



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 01:34 AM GMT

PDB ID : 2DD4
Title : Thiocyanate hydrolase (SCNase) from Thiobacillus thioparus recombinant apo-enzyme
Authors : Arakawa, T.; Kawano, Y.; Kataoka, S.; Katayama, Y.; Kamiya, N.; Yohda, M.; Odaka, M.
Deposited on : 2006-01-19
Resolution : 2.06 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

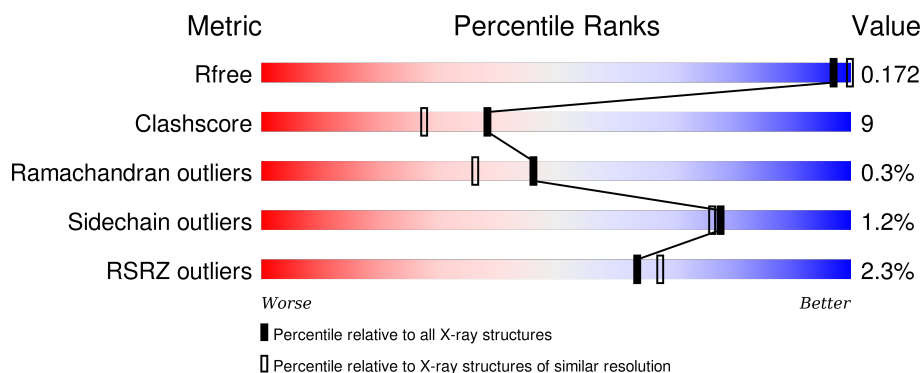
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.06 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	1799 (2.08-2.04)
Clashscore	102246	1910 (2.08-2.04)
Ramachandran outliers	100387	1893 (2.08-2.04)
Sidechain outliers	100360	1893 (2.08-2.04)
RSRZ outliers	91569	1802 (2.08-2.04)

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	126	<div> <div>2%</div> <div>82% 11% 6%</div> </div>
1	D	126	<div> <div>2%</div> <div>85% 10% 6%</div> </div>
1	G	126	<div> <div>3%</div> <div>82% 13% 5%</div> </div>
1	J	126	<div> <div>2%</div> <div>85% 10% 5%</div> </div>
2	B	157	<div> <div>0%</div> <div>85% 10% . .</div> </div>

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Mol	Chain	Length	Quality of chain
2	E	157	
2	H	157	
2	K	157	
3	C	243	
3	F	243	
3	I	243	
3	L	243	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	FRU	B	3002	-	-	-	X
4	FRU	B	3008	-	-	-	X
4	FRU	C	3001	-	-	-	X
4	FRU	H	3004	-	-	-	X
4	FRU	H	3006	-	-	-	X
4	FRU	H	3007	-	-	-	X
4	FRU	K	3003	-	-	-	X
4	FRU	K	3005	-	-	-	X
5	TAR	C	3401	X	-	-	-
5	TAR	C	3501	X	-	-	-
5	TAR	F	4401	X	-	-	-
5	TAR	F	4501	X	-	-	-
5	TAR	I	5401	X	-	-	-
5	TAR	I	5501	X	-	-	-
5	TAR	L	6401	X	-	-	-
5	TAR	L	6501	X	-	-	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 18077 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 Thiocyanate hydrolase alpha subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	118	Total	C	N	O	S	0	0	0
			958	609	159	186	4			
1	D	119	Total	C	N	O	S	0	0	0
			965	614	160	187	4			
1	G	120	Total	C	N	O	S	0	0	0
			974	620	162	188	4			
1	J	120	Total	C	N	O	S	0	0	0
			974	620	162	188	4			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	INITIATING METHIONINE	UNP O66187
D	1	MET	-	INITIATING METHIONINE	UNP O66187
G	1	MET	-	INITIATING METHIONINE	UNP O66187
J	1	MET	-	INITIATING METHIONINE	UNP O66187

