



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 07:50 PM UTC

PDB ID : 6ERF / pdb_00006erf
Title : Complex of APLF factor and Ku heterodimer bound to DNA
Authors : Nemoz, C.; Legrand, P.; Ropars, V.; Charbonnier, J.B.
Deposited on : 2017-10-18
Resolution : 3.01 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

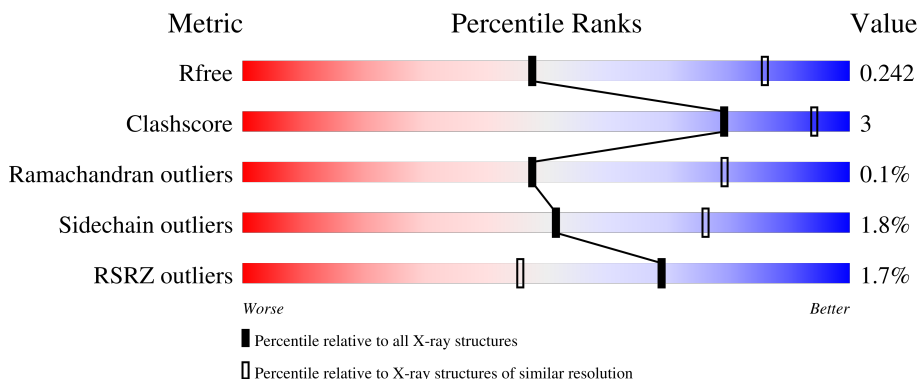
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.01 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	3131 (3.04-3.00)
Clashscore	190562	3444 (3.04-3.00)
Ramachandran outliers	187476	3319 (3.04-3.00)
Sidechain outliers	187428	3322 (3.04-3.00)
RSRZ outliers	180081	3130 (3.04-3.00)

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	A	544	 2% 81% 9% 9%
1	C	544	 % 83% 9% 8%
1	E	544	 % 82% 9% 9%
1	G	544	 2% 82% 9% 9%
2	B	572	 2% 83% 8% 9%

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Mol	Chain	Length	Quality of chain
2	D	572	<p>2% 82% 8% 9%</p>
2	F	572	<p>1% 81% 10% 8%</p>
2	H	572	<p>1% 83% 8% 8%</p>
3	I	21	<p>57% 10% 33%</p>
3	K	21	<p>5% 52% 10% 38%</p>
3	M	21	<p>48% 14% 38%</p>
3	O	21	<p>19% 52% 14% 33%</p>
4	J	34	<p>35% 65%</p>
4	L	34	<p>29% 71%</p>
4	N	34	<p>3% 38% 59%</p>
4	P	34	<p>6% 44% 53%</p>
5	Q	18	<p>56% 11% 33%</p>
5	R	18	<p>72% 28%</p>
5	S	18	<p>67% 33%</p>
5	T	18	<p>67% 33%</p>

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 35411 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 X-ray repair cross-complementing protein 6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	493	Total 3988	C 2547	N 677	O 747	S 17	0	0	0
1	C	500	Total 4035	C 2578	N 684	O 756	S 17	0	0	0
1	E	497	Total 4016	C 2565	N 682	O 752	S 17	0	0	0
1	G	495	Total 4000	C 2557	N 678	O 748	S 17	0	0	0

- Molecule 2 is a protein called X-ray repair cross-complementing protein 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	521	Total 4168	C 2666	N 701	O 778	S 23	0	0	0
2	D	520	Total 4168	C 2667	N 701	O 777	S 23	0	0	0
2	F	526	Total 4211	C 2697	N 707	O 784	S 23	0	0	0
2	H	526	Total 4211	C 2697	N 707	O 784	S 23	0	0	0

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-16	MET	-	initiating methionine	UNP P13010
B	-15	HIS	-	expression tag	UNP P13010
B	-14	HIS	-	expression tag	UNP P13010
B	-13	HIS	-	expression tag	UNP P13010
B	-12	HIS	-	expression tag	UNP P13010
B	-11	HIS	-	expression tag	UNP P13010
B	-10	HIS	-	expression tag	UNP P13010
B	-9	HIS	-	expression tag	UNP P13010

