



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 07:18 AM GMT

PDB ID : 3A8I
Title : Crystal Structure of ET-EHred-5-CH3-THF complex
Authors : Okamura-Ikeda, K.; Hosaka, H.
Deposited on : 2009-10-06
Resolution : 1.99 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (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

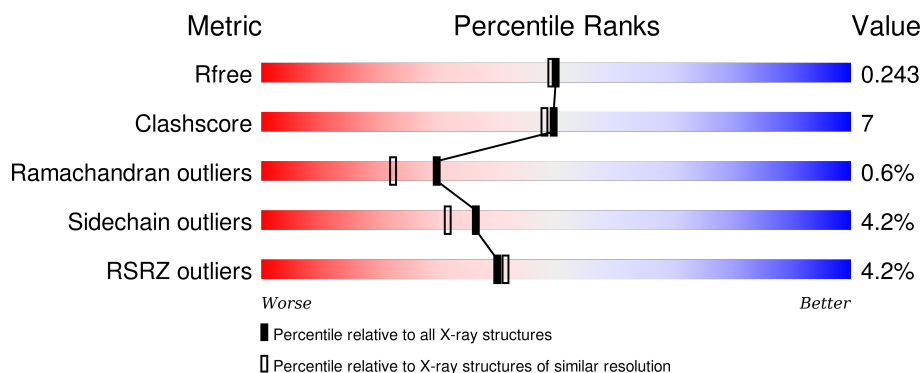
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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 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 $\leq 5\%$. 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	364	<div> <div>4%</div> <div>81% 17% •</div> </div>
1	B	364	<div> <div>3%</div> <div>83% 15% •</div> </div>
1	C	364	<div> <div>3%</div> <div>82% 15% •</div> </div>
1	D	364	<div> <div>4%</div> <div>80% 18% •</div> </div>
2	E	129	<div> <div>10%</div> <div>81% 16% •••</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	129	 A horizontal bar chart showing the quality of chain F. The bar is divided into three segments: a red segment at the beginning labeled '7%', a green segment in the middle labeled '73%', and a yellow segment at the end labeled '25%'. The bar ends with a small grey segment and three dots '...'. The segments are separated by thin white lines.

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14524 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.

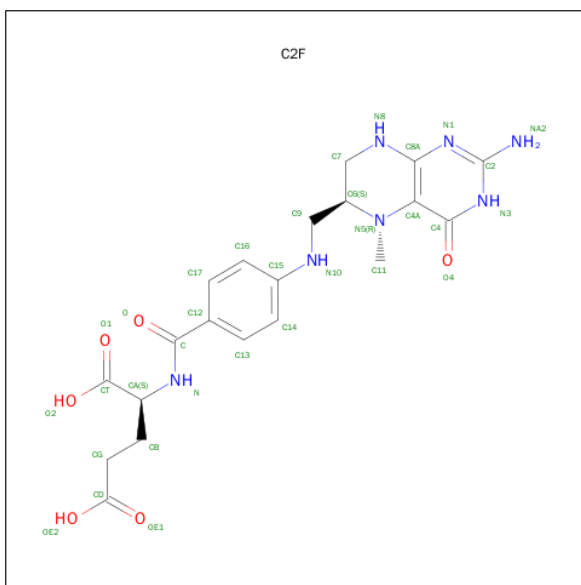
- Molecule 1 is a protein called Aminomethyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	363	Total	C	N	O	S	0	0	0
			2815	1777	492	531	15			
1	B	363	Total	C	N	O	S	0	7	0
			2865	1807	502	541	15			
1	C	363	Total	C	N	O	S	0	0	0
			2815	1777	492	531	15			
1	D	363	Total	C	N	O	S	0	0	0
			2815	1777	492	531	15			

- Molecule 2 is a protein called Glycine cleavage system H protein.

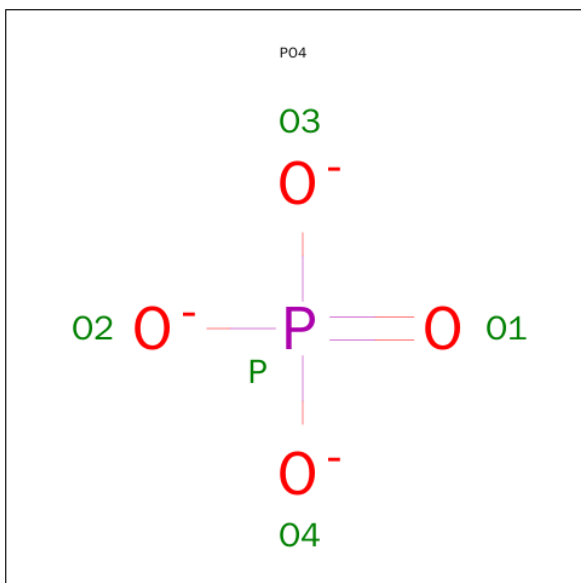
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	128	Total	C	N	O	S	0	0	0
			974	611	147	212	4			
2	F	128	Total	C	N	O	S	0	0	0
			974	611	147	212	4			

