



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 22, 2024 – 09:11 AM EDT

PDB ID : 4IC1
Title : Crystal structure of SSO0001
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Deposited on : 2012-12-09
Resolution : 2.35 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

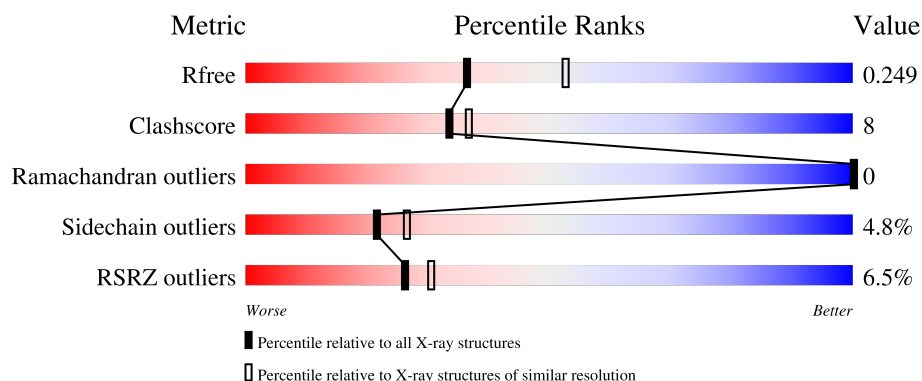
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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}	164625	1460 (2.36-2.36)
Clashscore	180529	1571 (2.36-2.36)
Ramachandran outliers	177936	1559 (2.36-2.36)
Sidechain outliers	177891	1559 (2.36-2.36)
RSRZ outliers	164620	1460 (2.36-2.36)

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	206	 2% 84% 12% ..
1	B	206	 2% 86% 12% .
1	C	206	 6% 78% 20% .
1	D	206	 2% 83% 16%
1	F	206	 6% 83% 15% ..

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Mol	Chain	Length	Quality of chain
1	G	206	<div> <div>5%</div> <div>80%</div> <div>17%</div> <div>• •</div> </div>
1	H	206	<div> <div>3%</div> <div>79%</div> <div>18%</div> <div>• •</div> </div>
1	I	206	<div> <div>14%</div> <div>77%</div> <div>17%</div> <div>• •</div> </div>
1	J	206	<div> <div>15%</div> <div>79%</div> <div>17%</div> <div>• •</div> </div>
1	K	206	<div> <div>7%</div> <div>72%</div> <div>25%</div> <div>•</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 16484 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 Uncharacterized protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	202	Total	C	N	O	S	Se	0	0	0
			1621	1046	269	299	4	3			
1	B	203	Total	C	N	O	S	Se	0	1	0
			1626	1047	270	302	4	3			
1	C	202	Total	C	N	O	S	Se	0	2	0
			1621	1043	272	299	4	3			
1	D	206	Total	C	N	O	S	Se	0	0	0
			1639	1053	273	306	4	3			
1	F	203	Total	C	N	O	S	Se	0	0	0
			1610	1036	270	297	4	3			
1	G	202	Total	C	N	O	S	Se	0	0	0
			1580	1020	265	288	4	3			
1	H	203	Total	C	N	O	S	Se	0	0	0
			1618	1040	270	301	4	3			
1	I	202	Total	C	N	O	S	Se	0	2	0
			1583	1018	262	296	4	3			
1	J	202	Total	C	N	O	S	Se	0	1	0
			1594	1027	267	293	4	3			
1	K	202	Total	C	N	O	S	Se	0	0	0
			1610	1037	270	296	4	3			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	TYR	-	expression tag	UNP Q97TX9
A	-2	PHE	-	expression tag	UNP Q97TX9
A	-1	GLN	-	expression tag	UNP Q97TX9
A	0	GLY	-	expression tag	UNP Q97TX9
B	-3	TYR	-	expression tag	UNP Q97TX9
B	-2	PHE	-	expression tag	UNP Q97TX9
B	-1	GLN	-	expression tag	UNP Q97TX9
B	0	GLY	-	expression tag	UNP Q97TX9
C	-3	TYR	-	expression tag	UNP Q97TX9