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-8	HIS	-	expression tag	UNP P13010
B	-7	HIS	-	expression tag	UNP P13010
B	-6	HIS	-	expression tag	UNP P13010
B	-5	GLU	-	expression tag	UNP P13010
B	-4	ASN	-	expression tag	UNP P13010
B	-3	LEU	-	expression tag	UNP P13010
B	-2	TYR	-	expression tag	UNP P13010
B	-1	PHE	-	expression tag	UNP P13010
B	0	GLN	-	expression tag	UNP P13010
B	1	GLY	-	expression tag	UNP P13010
D	-16	MET	-	initiating methionine	UNP P13010
D	-15	HIS	-	expression tag	UNP P13010
D	-14	HIS	-	expression tag	UNP P13010
D	-13	HIS	-	expression tag	UNP P13010
D	-12	HIS	-	expression tag	UNP P13010
D	-11	HIS	-	expression tag	UNP P13010
D	-10	HIS	-	expression tag	UNP P13010
D	-9	HIS	-	expression tag	UNP P13010
D	-8	HIS	-	expression tag	UNP P13010
D	-7	HIS	-	expression tag	UNP P13010
D	-6	HIS	-	expression tag	UNP P13010
D	-5	GLU	-	expression tag	UNP P13010
D	-4	ASN	-	expression tag	UNP P13010
D	-3	LEU	-	expression tag	UNP P13010
D	-2	TYR	-	expression tag	UNP P13010
D	-1	PHE	-	expression tag	UNP P13010
D	0	GLN	-	expression tag	UNP P13010
D	1	GLY	-	expression tag	UNP P13010
F	-16	MET	-	initiating methionine	UNP P13010
F	-15	HIS	-	expression tag	UNP P13010
F	-14	HIS	-	expression tag	UNP P13010
F	-13	HIS	-	expression tag	UNP P13010
F	-12	HIS	-	expression tag	UNP P13010
F	-11	HIS	-	expression tag	UNP P13010
F	-10	HIS	-	expression tag	UNP P13010
F	-9	HIS	-	expression tag	UNP P13010
F	-8	HIS	-	expression tag	UNP P13010
F	-7	HIS	-	expression tag	UNP P13010
F	-6	HIS	-	expression tag	UNP P13010
F	-5	GLU	-	expression tag	UNP P13010
F	-4	ASN	-	expression tag	UNP P13010
F	-3	LEU	-	expression tag	UNP P13010

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-2	TYR	-	expression tag	UNP P13010
F	-1	PHE	-	expression tag	UNP P13010
F	0	GLN	-	expression tag	UNP P13010
F	1	GLY	-	expression tag	UNP P13010
H	-16	MET	-	initiating methionine	UNP P13010
H	-15	HIS	-	expression tag	UNP P13010
H	-14	HIS	-	expression tag	UNP P13010
H	-13	HIS	-	expression tag	UNP P13010
H	-12	HIS	-	expression tag	UNP P13010
H	-11	HIS	-	expression tag	UNP P13010
H	-10	HIS	-	expression tag	UNP P13010
H	-9	HIS	-	expression tag	UNP P13010
H	-8	HIS	-	expression tag	UNP P13010
H	-7	HIS	-	expression tag	UNP P13010
H	-6	HIS	-	expression tag	UNP P13010
H	-5	GLU	-	expression tag	UNP P13010
H	-4	ASN	-	expression tag	UNP P13010
H	-3	LEU	-	expression tag	UNP P13010
H	-2	TYR	-	expression tag	UNP P13010
H	-1	PHE	-	expression tag	UNP P13010
H	0	GLN	-	expression tag	UNP P13010
H	1	GLY	-	expression tag	UNP P13010

- Molecule 3 is a DNA chain called DNA (5'-D(*GP*TP*TP*TP*TP*TP*AP*GP*TP*TP*TP*AP*TP*TP*GP*GP*GP*CP*GP*CP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	I	14	Total 286	C 140	N 40	O 92	P 14	0	0	0
3	K	13	Total 268	C 130	N 41	O 84	P 13	0	0	0
3	M	13	Total 268	C 130	N 41	O 84	P 13	0	0	0
3	O	14	Total 286	C 140	N 40	O 92	P 14	0	0	0