- Molecule 3 is 5-METHYL-5,6,7,8-TETRAHYDROFOLIC ACID (three-letter code: C2F) (formula: C₂₀H₂₅N₇O₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			33	20	7	6		
3	B	1	Total	C	N	O	0	0
			33	20	7	6		
3	C	1	Total	C	N	O	0	0
			33	20	7	6		
3	D	1	Total	C	N	O	0	0
			33	20	7	6		

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	O	P	0	0
			5	4	1		
4	D	1	Total	O	P	0	0
			5	4	1		

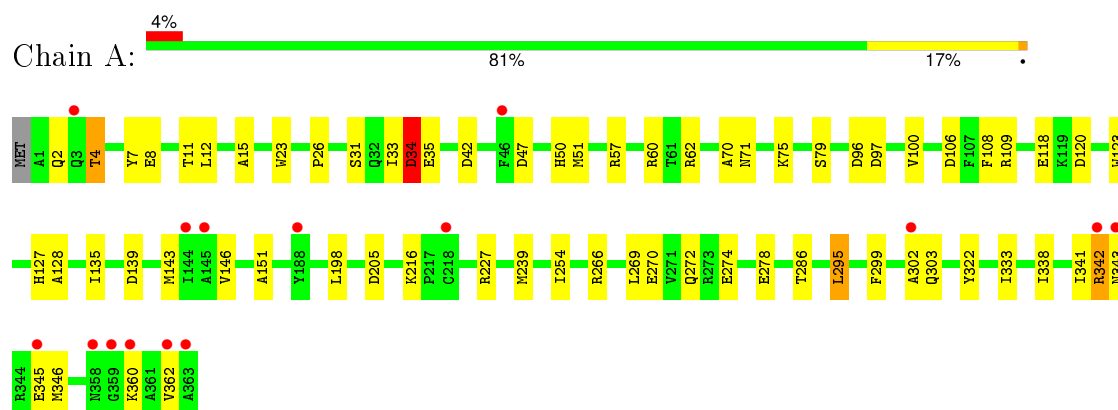
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	282	Total	O	0	0
			282	282		
5	B	251	Total	O	0	0
			251	251		
5	C	249	Total	O	0	0
			249	249		
5	D	246	Total	O	0	0
			246	246		
5	E	61	Total	O	0	0
			61	61		
5	F	35	Total	O	0	0
			35	35		

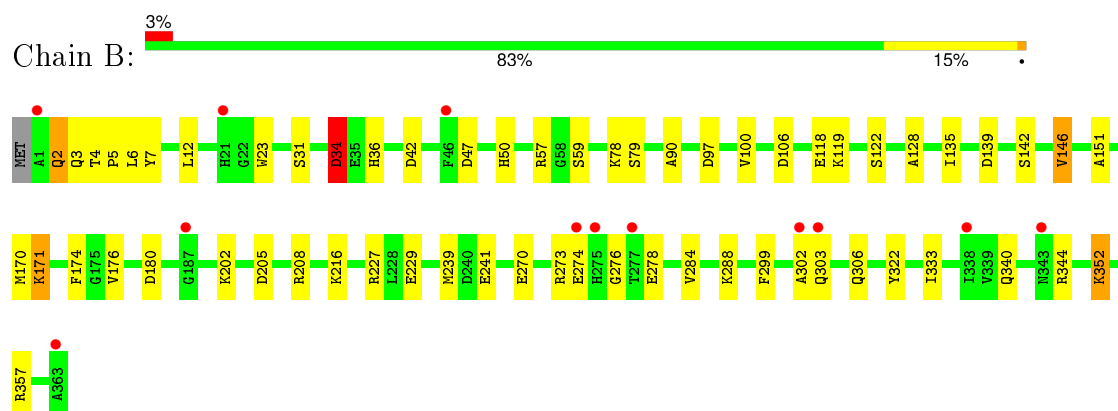
3 Residue-property plots

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.