- Molecule 2 is a protein called Thiocyanate hydrolase beta subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	152	Total	C	N	O	S	0	0	0
			1232	778	222	226	6			
2	E	151	Total	C	N	O	S	0	0	0
			1226	775	221	224	6			
2	H	156	Total	C	N	O	S	0	0	0
			1262	796	228	232	6			
2	K	152	Total	C	N	O	S	0	0	0
			1232	778	222	226	6			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	INITIATING METHIONINE	UNP O66186
E	1	MET	-	INITIATING METHIONINE	UNP O66186
H	1	MET	-	INITIATING METHIONINE	UNP O66186
K	1	MET	-	INITIATING METHIONINE	UNP O66186

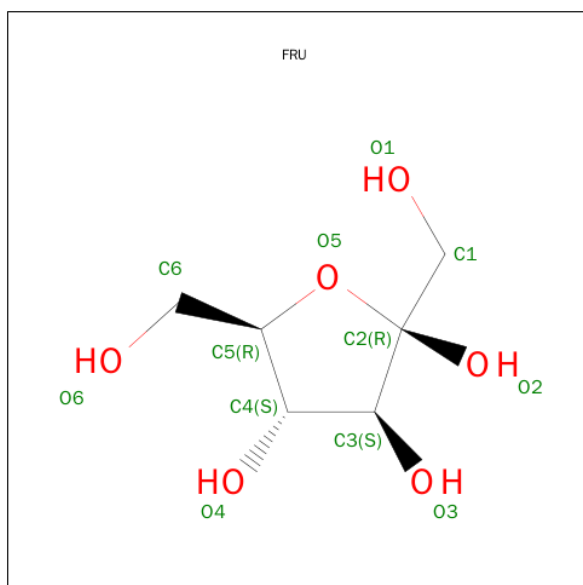
- Molecule 3 is a protein called Thiocyanate hydrolase gamma subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	217	Total	C	N	O	S	0	0	0
			1721	1098	304	311	8			
3	F	216	Total	C	N	O	S	0	0	0
			1712	1093	303	308	8			
3	I	217	Total	C	N	O	S	0	0	0
			1721	1098	304	311	8			
3	L	216	Total	C	N	O	S	0	0	0
			1712	1093	303	308	8			

There are 4 discrepancies between the modelled and reference sequences:

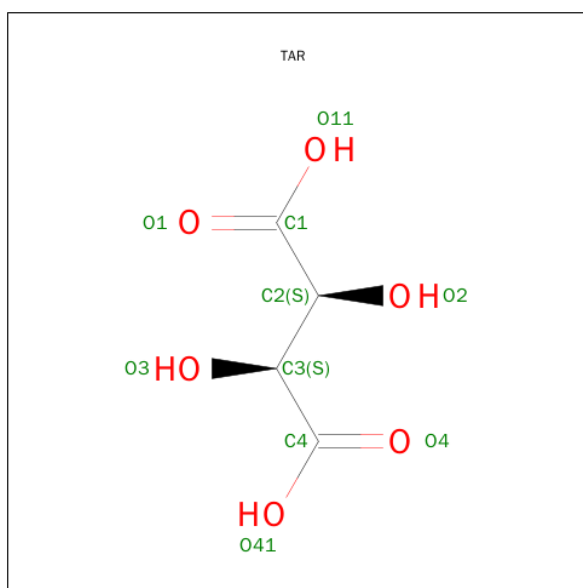
Chain	Residue	Modelled	Actual	Comment	Reference
C	1	MET	-	INITIATING METHIONINE	UNP O66188
F	1	MET	-	INITIATING METHIONINE	UNP O66188
I	1	MET	-	INITIATING METHIONINE	UNP O66188
L	1	MET	-	INITIATING METHIONINE	UNP O66188

- Molecule 4 is SUGAR (FRUCTOSE) (three-letter code: FRU) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	1	Total C O 12 6 6	0	0
4	B	1	Total C O 12 6 6	0	0
4	K	1	Total C O 12 6 6	0	0
4	H	1	Total C O 12 6 6	0	0
4	K	1	Total C O 12 6 6	0	0
4	H	1	Total C O 12 6 6	0	0
4	H	1	Total C O 12 6 6	0	0
4	B	1	Total C O 12 6 6	0	0