- Molecule 4 is a DNA chain called DNA (34-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
4	J	12	Total 248	C 119	N 52	O 65	P 12	0	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	L	10	Total	C	N	O	P	0	0	0
			206	99	42	55	10			
4	N	14	Total	C	N	O	P	0	0	0
			289	139	59	77	14			
4	P	16	Total	C	N	O	P	0	0	0
			327	157	65	89	16			

- Molecule 5 is a protein called Aprataxin and PNK-like factor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	Q	12	Total	C	N	O	S	0	0	0
			105	69	20	15	1			
5	R	13	Total	C	N	O	S	0	0	0
			113	75	21	16	1			
5	S	12	Total	C	N	O	S	0	0	0
			105	69	20	15	1			
5	T	12	Total	C	N	O	S	0	0	0
			105	69	20	15	1			

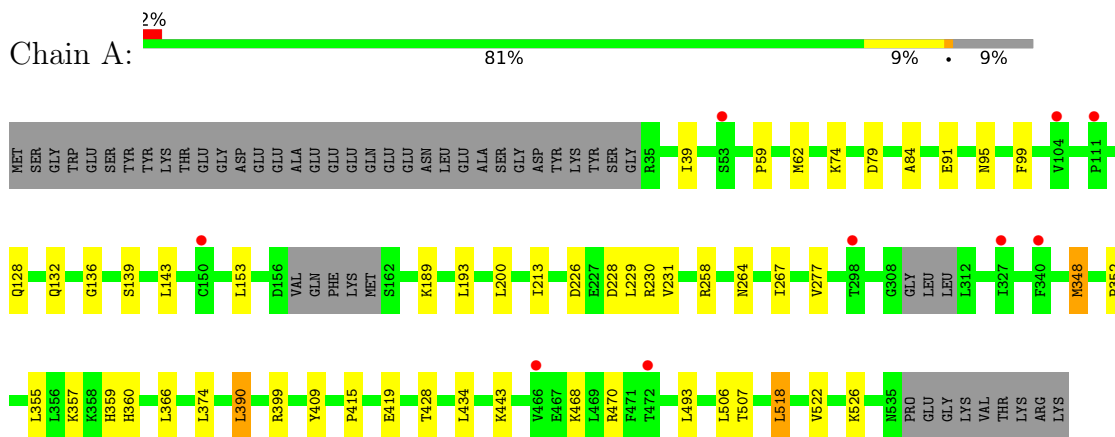
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total	O	0	0
			1	1		
6	E	1	Total	O	1	0
			1	1		
6	F	2	Total	O	0	0
			2	2		
6	G	2	Total	O	0	0
			2	2		
6	H	2	Total	O	0	0
			2	2		

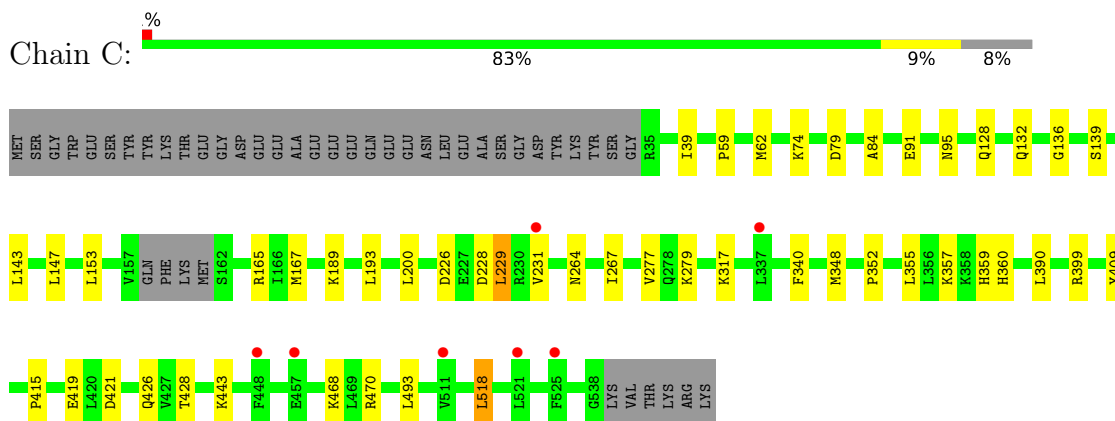
3 Residue-property plots [i](#)

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.

