



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 20, 2026 – 05:51 AM UTC

PDB ID : 4NFW / pdb_00004nfw
Title : Structure and atypical hydrolysis mechanism of the Nudix hydrolase Orf153 (YmfB) from Escherichia coli
Authors : Hong, M.K.; Kim, J.K.; Kang, L.W.
Deposited on : 2013-11-01
Resolution : 2.30 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

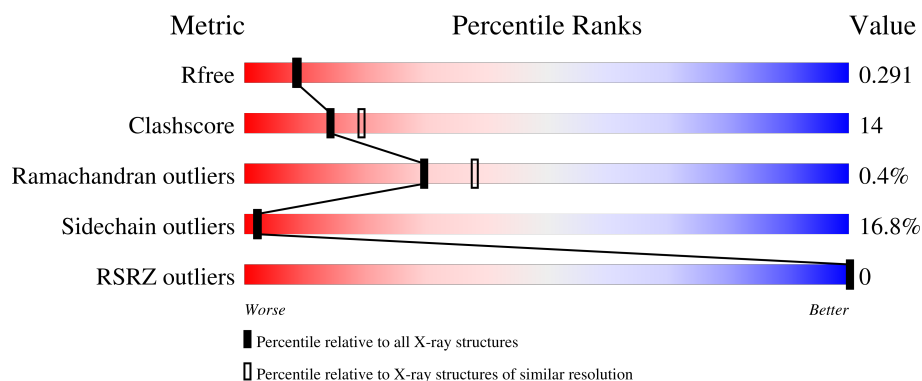
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	153	
1	B	153	
1	C	153	
1	D	153	
1	E	153	

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Mol	Chain	Length	Quality of chain
1	F	153	59%34%7% .
1	G	153	66%25%7% . .
1	H	153	63%29%5% . .
1	I	153	44%41%5% . 10%
1	J	153	60%29%10% .
1	K	153	64%30%. .
1	L	153	50%35%6% . 8%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 14906 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 Putative Nudix hydrolase ymfB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	150	Total	C	N	O	S	0	0	0
			1208	773	206	221	8			
1	B	150	Total	C	N	O	S	0	0	0
			1208	773	206	221	8			
1	C	150	Total	C	N	O	S	0	0	0
			1208	773	206	221	8			
1	D	150	Total	C	N	O	S	0	0	0
			1208	773	206	221	8			
1	E	150	Total	C	N	O	S	0	0	0
			1208	773	206	221	8			
1	F	153	Total	C	N	O	S	0	0	0
			1227	786	209	224	8			
1	G	150	Total	C	N	O	S	0	0	0
			1208	773	206	221	8			
1	H	150	Total	C	N	O	S	0	0	0
			1208	773	206	221	8			
1	I	138	Total	C	N	O	S	0	0	0
			1122	723	192	200	7			
1	J	152	Total	C	N	O	S	0	0	0
			1219	780	208	223	8			
1	K	150	Total	C	N	O	S	0	0	0
			1208	773	206	221	8			
1	L	141	Total	C	N	O	S	0	0	0
			1143	734	195	206	8			

- Molecule 2 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn).

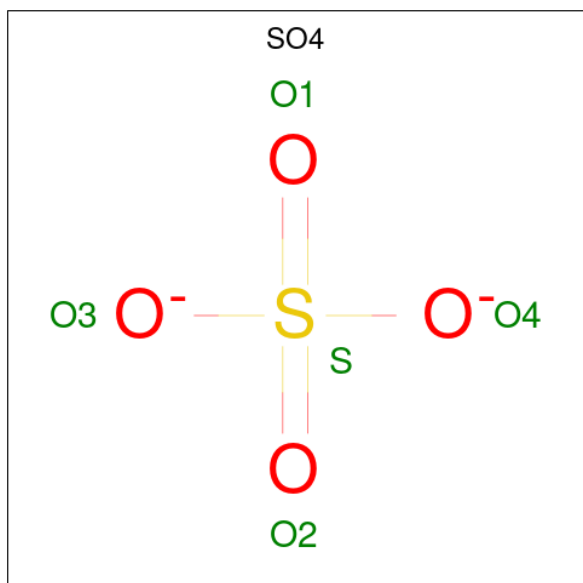
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Mn	0	0
			2	2		
2	B	2	Total	Mn	0	0
			2	2		