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	PHE	-	expression tag	UNP Q97TX9
C	-1	GLN	-	expression tag	UNP Q97TX9
C	0	GLY	-	expression tag	UNP Q97TX9
D	-3	TYR	-	expression tag	UNP Q97TX9
D	-2	PHE	-	expression tag	UNP Q97TX9
D	-1	GLN	-	expression tag	UNP Q97TX9
D	0	GLY	-	expression tag	UNP Q97TX9
F	-3	TYR	-	expression tag	UNP Q97TX9
F	-2	PHE	-	expression tag	UNP Q97TX9
F	-1	GLN	-	expression tag	UNP Q97TX9
F	0	GLY	-	expression tag	UNP Q97TX9
G	-3	TYR	-	expression tag	UNP Q97TX9
G	-2	PHE	-	expression tag	UNP Q97TX9
G	-1	GLN	-	expression tag	UNP Q97TX9
G	0	GLY	-	expression tag	UNP Q97TX9
H	-3	TYR	-	expression tag	UNP Q97TX9
H	-2	PHE	-	expression tag	UNP Q97TX9
H	-1	GLN	-	expression tag	UNP Q97TX9
H	0	GLY	-	expression tag	UNP Q97TX9
I	-3	TYR	-	expression tag	UNP Q97TX9
I	-2	PHE	-	expression tag	UNP Q97TX9
I	-1	GLN	-	expression tag	UNP Q97TX9
I	0	GLY	-	expression tag	UNP Q97TX9
J	-3	TYR	-	expression tag	UNP Q97TX9
J	-2	PHE	-	expression tag	UNP Q97TX9
J	-1	GLN	-	expression tag	UNP Q97TX9
J	0	GLY	-	expression tag	UNP Q97TX9
K	-3	TYR	-	expression tag	UNP Q97TX9
K	-2	PHE	-	expression tag	UNP Q97TX9
K	-1	GLN	-	expression tag	UNP Q97TX9
K	0	GLY	-	expression tag	UNP Q97TX9

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

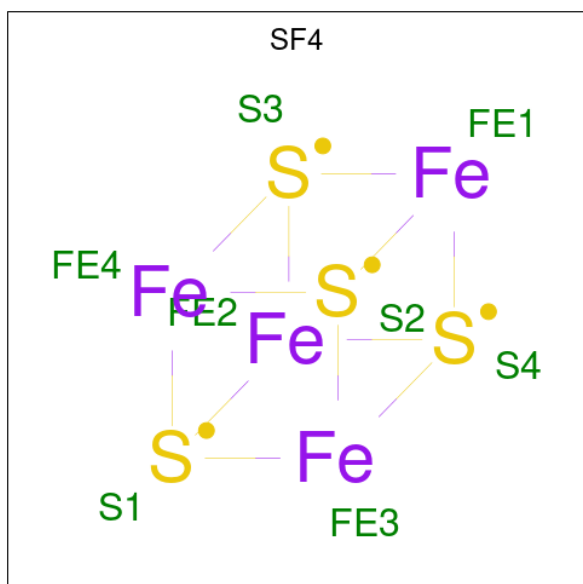
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Mn 1 1	0	0
2	B	1	Total Mn 1 1	0	0
2	C	1	Total Mn 1 1	0	0
2	D	1	Total Mn 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	F	1	Total	Mn	0	0
			1	1		
2	G	1	Total	Mn	0	0
			1	1		
2	H	1	Total	Mn	0	0
			1	1		
2	I	1	Total	Mn	0	0
			1	1		
2	J	1	Total	Mn	0	0
			1	1		
2	K	1	Total	Mn	0	0
			1	1		

- Molecule 3 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe₄S₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	Fe	S	0	0
			8	4	4		
3	B	1	Total	Fe	S	0	0
			8	4	4		
3	C	1	Total	Fe	S	0	0
			8	4	4		
3	D	1	Total	Fe	S	0	0
			8	4	4		
3	F	1	Total	Fe	S	0	0
			8	4	4		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	G	1	Total 8	Fe 4	S 4	0	0
3	H	1	Total 8	Fe 4	S 4	0	0
3	I	1	Total 8	Fe 4	S 4	0	0
3	J	1	Total 8	Fe 4	S 4	0	0
3	K	1	Total 8	Fe 4	S 4	0	0