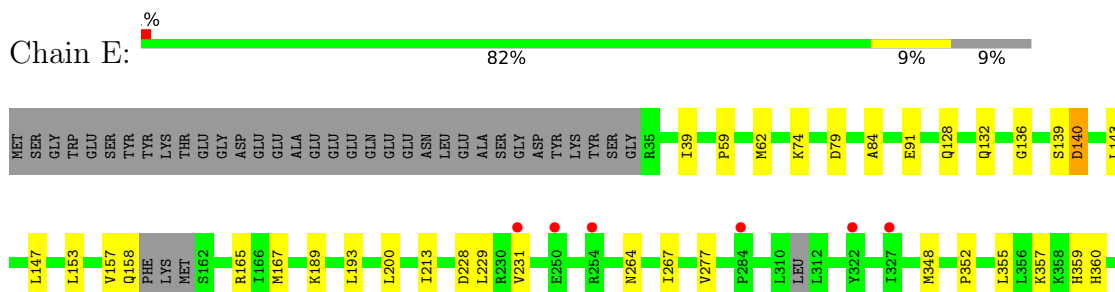
- Molecule 1: X-ray repair cross-complementing protein 6



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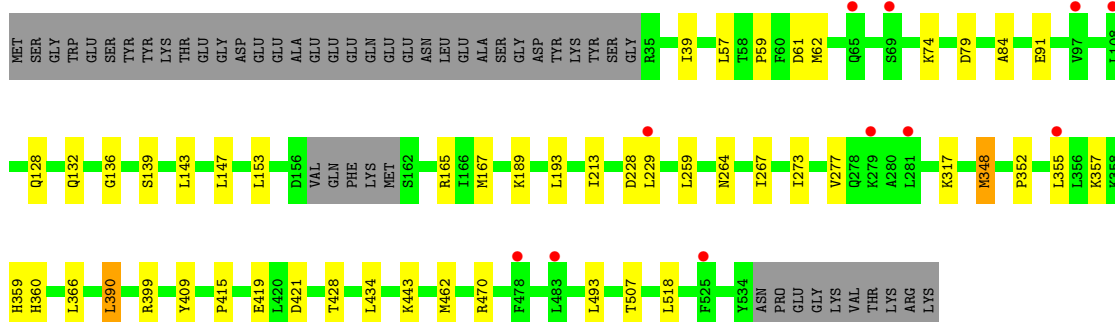
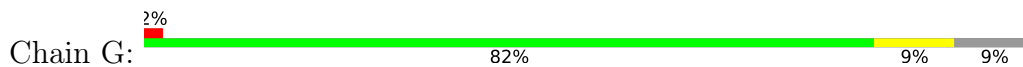


- Molecule 1: X-ray repair cross-complementing protein 6

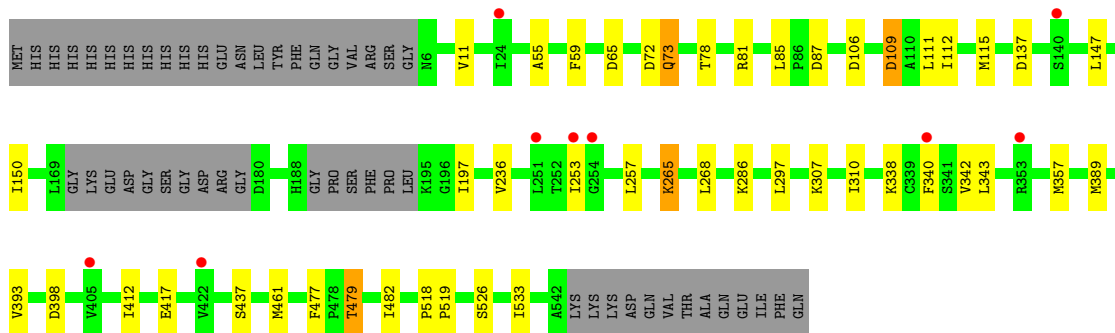
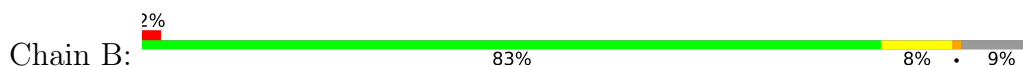