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

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	I	1	Total	O	S	0	0
			5	4	1		
3	I	1	Total	O	S	0	0
			5	4	1		
3	J	1	Total	O	S	0	0
			5	4	1		
3	J	1	Total	O	S	0	0
			5	4	1		
3	J	1	Total	O	S	0	0
			5	4	1		
3	K	1	Total	O	S	0	0
			5	4	1		
3	K	1	Total	O	S	0	0
			5	4	1		
3	K	1	Total	O	S	0	0
			5	4	1		
3	L	1	Total	O	S	0	0
			5	4	1		
3	L	1	Total	O	S	0	0
			5	4	1		
3	L	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	42	Total	O	0	0
			42	42		
4	B	34	Total	O	0	0
			34	34		
4	C	36	Total	O	0	0
			36	36		
4	D	23	Total	O	0	0
			23	23		
4	E	37	Total	O	0	0
			37	37		
4	F	17	Total	O	0	0
			17	17		

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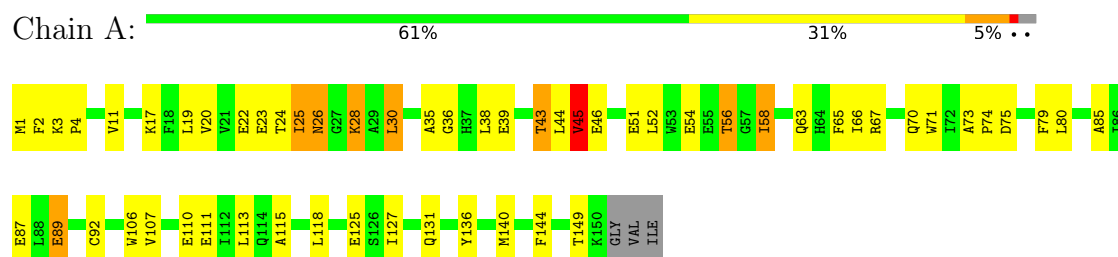
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	G	29	Total 29	O 29	0	0
4	H	25	Total 25	O 25	0	0
4	I	19	Total 19	O 19	0	0
4	J	17	Total 17	O 17	0	0
4	K	37	Total 37	O 37	0	0
4	L	18	Total 18	O 18	0	0

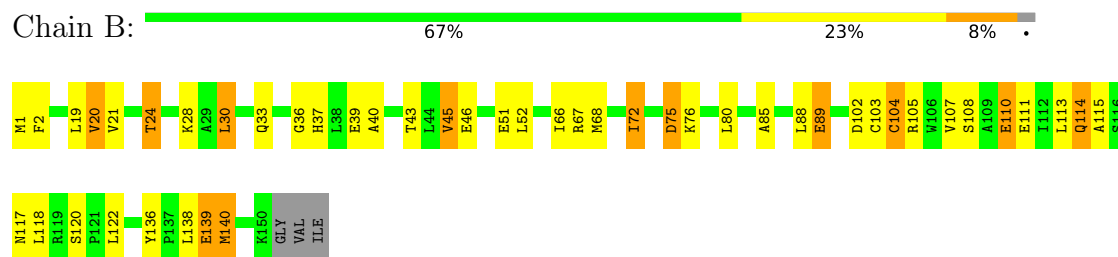
3 Residue-property plots

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.