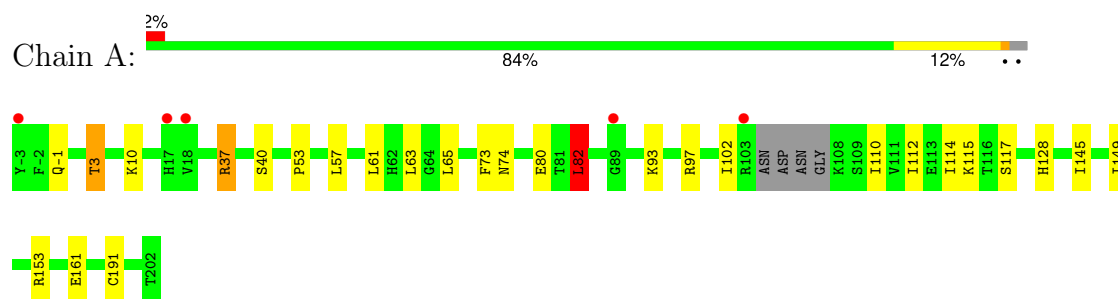
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	49	Total 49	O 49	0	0
4	B	62	Total 62	O 62	0	0
4	C	22	Total 22	O 22	0	0
4	D	49	Total 49	O 49	0	0
4	F	19	Total 19	O 19	0	0
4	G	21	Total 21	O 21	0	0
4	H	27	Total 27	O 27	0	0
4	I	8	Total 8	O 8	0	0
4	J	10	Total 10	O 10	0	0
4	K	25	Total 25	O 25	0	0

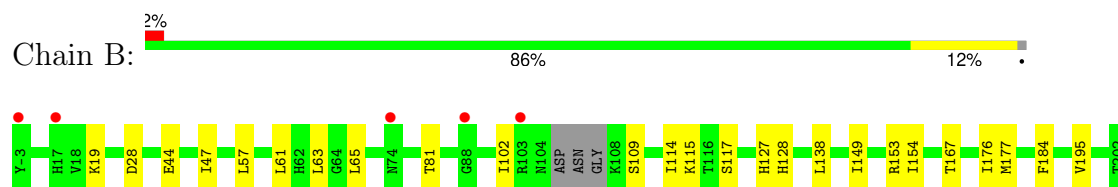
3 Residue-property plots [i](#)

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.

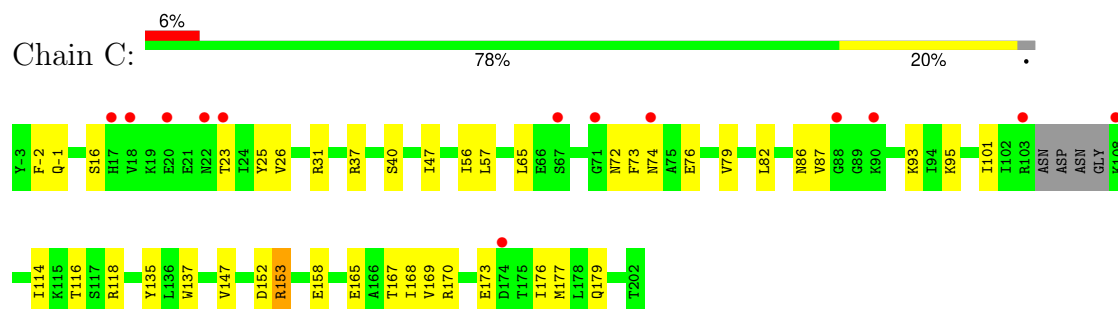
- Molecule 1: Uncharacterized protein



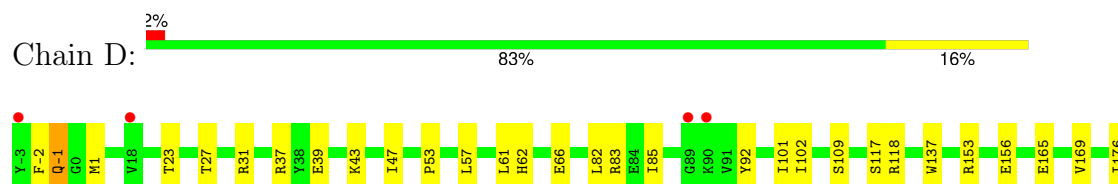
- Molecule 1: Uncharacterized protein

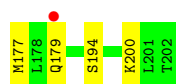


- Molecule 1: Uncharacterized protein

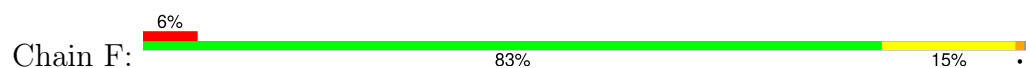


- Molecule 1: Uncharacterized protein

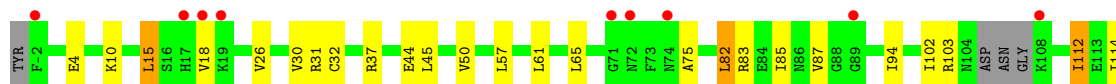
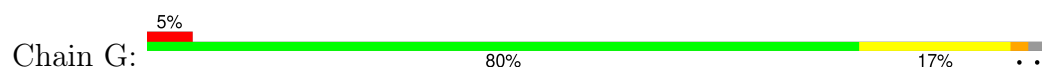