- Molecule 5 is D(-)-TARTARIC ACID (three-letter code: TAR) (formula: C₄H₆O₆).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	C	1	Total C O 10 4 6	0	0
5	C	1	Total C O 10 4 6	0	0
5	F	1	Total C O 10 4 6	0	0
5	F	1	Total C O 10 4 6	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	I	1	Total	C	O	0	0
			10	4	6		
5	I	1	Total	C	O	0	0
			10	4	6		
5	L	1	Total	C	O	0	0
			10	4	6		
5	L	1	Total	C	O	0	0
			10	4	6		

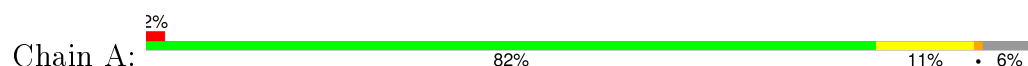
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	120	Total	O	0	0
			120	120		
6	B	182	Total	O	0	0
			182	182		
6	C	257	Total	O	0	0
			257	257		
6	D	123	Total	O	0	0
			123	123		
6	E	166	Total	O	0	0
			166	166		
6	F	209	Total	O	0	0
			209	209		
6	G	122	Total	O	0	0
			122	122		
6	H	185	Total	O	0	0
			185	185		
6	I	281	Total	O	0	0
			281	281		
6	J	132	Total	O	0	0
			132	132		
6	K	183	Total	O	0	0
			183	183		
6	L	252	Total	O	0	0
			252	252		

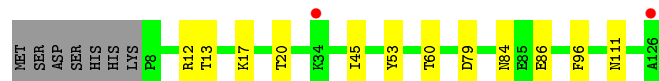
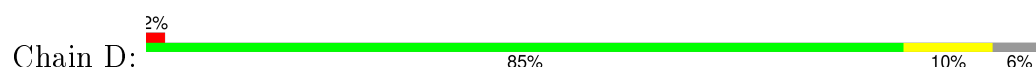
3 Residue-property plots [i](#)

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.

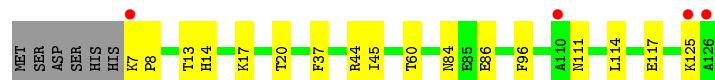
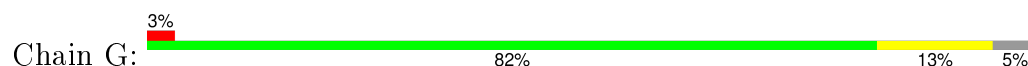
- Molecule 1: Thiocyanate hydrolase alpha subunit



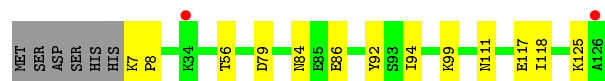
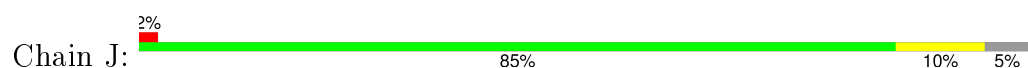
- Molecule 1: Thiocyanate hydrolase alpha subunit



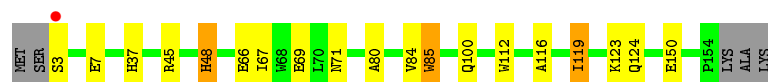
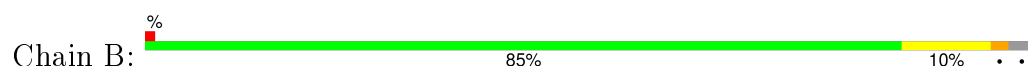
- Molecule 1: Thiocyanate hydrolase alpha subunit