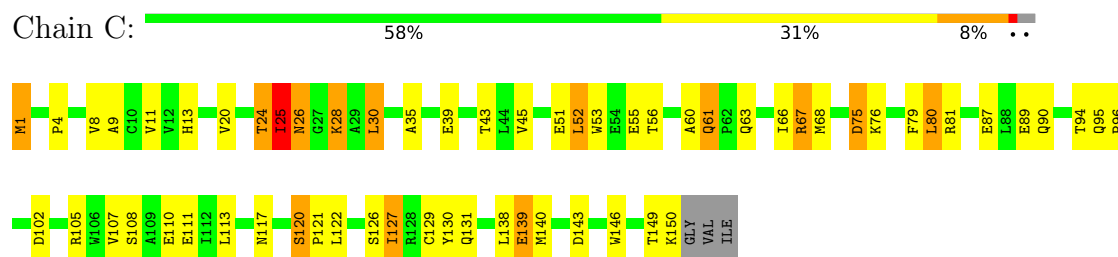
• Molecule 1: Putative Nudix hydrolase ymfB



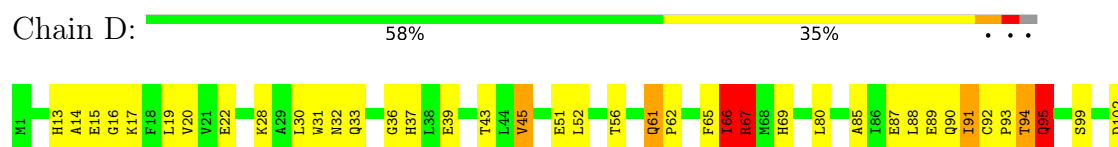
• Molecule 1: Putative Nudix hydrolase ymfB



• Molecule 1: Putative Nudix hydrolase ymfB



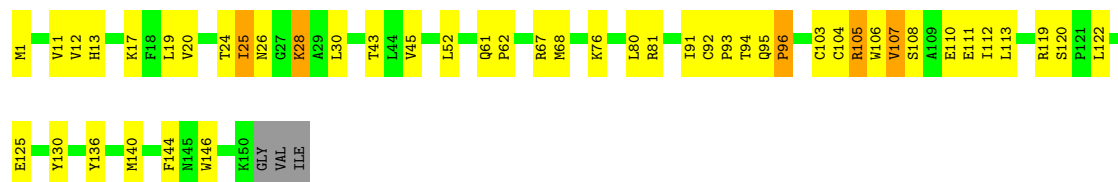
• Molecule 1: Putative Nudix hydrolase ymfB





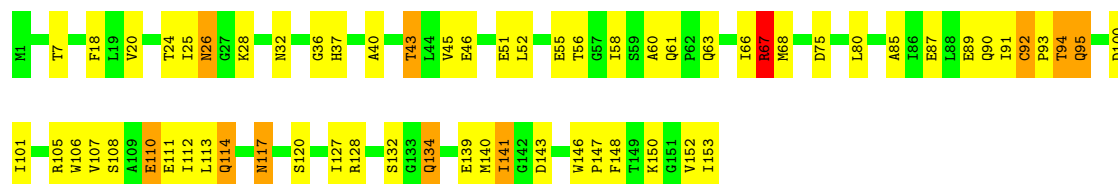
- Molecule 1: Putative Nudix hydrolase ymfB

Chain E: 67% 27% ..



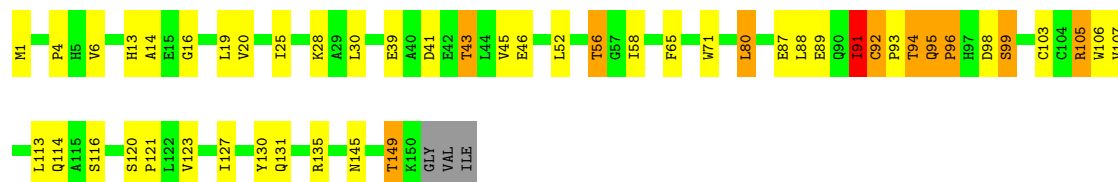
- Molecule 1: Putative Nudix hydrolase ymfB

Chain F: 59% 34% 7% .



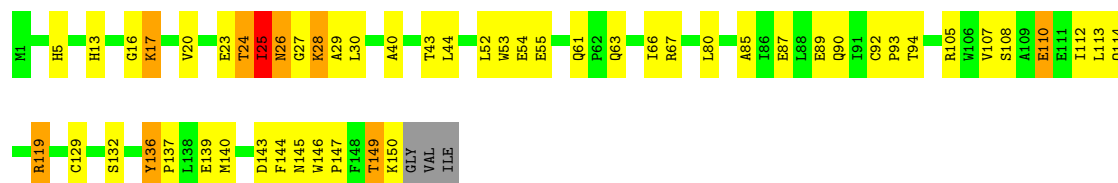
- Molecule 1: Putative Nudix hydrolase ymfB

Chain G: 66% 25% 7% ..