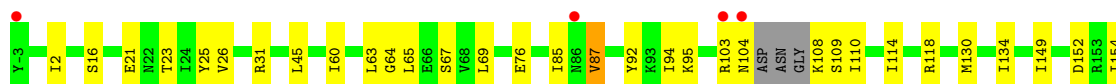
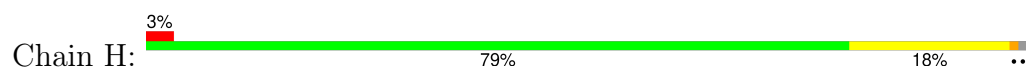
- Molecule 1: Uncharacterized protein



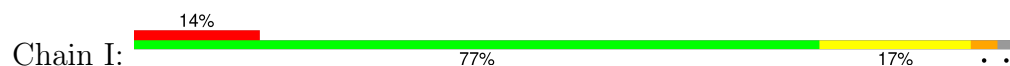
- Molecule 1: Uncharacterized protein



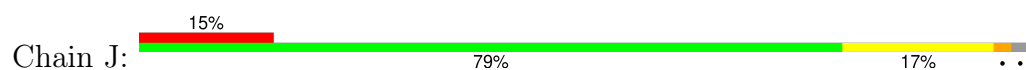
- Molecule 1: Uncharacterized protein

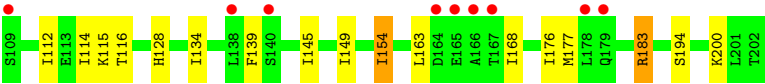
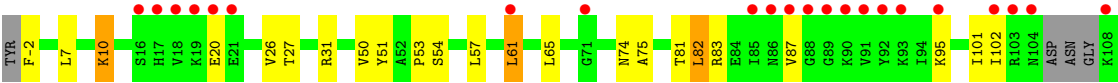


- Molecule 1: Uncharacterized protein

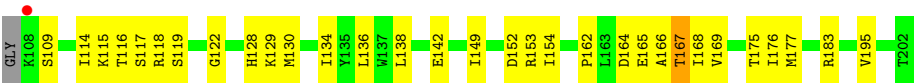
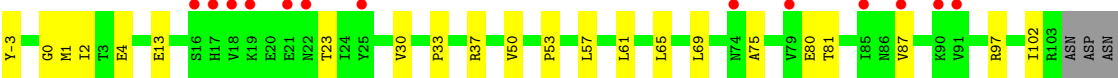


- Molecule 1: Uncharacterized protein





● Molecule 1: Uncharacterized protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	86.15Å 197.76Å 89.41Å 90.00° 100.88° 90.00°	Depositor
Resolution (Å)	40.00 – 2.35 40.00 – 2.35	Depositor EDS
% Data completeness (in resolution range)	82.3 (40.00-2.35) 82.6 (40.00-2.35)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.75 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.201 , 0.249 0.203 , 0.249	Depositor DCC
R_{free} test set	6111 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	30.6	Xtriage
Anisotropy	0.323	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.017 for l,-k,h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	16484	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.79% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SF4, MN

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	1.10	2/1648 (0.1%)	0.89	3/2223 (0.1%)
1	B	1.14	0/1655	0.94	2/2233 (0.1%)
1	C	0.98	3/1653 (0.2%)	0.91	4/2231 (0.2%)
1	D	1.11	2/1666 (0.1%)	0.94	2/2252 (0.1%)
1	F	0.93	0/1636	0.84	0/2210
1	G	0.96	0/1605	0.86	0/2172
1	H	0.97	0/1644	0.88	1/2220 (0.0%)
1	I	0.78	0/1614	0.76	1/2186 (0.0%)
1	J	0.84	0/1623	0.80	0/2195
1	K	0.96	1/1637 (0.1%)	0.86	2/2211 (0.1%)
All	All	0.99	8/16381 (0.0%)	0.87	15/22133 (0.1%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	191	CYS	CB-SG	-5.98	1.72	1.81
1	A	161	GLU	CG-CD	5.75	1.60	1.51
1	D	153	ARG	CZ-NH1	-5.75	1.25	1.33
1	K	13	GLU	CG-CD	5.38	1.60	1.51
1	D	153	ARG	CZ-NH2	-5.36	1.26	1.33