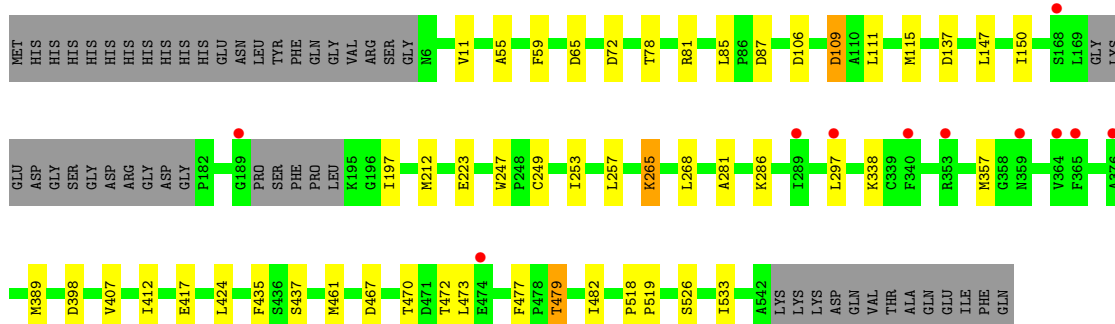
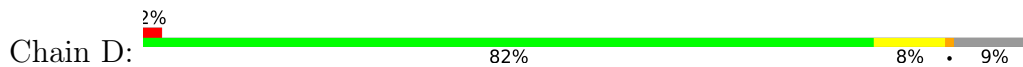
- Molecule 1: X-ray repair cross-complementing protein 6



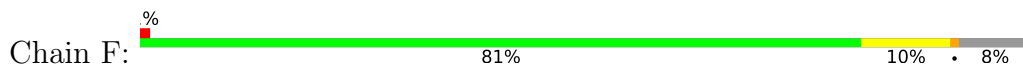
- Molecule 2: X-ray repair cross-complementing protein 5



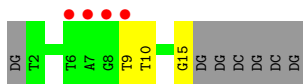
- Molecule 2: X-ray repair cross-complementing protein 5



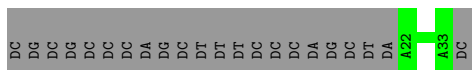
- Molecule 2: X-ray repair cross-complementing protein 5



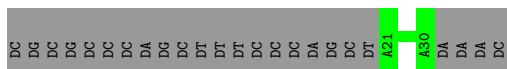
- Molecule 3: DNA (5'-D(*GP*TP*TP*TP*TP*TP*AP*GP*TP*TP*TP*AP*TP*TP*GP*GP*GP*CP*GP*CP*G)-3')



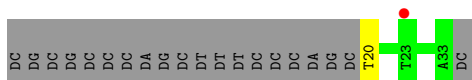
- Molecule 4: DNA (34-MER)



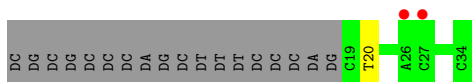
- Molecule 4: DNA (34-MER)



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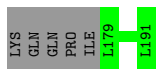