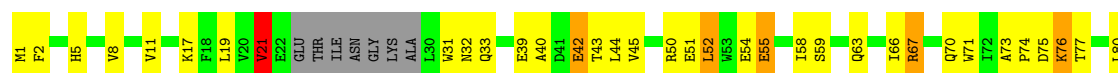
- Molecule 1: Putative Nudix hydrolase ymfB

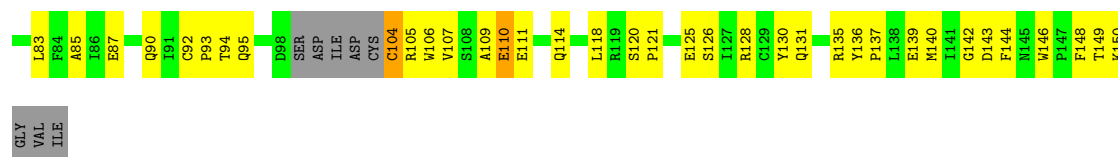
Chain H: 63% 29% 5% ..



- Molecule 1: Putative Nudix hydrolase ymfB

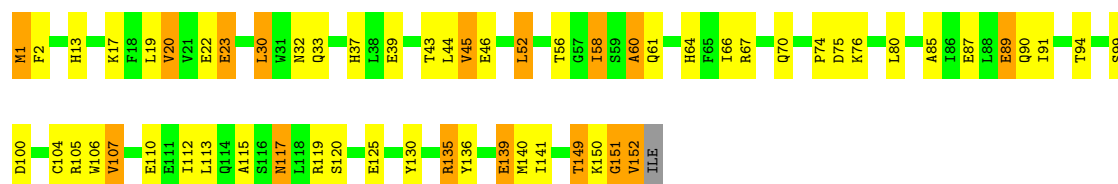
Chain I: 44% 41% 5% . 10%





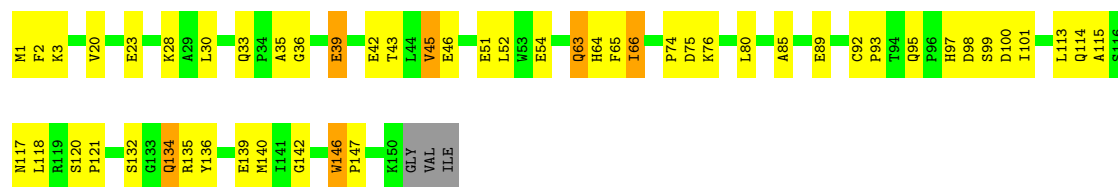
• Molecule 1: Putative Nudix hydrolase ymfB

Chain J: 60% 29% 10% .



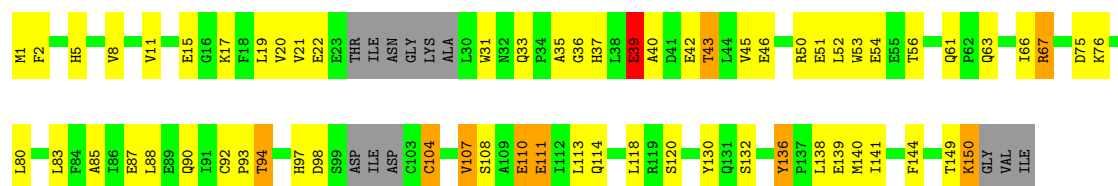
• Molecule 1: Putative Nudix hydrolase ymfB

Chain K: 64% 30% . .