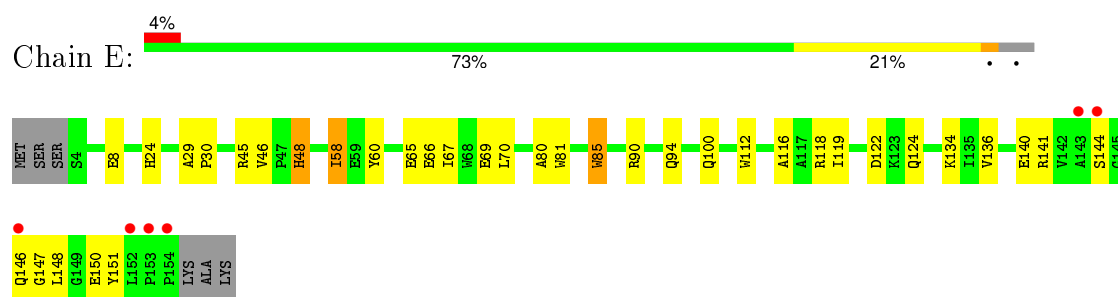
- Molecule 1: Thiocyanate hydrolase alpha subunit



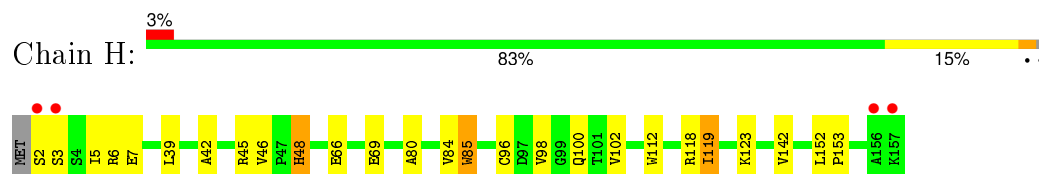
- Molecule 2: Thiocyanate hydrolase beta subunit



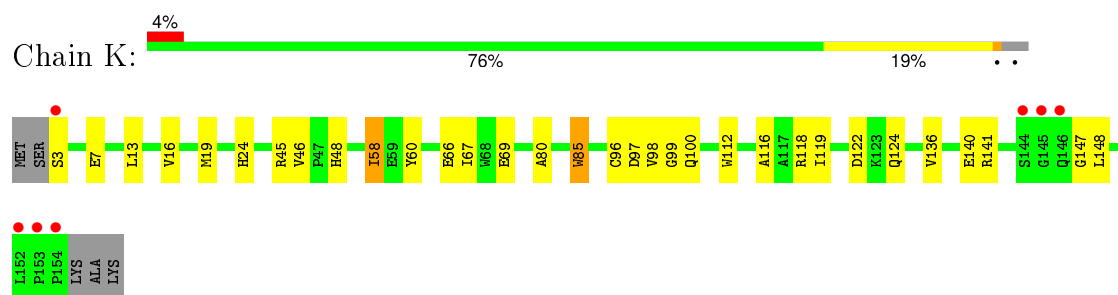
- Molecule 2: Thiocyanate hydrolase beta subunit



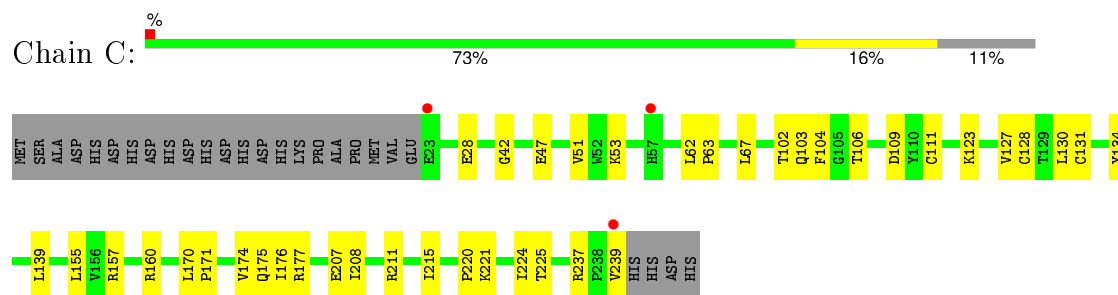
- Molecule 2: Thiocyanate hydrolase beta subunit