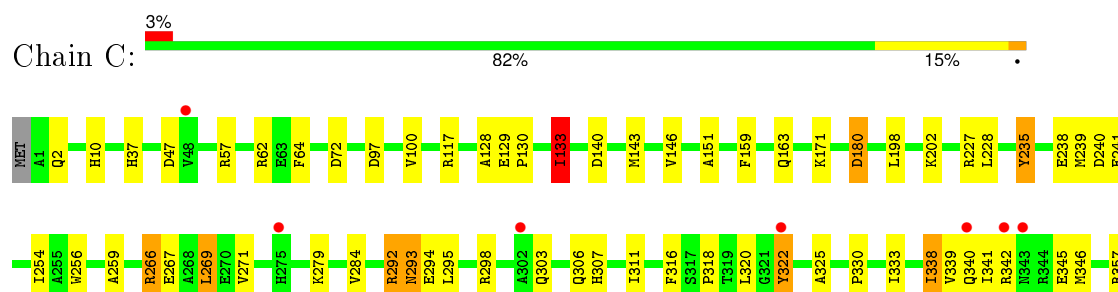
• Molecule 1: Aminomethyltransferase



• Molecule 1: Aminomethyltransferase

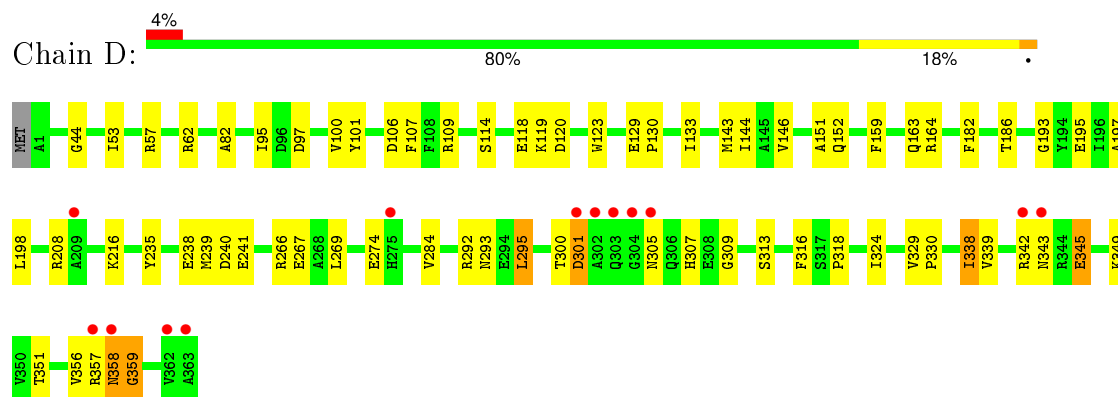


• Molecule 1: Aminomethyltransferase

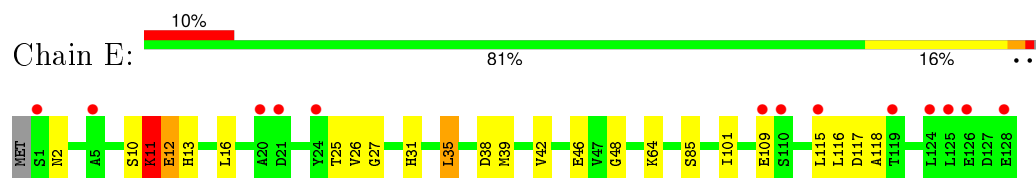




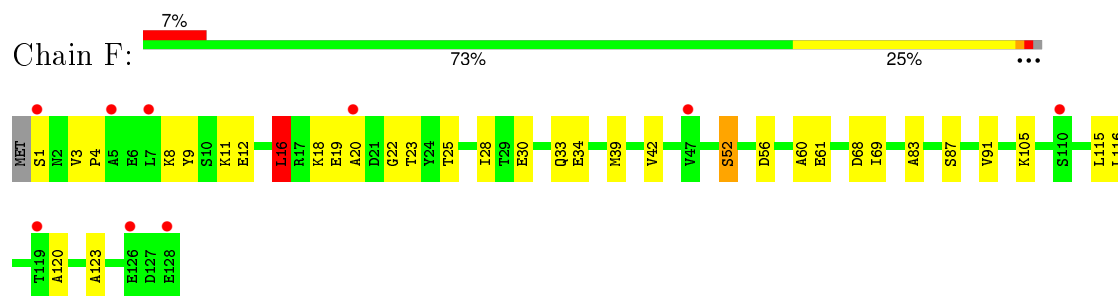
- Molecule 1: Aminomethyltransferase



- Molecule 2: Glycine cleavage system H protein



- Molecule 2: Glycine cleavage system H protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	53.98Å 88.93Å 97.99Å 91.53° 102.47° 89.59°	Depositor
Resolution (Å)	29.77 – 1.99 29.77 – 1.99	Depositor EDS
% Data completeness (in resolution range)	84.4 (29.77-1.99) 84.0 (29.77-1.99)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.74 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.182 , 0.244 0.182 , 0.243	Depositor DCC
R_{free} test set	5115 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	21.4	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 50.6	EDS
Estimated twinning fraction	0.148 for -h,k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 102296 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14524	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.36% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: PO4, C2F, LA2