• Molecule 1: Putative Nudix hydrolase ymfB

Chain L: 50% 35% 6% . 8%



4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	111.39Å 111.39Å 247.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.42 – 2.30 32.42 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.8 (32.42-2.30) 96.9 (32.42-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.94 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.240 , 0.289 0.243 , 0.291	Depositor DCC
R_{free} test set	6505 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	22.6	Xtriage
Anisotropy	0.108	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 15.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.478 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14906	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.75% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MN, SO4

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	1.24	3/1243 (0.2%)	1.19	4/1693 (0.2%)
1	B	1.23	3/1243 (0.2%)	1.26	6/1693 (0.4%)
1	C	1.04	3/1243 (0.2%)	1.15	8/1693 (0.5%)
1	D	1.22	7/1243 (0.6%)	1.17	2/1693 (0.1%)
1	E	1.12	3/1243 (0.2%)	1.13	4/1693 (0.2%)
1	F	1.04	0/1262	1.16	7/1719 (0.4%)
1	G	1.01	0/1243	1.21	5/1693 (0.3%)
1	H	1.04	1/1243 (0.1%)	1.11	2/1693 (0.1%)
1	I	1.06	2/1155 (0.2%)	1.17	7/1571 (0.4%)
1	J	1.08	0/1254	1.15	4/1708 (0.2%)
1	K	1.11	4/1243 (0.3%)	1.13	4/1693 (0.2%)
1	L	1.13	3/1176 (0.3%)	1.18	10/1599 (0.6%)
All	All	1.11	29/14791 (0.2%)	1.17	63/20141 (0.3%)

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	E	0	1
1	I	0	1
1	J	0	1
All	All	0	3

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	69	HIS	CG-ND1	-8.06	1.29	1.38
1	L	107	VAL	C-O	-7.16	1.16	1.23
1	B	104	CYS	CA-C	-6.53	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	136	TYR	C-O	-6.43	1.18	1.24
1	C	90	GLN	CA-C	-6.41	1.45	1.52

The worst 5 of 63 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	94	THR	N-CA-C	10.37	126.03	111.52
1	I	55	GLU	N-CA-C	7.97	121.07	111.82
1	K	142	GLY	N-CA-C	7.87	120.99	112.33
1	L	92	CYS	CA-C-N	7.49	129.21	119.84
1	L	92	CYS	C-N-CA	7.49	129.21	119.84

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	25	ILE	Peptide
1	I	21	VAL	Peptide
1	J	151	GLY	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	1208	0	1167	36	0
1	B	1208	0	1167	28	0
1	C	1208	0	1167	42	0
1	D	1208	0	1167	45	0
1	E	1208	0	1167	24	0
1	F	1227	0	1190	35	0
1	G	1208	0	1167	42	0
1	H	1208	0	1167	39	0
1	I	1122	0	1085	45	0
1	J	1219	0	1179	40	0
1	K	1208	0	1167	31	0
1	L	1143	0	1101	47	0
2	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
2	G	2	0	0	0	0
2	H	2	0	0	0	0
2	I	1	0	0	0	0
2	J	2	0	0	0	0
2	K	2	0	0	0	0
2	L	1	0	0	0	0
3	A	15	0	0	1	0
3	B	15	0	0	1	0
3	C	15	0	0	1	0
3	D	15	0	0	0	0
3	E	15	0	0	1	0
3	F	15	0	0	0	0
3	G	15	0	0	0	0
3	H	15	0	0	1	0
3	I	10	0	0	0	0
3	J	15	0	0	1	0
3	K	15	0	0	0	0
3	L	15	0	0	2	0
4	A	42	0	0	3	0
4	B	34	0	0	0	0
4	C	36	0	0	2	0
4	D	23	0	0	0	0
4	E	37	0	0	1	0
4	F	17	0	0	0	0
4	G	29	0	0	3	0
4	H	25	0	0	2	0
4	I	19	0	0	3	0
4	J	17	0	0	0	0
4	K	37	0	0	5	0
4	L	18	0	0	1	0
All	All	14906	0	13891	404	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 14.