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	153	ARG	NE-CZ-NH1	6.41	123.50	120.30
1	A	153	ARG	NE-CZ-NH2	-5.88	117.36	120.30
1	D	82	LEU	CA-CB-CG	5.84	128.74	115.30
1	A	82	LEU	CA-CB-CG	5.78	128.59	115.30
1	A	37	ARG	NE-CZ-NH1	-5.67	117.47	120.30

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	1621	0	1644	16	0
1	B	1626	0	1646	20	0
1	C	1621	0	1641	27	0
1	D	1639	0	1642	23	0
1	F	1610	0	1619	40	0
1	G	1580	0	1585	32	0
1	H	1618	0	1627	32	0
1	I	1583	0	1566	37	0
1	J	1594	0	1596	33	0
1	K	1610	0	1615	37	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
3	A	8	0	0	0	0
3	B	8	0	0	0	0
3	C	8	0	0	0	0
3	D	8	0	0	0	0
3	F	8	0	0	0	0
3	G	8	0	0	0	0
3	H	8	0	0	0	0
3	I	8	0	0	0	0
3	J	8	0	0	0	0
3	K	8	0	0	0	0
4	A	49	0	0	0	0
4	B	62	0	0	0	0
4	C	22	0	0	2	0
4	D	49	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	F	19	0	0	0	0
4	G	21	0	0	1	0
4	H	27	0	0	0	0
4	I	8	0	0	0	0
4	J	10	0	0	0	0
4	K	25	0	0	1	0
All	All	16484	0	16181	247	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 8.

The worst 5 of 247 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:F:61:LEU:HD12	1:G:61:LEU:CD2	1.72	1.18
1:F:61:LEU:CD1	1:G:61:LEU:HD21	1.74	1.16
1:B:176:ILE:HG22	1:B:177:MSE:HE3	1.38	1.05
1:H:176:ILE:HG22	1:H:177:MSE:HE3	1.34	1.05
1:F:102:ILE:HD11	1:F:110:ILE:HD12	1.37	1.03

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	198/206 (96%)	195 (98%)	3 (2%)	0	100	100
1	B	200/206 (97%)	199 (100%)	1 (0%)	0	100	100
1	C	200/206 (97%)	188 (94%)	12 (6%)	0	100	100
1	D	204/206 (99%)	195 (96%)	9 (4%)	0	100	100
1	F	199/206 (97%)	192 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	G	198/206 (96%)	189 (96%)	9 (4%)	0	100	100
1	H	199/206 (97%)	192 (96%)	7 (4%)	0	100	100
1	I	200/206 (97%)	191 (96%)	9 (4%)	0	100	100
1	J	199/206 (97%)	194 (98%)	5 (2%)	0	100	100
1	K	198/206 (96%)	189 (96%)	9 (4%)	0	100	100
All	All	1995/2060 (97%)	1924 (96%)	71 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	177/182 (97%)	169 (96%)	8 (4%)	23	29
1	B	178/182 (98%)	175 (98%)	3 (2%)	56	69
1	C	177/182 (97%)	171 (97%)	6 (3%)	32	41
1	D	177/182 (97%)	168 (95%)	9 (5%)	20	24
1	F	174/182 (96%)	167 (96%)	7 (4%)	27	34
1	G	168/182 (92%)	159 (95%)	9 (5%)	18	21
1	H	176/182 (97%)	168 (96%)	8 (4%)	23	29
1	I	169/182 (93%)	157 (93%)	12 (7%)	12	12
1	J	171/182 (94%)	159 (93%)	12 (7%)	12	13
1	K	173/182 (95%)	163 (94%)	10 (6%)	17	19
All	All	1740/1820 (96%)	1656 (95%)	84 (5%)	21	26

5 of 84 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	147	VAL
1	J	154	ILE