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	1.16	4/2873 (0.1%)	1.02	12/3891 (0.3%)
1	B	1.12	3/2928 (0.1%)	0.99	8/3967 (0.2%)
1	C	1.15	5/2873 (0.2%)	0.98	6/3891 (0.2%)
1	D	1.15	3/2873 (0.1%)	1.02	11/3891 (0.3%)
2	E	0.96	0/970	0.93	3/1321 (0.2%)
2	F	0.91	0/970	0.88	1/1321 (0.1%)
All	All	1.12	15/13487 (0.1%)	0.99	41/18282 (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	C	0	1

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	238	GLU	CB-CG	7.43	1.66	1.52
1	C	241	GLU	CB-CG	6.09	1.63	1.52
1	A	118	GLU	CB-CG	5.73	1.63	1.52
1	C	2	GLN	CB-CG	-5.71	1.37	1.52
1	D	144	ILE	CB-CG2	5.69	1.70	1.52

The worst 5 of 41 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	62	ARG	NE-CZ-NH1	12.93	126.76	120.30
1	D	266	ARG	NE-CZ-NH2	-12.58	114.01	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	35	LEU	CA-CB-CG	9.30	136.70	115.30
1	D	266	ARG	NE-CZ-NH1	8.81	124.71	120.30
1	B	208	ARG	NE-CZ-NH1	7.37	123.98	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	292	ARG	Peptide

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	2815	0	2771	36	0
1	B	2865	0	2818	37	0
1	C	2815	0	2771	42	0
1	D	2815	0	2771	35	0
2	E	974	0	922	16	0
2	F	974	0	923	22	0
3	A	33	0	23	1	0
3	B	33	0	23	2	0
3	C	33	0	23	1	0
3	D	33	0	23	2	0
4	C	5	0	0	0	0
4	D	5	0	0	1	0
5	A	282	0	0	4	0
5	B	251	0	0	5	0
5	C	249	0	0	7	1
5	D	246	0	0	2	1
5	E	61	0	0	2	0
5	F	35	0	0	2	0
All	All	14524	0	13068	187	1

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 7.

The worst 5 of 187 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:C:266:ARG:HH11	1:C:266:ARG:HG3	1.16	1.10
1:C:298:ARG:HB2	1:C:338:ILE:CD1	2.01	0.91
2:F:11:LYS:HG3	2:F:12:GLU:OE2	1.75	0.85
1:C:292:ARG:H	1:C:295:LEU:HD22	1.43	0.83
2:F:116:LEU:HD23	2:F:120:ALA:HB1	1.60	0.83

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:849:HOH:O	5:D:699:HOH:O 1_656	2.01	0.19

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	361/364 (99%)	347 (96%)	11 (3%)	3 (1%)	24	15
1	B	367/364 (101%)	353 (96%)	9 (2%)	5 (1%)	14	6
1	C	361/364 (99%)	350 (97%)	10 (3%)	1 (0%)	46	41
1	D	361/364 (99%)	346 (96%)	13 (4%)	2 (1%)	30	22
2	E	125/129 (97%)	119 (95%)	6 (5%)	0	100	100
2	F	125/129 (97%)	118 (94%)	6 (5%)	1 (1%)	24	15
All	All	1700/1714 (99%)	1633 (96%)	55 (3%)	12 (1%)	30	19

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	278	GLU
1	D	358	ASN

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Mol	Chain	Res	Type
2	F	20	ALA
1	C	293	ASN
1	A	278	GLU

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	291/292 (100%)	279 (96%)	12 (4%)	37	32
1	B	297/292 (102%)	286 (96%)	11 (4%)	41	38
1	C	291/292 (100%)	278 (96%)	13 (4%)	34	29
1	D	291/292 (100%)	279 (96%)	12 (4%)	37	32
2	E	102/103 (99%)	96 (94%)	6 (6%)	24	18
2	F	102/103 (99%)	99 (97%)	3 (3%)	50	49
All	All	1374/1374 (100%)	1317 (96%)	57 (4%)	36	32