The worst 5 of 404 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:D:15:GLU:OE2	1:D:91:ILE:N	1.73	1.22
1:H:25:ILE:HD12	1:H:119:ARG:NH2	1.66	1.10
1:D:92:CYS:HB2	1:D:93:PRO:HD2	1.32	1.06
1:C:25:ILE:HG22	1:C:26:ASN:H	1.20	1.02
1:H:66:ILE:HD11	1:H:85:ALA:HB2	1.42	1.00

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	148/153 (97%)	139 (94%)	7 (5%)	2 (1%)	9	9
1	B	148/153 (97%)	138 (93%)	9 (6%)	1 (1%)	18	23
1	C	148/153 (97%)	135 (91%)	13 (9%)	0	100	100
1	D	148/153 (97%)	132 (89%)	16 (11%)	0	100	100
1	E	148/153 (97%)	142 (96%)	5 (3%)	1 (1%)	18	23
1	F	151/153 (99%)	138 (91%)	12 (8%)	1 (1%)	18	23
1	G	148/153 (97%)	135 (91%)	12 (8%)	1 (1%)	18	23
1	H	148/153 (97%)	140 (95%)	8 (5%)	0	100	100
1	I	132/153 (86%)	120 (91%)	12 (9%)	0	100	100
1	J	150/153 (98%)	138 (92%)	12 (8%)	0	100	100
1	K	148/153 (97%)	135 (91%)	13 (9%)	0	100	100
1	L	135/153 (88%)	122 (90%)	12 (9%)	1 (1%)	18	23
All	All	1752/1836 (95%)	1614 (92%)	131 (8%)	7 (0%)	30	38

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	4	PRO

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Mol	Chain	Res	Type
1	A	26	ASN
1	F	67	ARG
1	G	96	PRO
1	L	93	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	
1	A	130/132 (98%)	110 (85%)	20 (15%)	2	3
1	B	130/132 (98%)	112 (86%)	18 (14%)	3	4
1	C	130/132 (98%)	105 (81%)	25 (19%)	1	1
1	D	130/132 (98%)	106 (82%)	24 (18%)	1	1
1	E	130/132 (98%)	110 (85%)	20 (15%)	2	3
1	F	132/132 (100%)	110 (83%)	22 (17%)	2	2
1	G	130/132 (98%)	109 (84%)	21 (16%)	2	2
1	H	130/132 (98%)	106 (82%)	24 (18%)	1	1
1	I	120/132 (91%)	97 (81%)	23 (19%)	1	1
1	J	131/132 (99%)	104 (79%)	27 (21%)	1	1
1	K	130/132 (98%)	114 (88%)	16 (12%)	4	5
1	L	123/132 (93%)	104 (85%)	19 (15%)	2	3
All	All	1546/1584 (98%)	1287 (83%)	259 (17%)	2	2

5 of 259 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	52	LEU
1	K	134	GLN
1	E	76	LYS
1	E	62	PRO
1	L	22	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	63	GLN
1	L	69	HIS
1	H	63	GLN
1	L	63	GLN
1	L	134	GLN

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](#)

