEU
3	B	271	GLU
3	B	278	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	40	GLN
3	A	56	ASN
3	A	60	ASN
3	A	92	ASN
3	A	116	HIS
3	A	166	HIS
3	A	240	ASN
3	B	56	ASN
3	B	59	ASN
3	B	60	ASN
3	B	92	ASN
3	B	116	HIS
3	B	161	ASN
3	B	166	HIS
3	B	200	HIS
3	B	290	ASN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 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 [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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2		OWAB(Å²)	Q<0.9
1	C	27/27 (100%)	-0.44	0	100100	29, 52, 84, 130	0
1	E	27/27 (100%)	-0.38	0	100100	29, 53, 70, 95	0
2	D	26/27 (96%)	-0.66	0	100100	32, 49, 79, 107	0
2	F	26/27 (96%)	-0.59	0	100100	28, 47, 76, 94	0
3	A	291/300 (97%)	-0.22	8 (2%)	5646	19, 38, 77, 130	0
3	B	291/300 (97%)	-0.23	1 (0%)	9086	21, 41, 72, 95	0
All	All	688/708 (97%)	-0.27	9 (1%)	7566	19, 41, 76, 130	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	A	120	GLU	4.0
3	B	123	ALA	3.9
3	A	121	VAL	3.3
3	A	117	LEU	2.7
3	A	118	SER	2.6
3	A	119	TYR	2.4
3	A	116	HIS	2.4
3	A	123	ALA	2.3
3	A	29	ASN	2.2

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 oligosaccharides 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(Å ²)	Q<0.9
4	CA	A	401	1/1	0.97	0.04	27,27,27,27	0
4	CA	C	101	1/1	0.99	0.03	41,41,41,41	0
4	CA	A	402	1/1	0.99	0.05	31,31,31,31	0
4	CA	B	401	1/1	0.99	0.05	37,37,37,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.