- Molecule 5: Aprataxin and PNK-like factor

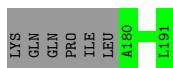


- Molecule 5: Aprataxin and PNK-like factor

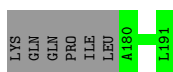




- Molecule 5: Aprataxin and PNK-like factor



- Molecule 5: Aprataxin and PNK-like factor



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	98.92Å 140.86Å 150.31Å 68.64° 80.85° 81.23°	Depositor
Resolution (Å)	49.47 – 3.01 49.47 – 3.08	Depositor EDS
% Data completeness (in resolution range)	61.9 (49.47-3.01) 66.1 (49.47-3.08)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.12 (at 3.07Å)	Xtrriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.209 , 0.227 0.221 , 0.242	Depositor DCC
R_{free} test set	4537 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	97.5	Xtrriage
Anisotropy	0.009	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 72.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	35411	wwPDB-VP
Average B, all atoms (Å ²)	121.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.51% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.71	1/4064 (0.0%)	1.27	5/5474 (0.1%)
1	C	0.71	0/4113	1.28	4/5543 (0.1%)
1	E	0.72	0/4092	1.28	5/5512 (0.1%)
1	G	0.71	1/4077 (0.0%)	1.28	3/5493 (0.1%)
2	B	0.71	0/4251	1.25	7/5734 (0.1%)
2	D	0.70	0/4251	1.25	7/5732 (0.1%)
2	F	0.71	0/4298	1.27	9/5800 (0.2%)
2	H	0.71	0/4298	1.25	10/5800 (0.2%)
3	I	0.43	0/317	0.80	0/488
3	K	0.45	0/298	0.79	0/459
3	M	0.45	0/298	0.78	0/459
3	O	0.44	0/317	0.80	0/488
4	J	0.37	0/280	0.60	0/429
4	L	0.39	0/232	0.63	0/355
4	N	0.39	0/326	0.61	0/500
4	P	0.40	0/368	0.61	0/564
5	Q	0.68	0/107	1.03	0/143
5	R	0.71	0/115	1.10	0/154
5	S	0.63	0/107	0.98	0/143
5	T	0.65	0/107	0.93	0/143
All	All	0.69	2/36316 (0.0%)	1.23	50/49413 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	348	MET	SD-CE	-5.16	1.66	1.79
1	A	348	MET	SD-CE	-5.11	1.66	1.79

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	18	PHE	CA-CB-CG	6.28	120.08	113.80
1	E	510	LYS	CA-C-N	5.92	128.53	120.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	510	LYS	C-N-CA	5.92	128.53	120.77
1	E	140	ASP	CA-CB-CG	5.52	118.12	112.60
1	E	390	LEU	CA-C-N	5.48	127.56	120.44

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3988	0	4053	24	0
1	C	4035	0	4104	26	0
1	E	4016	0	4084	26	0
1	G	4000	0	4073	25	0
2	B	4168	0	4199	25	0
2	D	4168	0	4210	26	0
2	F	4211	0	4252	32	0
2	H	4211	0	4252	25	0
3	I	286	0	165	1	0
3	K	268	0	152	1	0
3	M	268	0	152	2	0
3	O	286	0	165	2	0
4	J	248	0	135	0	0
4	L	206	0	113	0	0
4	N	289	0	158	1	0
4	P	327	0	180	1	0
5	Q	105	0	115	3	0
5	R	113	0	126	0	0
5	S	105	0	115	0	0
5	T	105	0	115	0	0
6	B	1	0	0	0	0
6	E	1	0	0	0	0
6	F	2	0	0	0	0
6	G	2	0	0	0	0
6	H	2	0	0	0	0
All	All	35411	0	34918	190	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 3.

The worst 5 of 190 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:M:15:DG:H1	4:N:20:DT:H3	1.22	0.87
3:O:15:DG:H1	4:P:20:DT:H3	1.22	0.84
1:C:228:ASP:HB3	2:D:437:SER:HB2	1.63	0.81
2:D:467:ASP:HB3	2:D:470:THR:HG22	1.64	0.80
2:H:347:LYS:HG2	2:H:350:GLN:HE21	1.51	0.75

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	487/544 (90%)	474 (97%)	12 (2%)	1 (0%)	43	75
1	C	496/544 (91%)	484 (98%)	11 (2%)	1 (0%)	43	75
1	E	491/544 (90%)	477 (97%)	13 (3%)	1 (0%)	43	75
1	G	491/544 (90%)	479 (98%)	11 (2%)	1 (0%)	43	75
2	B	515/572 (90%)	505 (98%)	10 (2%)	0	100	100
2	D	514/572 (90%)	503 (98%)	11 (2%)	0	100	100
2	F	522/572 (91%)	514 (98%)	8 (2%)	0	100	100
2	H	522/572 (91%)	512 (98%)	10 (2%)	0	100	100
5	Q	10/18 (56%)	10 (100%)	0	0	100	100
5	R	11/18 (61%)	10 (91%)	1 (9%)	0	100	100
5	S	10/18 (56%)	10 (100%)	0	0	100	100
5	T	10/18 (56%)	10 (100%)	0	0	100	100
All	All	4079/4536 (90%)	3988 (98%)	87 (2%)	4 (0%)	48	79