Of 57 ligands modelled in this entry, 22 are monoatomic - leaving 35 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	SO4	E	205	-	4,4,4	0.52	0	6,6,6	0.32	0
3	SO4	F	205	-	4,4,4	0.75	0	6,6,6	0.30	0
3	SO4	L	202	2	4,4,4	0.43	0	6,6,6	0.18	0
3	SO4	H	205	-	4,4,4	0.71	0	6,6,6	0.47	0
3	SO4	D	204	-	4,4,4	0.51	0	6,6,6	0.25	0
3	SO4	K	204	2	4,4,4	0.45	0	6,6,6	0.26	0
3	SO4	A	205	-	4,4,4	0.53	0	6,6,6	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	A	203	2	4,4,4	0.73	0	6,6,6	0.31	0
3	SO4	C	204	-	4,4,4	0.47	0	6,6,6	0.47	0
3	SO4	C	205	-	4,4,4	0.52	0	6,6,6	0.31	0
3	SO4	I	202	2	4,4,4	0.48	0	6,6,6	0.10	0
3	SO4	B	204	-	4,4,4	0.55	0	6,6,6	0.32	0
3	SO4	L	203	-	4,4,4	0.50	0	6,6,6	0.31	0
3	SO4	B	203	2	4,4,4	0.60	0	6,6,6	0.54	0
3	SO4	K	203	2	4,4,4	0.36	0	6,6,6	0.63	0
3	SO4	G	203	2	4,4,4	0.40	0	6,6,6	0.54	0
3	SO4	K	205	-	4,4,4	0.58	0	6,6,6	0.41	0
3	SO4	L	204	-	4,4,4	0.49	0	6,6,6	0.38	0
3	SO4	G	205	-	4,4,4	0.52	0	6,6,6	0.24	0
3	SO4	I	203	-	4,4,4	0.48	0	6,6,6	0.19	0
3	SO4	B	205	-	4,4,4	0.67	0	6,6,6	0.58	0
3	SO4	E	203	-	4,4,4	0.51	0	6,6,6	0.35	0
3	SO4	H	203	2	4,4,4	0.42	0	6,6,6	0.76	0
3	SO4	J	203	2	4,4,4	0.47	0	6,6,6	0.52	0
3	SO4	J	204	2	4,4,4	0.45	0	6,6,6	0.20	0
3	SO4	D	205	-	4,4,4	0.58	0	6,6,6	0.51	0
3	SO4	J	205	-	4,4,4	0.61	0	6,6,6	0.43	0
3	SO4	A	204	2	4,4,4	0.54	0	6,6,6	0.45	0
3	SO4	D	203	2	4,4,4	0.48	0	6,6,6	0.73	0
3	SO4	C	203	2	4,4,4	0.51	0	6,6,6	0.50	0
3	SO4	F	204	-	4,4,4	0.54	0	6,6,6	0.18	0
3	SO4	G	204	-	4,4,4	0.58	0	6,6,6	0.44	0
3	SO4	F	203	2	4,4,4	0.42	0	6,6,6	0.26	0
3	SO4	H	204	-	4,4,4	0.56	0	6,6,6	0.28	0
3	SO4	E	204	2	4,4,4	0.50	0	6,6,6	0.29	0

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.

10 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	L	202	SO4	1	0
3	C	204	SO4	1	0
3	B	204	SO4	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	L	203	SO4	1	0
3	B	203	SO4	1	0
3	E	203	SO4	1	0
3	J	203	SO4	1	0
3	A	204	SO4	1	0
3	H	204	SO4	1	0
3	E	204	SO4	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 [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	150/153 (98%)	-1.47	0 100 100	9, 21, 40, 62	2 (1%)
1	B	150/153 (98%)	-1.48	0 100 100	9, 21, 42, 60	2 (1%)
1	C	150/153 (98%)	-1.40	0 100 100	10, 27, 58, 74	2 (1%)
1	D	150/153 (98%)	-1.29	0 100 100	12, 32, 69, 78	2 (1%)
1	E	150/153 (98%)	-1.39	0 100 100	10, 25, 61, 80	2 (1%)
1	F	153/153 (100%)	-1.26	0 100 100	8, 30, 72, 107	2 (1%)
1	G	150/153 (98%)	-1.27	0 100 100	15, 33, 69, 82	2 (1%)
1	H	150/153 (98%)	-1.37	0 100 100	9, 30, 52, 78	2 (1%)
1	I	138/153 (90%)	-1.19	0 100 100	12, 39, 72, 89	2 (1%)
1	J	152/153 (99%)	-1.29	0 100 100	10, 29, 71, 83	2 (1%)
1	K	150/153 (98%)	-1.36	0 100 100	8, 30, 54, 70	2 (1%)
1	L	141/153 (92%)	-1.12	0 100 100	11, 40, 78, 96	2 (1%)
All	All	1784/1836 (97%)	-1.33	0 100 100	8, 29, 66, 107	24 (1%)

There are no RSRZ outliers to report.