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Mol	Chain	Res	Type
1	I	161	GLU
1	J	54[A]	SER
1	K	37	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	D	49	GLN
1	F	180	ASN
1	J	72	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 20 ligands modelled in this entry, 10 are monoatomic - leaving 10 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SF4	F	302	1	0,12,12	-	-	-		
3	SF4	K	302	1	0,12,12	-	-	-		
3	SF4	J	302	1	0,12,12	-	-	-		

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SF4	A	302	1	0,12,12	-	-	-		
3	SF4	C	302	1	0,12,12	-	-	-		
3	SF4	B	302	1	0,12,12	-	-	-		
3	SF4	H	302	1	0,12,12	-	-	-		
3	SF4	G	302	1	0,12,12	-	-	-		
3	SF4	D	302	1	0,12,12	-	-	-		
3	SF4	I	302	1	0,12,12	-	-	-		

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	SF4	F	302	1	-	-	0/6/5/5
3	SF4	K	302	1	-	-	0/6/5/5
3	SF4	J	302	1	-	-	0/6/5/5
3	SF4	A	302	1	-	-	0/6/5/5
3	SF4	C	302	1	-	-	0/6/5/5
3	SF4	B	302	1	-	-	0/6/5/5
3	SF4	H	302	1	-	-	0/6/5/5
3	SF4	G	302	1	-	-	0/6/5/5
3	SF4	D	302	1	-	-	0/6/5/5
3	SF4	I	302	1	-	-	0/6/5/5

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(Å ²)	Q<0.9
1	A	199/206 (96%)	-0.26	5 (2%) 58 64	8, 22, 49, 73	0
1	B	200/206 (97%)	-0.42	5 (2%) 58 64	4, 18, 42, 65	1 (0%)
1	C	199/206 (96%)	0.12	13 (6%) 26 30	11, 31, 65, 82	2 (1%)
1	D	203/206 (98%)	-0.25	5 (2%) 58 64	6, 22, 52, 69	0
1	F	200/206 (97%)	0.24	12 (6%) 29 33	11, 33, 67, 90	0
1	G	199/206 (96%)	0.27	10 (5%) 35 41	18, 34, 58, 69	0
1	H	200/206 (97%)	0.01	6 (3%) 52 58	17, 30, 53, 69	0
1	I	199/206 (96%)	0.92	29 (14%) 7 8	22, 48, 84, 99	2 (1%)
1	J	199/206 (96%)	0.74	31 (15%) 6 7	18, 43, 80, 88	1 (0%)
1	K	199/206 (96%)	0.28	14 (7%) 24 28	13, 34, 65, 81	0
All	All	1997/2060 (96%)	0.16	130 (6%) 26 30	4, 31, 67, 99	6 (0%)

The worst 5 of 130 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	-3	TYR	5.8
1	I	91	VAL	5.7
1	G	17	HIS	5.6
1	B	103	ARG	5.5
1	B	88	GLY	4.9

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 ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

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
2	MN	A	301	1/1	0.96	0.05	32,32,32,32	0
2	MN	K	301	1/1	0.96	0.04	28,28,28,28	1
3	SF4	C	302	8/8	0.96	0.04	12,16,20,21	0
3	SF4	H	302	8/8	0.96	0.05	12,13,18,18	0
3	SF4	J	302	8/8	0.96	0.06	33,36,39,39	0
2	MN	I	301	1/1	0.97	0.06	45,45,45,45	1
3	SF4	D	302	8/8	0.97	0.04	11,15,17,18	0
3	SF4	F	302	8/8	0.97	0.04	11,12,15,17	0
3	SF4	G	302	8/8	0.97	0.04	15,20,22,22	0
2	MN	C	301	1/1	0.97	0.03	37,37,37,37	1
3	SF4	I	302	8/8	0.97	0.05	24,30,32,33	0
3	SF4	B	302	8/8	0.97	0.04	6,7,9,10	0
2	MN	B	301	1/1	0.98	0.04	26,26,26,26	0
2	MN	J	301	1/1	0.98	0.03	43,43,43,43	1
2	MN	D	301	1/1	0.98	0.02	19,19,19,19	1
3	SF4	A	302	8/8	0.98	0.04	11,13,15,16	0
3	SF4	K	302	8/8	0.98	0.04	12,18,18,21	0
2	MN	G	301	1/1	0.99	0.03	25,25,25,25	1
2	MN	H	301	1/1	0.99	0.06	34,34,34,34	1
2	MN	F	301	1/1	0.99	0.02	35,35,35,35	1

6.5 Other polymers ⓘ

There are no such residues in this entry.