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	359	HIS
1	C	359	HIS
1	E	359	HIS
1	G	359	HIS

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	449/492 (91%)	439 (98%)	10 (2%)	45	73
1	C	454/492 (92%)	445 (98%)	9 (2%)	48	75
1	E	452/492 (92%)	440 (97%)	12 (3%)	39	70
1	G	450/492 (92%)	442 (98%)	8 (2%)	51	76
2	B	468/513 (91%)	459 (98%)	9 (2%)	50	75
2	D	469/513 (91%)	463 (99%)	6 (1%)	61	80
2	F	474/513 (92%)	467 (98%)	7 (2%)	57	79
2	H	474/513 (92%)	468 (99%)	6 (1%)	61	80
5	Q	11/17 (65%)	11 (100%)	0	100	100
5	R	12/17 (71%)	12 (100%)	0	100	100
5	S	11/17 (65%)	11 (100%)	0	100	100
5	T	11/17 (65%)	11 (100%)	0	100	100
All	All	3735/4088 (91%)	3668 (98%)	67 (2%)	51	76

5 of 67 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	229	LEU
1	G	493	LEU
2	H	479	THR
1	C	279	LYS
1	C	231	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 67 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	360	HIS
1	G	489	ASN
2	H	484	ASN
1	C	264	ASN
1	C	174	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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(Å ²)	Q<0.9
1	A	493/544 (90%)	0.23	9 (1%) 67 44	58, 121, 205, 236	0
1	C	500/544 (91%)	0.21	7 (1%) 73 51	66, 121, 189, 202	0
1	E	497/544 (91%)	0.21	6 (1%) 76 55	60, 112, 171, 233	0
1	G	495/544 (90%)	0.18	11 (2%) 62 39	62, 123, 194, 217	0
2	B	521/572 (91%)	0.11	9 (1%) 69 46	53, 103, 201, 237	0
2	D	520/572 (90%)	0.15	11 (2%) 63 40	54, 98, 182, 234	0
2	F	526/572 (91%)	0.01	7 (1%) 75 53	56, 88, 167, 229	0
2	H	526/572 (91%)	0.09	6 (1%) 78 57	47, 106, 181, 225	0
3	I	14/21 (66%)	0.67	0 100 100	180, 215, 256, 260	0
3	K	13/21 (61%)	1.16	1 (7%) 19 10	145, 191, 250, 251	0
3	M	13/21 (61%)	0.87	0 100 100	150, 183, 234, 239	0
3	O	14/21 (66%)	1.54	4 (28%) 1 1	184, 217, 255, 258	0
4	J	12/34 (35%)	0.76	0 100 100	207, 213, 223, 236	0
4	L	10/34 (29%)	0.68	0 100 100	162, 180, 196, 211	0
4	N	14/34 (41%)	0.98	1 (7%) 22 11	146, 181, 212, 219	0
4	P	16/34 (47%)	1.06	2 (12%) 8 5	182, 202, 236, 237	0
5	Q	12/18 (66%)	-0.03	0 100 100	99, 105, 128, 135	0
5	R	13/18 (72%)	0.12	0 100 100	83, 89, 126, 137	0
5	S	12/18 (66%)	0.02	0 100 100	86, 92, 118, 120	0
5	T	12/18 (66%)	0.08	0 100 100	94, 96, 117, 119	0
All	All	4233/4756 (89%)	0.17	74 (1%) 69 46	47, 110, 200, 260	0

The worst 5 of 74 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	525	PHE	4.6
2	B	340	PHE	3.8
1	G	279	LYS	3.6
2	H	359	ASN	3.3
2	H	72	ASP	3.2

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.