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

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
3	SO4	I	202	5/5	0.95	0.07	129,131,135,137	0
3	SO4	L	202	5/5	0.95	0.07	119,119,121,126	0
3	SO4	C	204	5/5	0.96	0.07	91,96,101,103	0
3	SO4	F	204	5/5	0.97	0.09	104,110,116,123	0
2	MN	D	201	1/1	0.97	0.07	100,100,100,100	0
3	SO4	E	204	5/5	0.97	0.06	87,95,104,105	0
3	SO4	L	203	5/5	0.97	0.06	106,109,118,119	0
3	SO4	D	203	5/5	0.98	0.05	53,54,62,63	0
3	SO4	I	203	5/5	0.98	0.08	103,110,116,116	0
3	SO4	J	204	5/5	0.98	0.05	97,99,104,104	0
3	SO4	K	204	5/5	0.98	0.06	97,98,105,106	0
3	SO4	G	205	5/5	0.98	0.05	78,82,96,101	0
3	SO4	H	204	5/5	0.98	0.07	102,104,111,116	0
3	SO4	L	204	5/5	0.98	0.07	85,89,93,98	0
2	MN	J	202	1/1	0.99	0.08	112,112,112,112	0
2	MN	K	202	1/1	0.99	0.03	72,72,72,72	0
3	SO4	A	203	5/5	0.99	0.03	45,45,48,50	0
3	SO4	A	204	5/5	0.99	0.08	60,61,71,75	0
3	SO4	B	204	5/5	0.99	0.05	61,63,71,79	0
3	SO4	B	205	5/5	0.99	0.05	41,43,48,48	0
3	SO4	C	203	5/5	0.99	0.04	66,68,74,77	0
2	MN	C	201	1/1	0.99	0.05	95,95,95,95	0
2	MN	C	202	1/1	0.99	0.04	92,92,92,92	0
3	SO4	D	204	5/5	0.99	0.06	93,98,106,107	0
3	SO4	D	205	5/5	0.99	0.06	46,46,52,56	0
3	SO4	E	203	5/5	0.99	0.04	55,58,62,66	0
2	MN	A	201	1/1	0.99	0.09	78,78,78,78	0
3	SO4	F	203	5/5	0.99	0.05	72,73,78,82	0
2	MN	E	201	1/1	0.99	0.05	82,82,82,82	0
3	SO4	F	205	5/5	0.99	0.04	38,41,46,48	0
3	SO4	G	203	5/5	0.99	0.04	56,60,63,66	0
3	SO4	G	204	5/5	0.99	0.06	44,46,53,53	0
2	MN	E	202	1/1	0.99	0.07	96,96,96,96	0
3	SO4	H	203	5/5	0.99	0.03	38,45,49,51	0
2	MN	F	201	1/1	0.99	0.07	86,86,86,86	0
2	MN	F	202	1/1	0.99	0.07	82,82,82,82	0
2	MN	G	201	1/1	0.99	0.04	88,88,88,88	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SO4	J	203	5/5	0.99	0.06	60,66,68,68	0
2	MN	G	202	1/1	0.99	0.05	86,86,86,86	0
3	SO4	J	205	5/5	0.99	0.04	51,52,62,64	0
2	MN	H	201	1/1	0.99	0.04	101,101,101,101	0
2	MN	H	202	1/1	0.99	0.02	87,87,87,87	0
2	MN	I	201	1/1	0.99	0.03	87,87,87,87	0
2	MN	J	201	1/1	0.99	0.07	87,87,87,87	0
3	SO4	B	203	5/5	1.00	0.03	45,46,49,51	0
3	SO4	H	205	5/5	1.00	0.03	26,29,31,31	0
2	MN	B	202	1/1	1.00	0.04	60,60,60,60	0
3	SO4	E	205	5/5	1.00	0.03	52,56,58,61	0
2	MN	K	201	1/1	1.00	0.03	81,81,81,81	0
2	MN	D	202	1/1	1.00	0.07	87,87,87,87	0
2	MN	L	201	1/1	1.00	0.03	77,77,77,77	0
3	SO4	K	203	5/5	1.00	0.03	43,46,48,49	0
3	SO4	C	205	5/5	1.00	0.04	49,50,51,53	0
3	SO4	K	205	5/5	1.00	0.04	31,33,37,39	0
2	MN	A	202	1/1	1.00	0.03	65,65,65,65	0
2	MN	B	201	1/1	1.00	0.04	75,75,75,75	0
3	SO4	A	205	5/5	1.00	0.04	36,36,37,38	0

6.5 Other polymers

There are no such residues in this entry.