5 of 57 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	180	ASP
1	C	303	GLN
2	E	109	GLU
1	C	198	LEU
1	C	239	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	303	GLN
1	A	358	ASN
1	C	343	ASN
1	A	272	GLN
1	C	303	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	LA2	E	64	2	16,19,20	0.98	0	14,21,23	1.39	2 (14%)
2	LA2	F	64	2	16,19,20	0.95	0	14,21,23	2.03	6 (42%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	LA2	E	64	2	-	0/16/20/22	0/0/0/0
2	LA2	F	64	2	-	0/16/20/22	0/0/0/0

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	64	LA2	O1-C1-NZ	-2.90	117.18	122.94
2	E	64	LA2	O-C-CA	-2.79	118.23	125.49
2	F	64	LA2	O-C-CA	-2.19	119.78	125.49
2	F	64	LA2	C3-C4-C5	2.02	120.84	113.66
2	F	64	LA2	C4-C3-C2	2.38	122.00	113.29

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	64	LA2	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

6 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	C2F	A	401	-	25,35,35	1.62	5 (20%)	27,49,49	2.40	9 (33%)
3	C2F	B	401	-	25,35,35	1.72	4 (16%)	27,49,49	2.42	6 (22%)
3	C2F	C	401	-	25,35,35	1.40	2 (8%)	27,49,49	2.26	6 (22%)
4	PO4	C	501	-	4,4,4	0.53	0	6,6,6	0.29	0
3	C2F	D	401	-	25,35,35	1.24	2 (8%)	27,49,49	2.16	6 (22%)
4	PO4	D	501	-	4,4,4	0.24	0	6,6,6	0.33	0

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	C2F	A	401	-	-	0/16/35/35	0/3/3/3
3	C2F	B	401	-	-	0/16/35/35	0/3/3/3
3	C2F	C	401	-	-	0/16/35/35	0/3/3/3
4	PO4	C	501	-	-	0/0/0/0	0/0/0/0
3	C2F	D	401	-	-	0/16/35/35	0/3/3/3
4	PO4	D	501	-	-	0/0/0/0	0/0/0/0

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	401	C2F	C6-N5	-2.94	1.44	1.47
3	A	401	C2F	C2-N1	-2.43	1.31	1.35
3	D	401	C2F	C6-N5	-2.12	1.45	1.47
3	A	401	C2F	C8A-N1	2.09	1.38	1.34
3	A	401	C2F	C7-N8	2.52	1.49	1.46

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	401	C2F	C7-C6-N5	-10.00	97.70	108.79
3	D	401	C2F	C7-C6-N5	-7.75	100.19	108.79
3	A	401	C2F	C7-C6-N5	-6.82	101.22	108.79
3	A	401	C2F	C9-C6-N5	-5.89	98.58	110.90
3	C	401	C2F	C7-C6-N5	-5.43	102.77	108.79

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	401	C2F	1	0
3	B	401	C2F	2	0
3	C	401	C2F	1	0
3	D	401	C2F	2	0
4	D	501	PO4	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	363/364 (99%)	0.10	15 (4%) 41 42	10, 17, 39, 56	0
1	B	363/364 (99%)	0.05	12 (3%) 50 51	9, 18, 40, 52	0
1	C	363/364 (99%)	0.08	10 (2%) 56 57	11, 20, 43, 63	0
1	D	363/364 (99%)	0.10	13 (3%) 46 48	10, 20, 42, 68	0
2	E	127/129 (98%)	0.47	13 (10%) 9 9	18, 28, 62, 70	0
2	F	127/129 (98%)	0.52	9 (7%) 19 20	22, 36, 52, 65	0
All	All	1706/1714 (99%)	0.14	72 (4%) 40 41	9, 20, 47, 70	0

The worst 5 of 72 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	363	ALA	7.3
1	A	363	ALA	7.1
1	C	302	ALA	6.1
1	D	363	ALA	6.0
1	D	302	ALA	5.8

6.2 Non-standard residues in protein, DNA, RNA chains

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, 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	LLDF	B-factors(Å ²)	Q<0.9
2	LA2	F	64	20/21	0.92	0.13	-	23,41,44,48	0
2	LA2	E	64	20/21	0.92	0.15	-	20,33,47,52	0

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, 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	LLDF	B-factors(\AA^2)	Q<0.9
3	C2F	A	401	33/33	0.88	0.19	1.15	9,21,44,47	0
3	C2F	C	401	33/33	0.89	0.21	1.13	11,26,43,48	0
3	C2F	D	401	33/33	0.93	0.16	0.95	11,25,48,50	0
3	C2F	B	401	33/33	0.93	0.15	0.64	10,19,42,45	0
4	PO4	C	501	5/5	0.97	0.09	-0.88	36,38,41,41	0
4	PO4	D	501	5/5	0.97	0.08	-1.66	37,38,39,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.