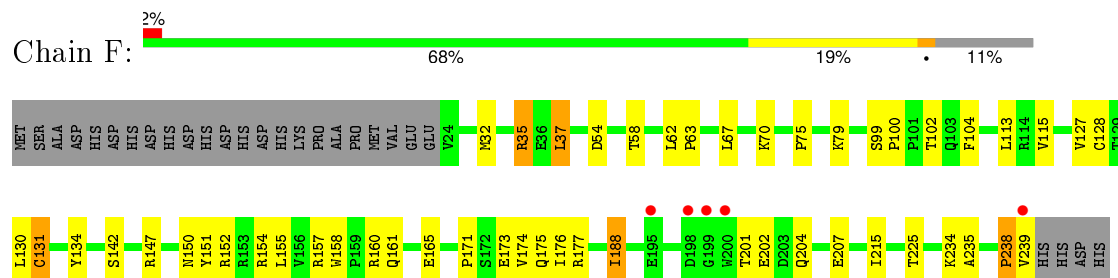
- Molecule 2: Thiocyanate hydrolase beta subunit



- Molecule 3: Thiocyanate hydrolase gamma subunit

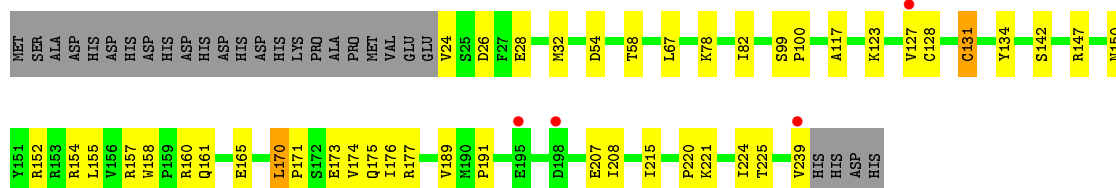


- Molecule 3: Thiocyanate hydrolase gamma subunit



- Molecule 3: Thiocyanate hydrolase gamma subunit





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	170.31Å 175.60Å 114.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.95 – 2.06 32.95 – 2.06	Depositor EDS
% Data completeness (in resolution range)	96.3 (32.95-2.06) 97.0 (32.95-2.06)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	8.56 (at 2.06Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.165 , 0.193 0.169 , 0.172	Depositor DCC
R_{free} test set	10298 reflections (5.03%)	DCC
Wilson B-factor (Å ²)	14.0	Xtriage
Anisotropy	0.610	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 61.6	EDS
Estimated twinning fraction	0.016 for k,h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 204859 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	18077	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.04% 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: FRU, TAR

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	0.34	0/983	0.61	0/1331
1	D	0.33	0/991	0.60	0/1342
1	G	0.32	0/1000	0.59	0/1354
1	J	0.34	0/1000	0.60	0/1354
2	B	0.30	0/1264	0.58	0/1720
2	E	0.30	0/1258	0.57	0/1712
2	H	0.31	0/1294	0.58	0/1757
2	K	0.31	0/1264	0.59	0/1720
3	C	0.29	0/1765	0.60	0/2410
3	F	0.29	0/1756	0.60	0/2398
3	I	0.29	0/1765	0.61	0/2410
3	L	0.29	0/1756	0.61	0/2398
All	All	0.31	0/16096	0.60	0/21906

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	958	0	906	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	965	0	914	12	0
1	G	974	0	926	18	0
1	J	974	0	926	13	0
2	B	1232	0	1198	20	0
2	E	1226	0	1193	31	0
2	H	1262	0	1234	22	0
2	K	1232	0	1198	29	0
3	C	1721	0	1739	41	0
3	F	1712	0	1733	50	0
3	I	1721	0	1739	29	0
3	L	1712	0	1733	38	0
4	B	24	0	24	2	0
4	C	12	0	12	1	0
4	H	36	0	36	6	0
4	K	24	0	24	4	0
5	C	20	0	8	1	0
5	F	20	0	8	1	0
5	I	20	0	8	1	0
5	L	20	0	8	1	0
6	A	120	0	0	3	0
6	B	182	0	0	1	0
6	C	257	0	0	3	0
6	D	123	0	0	1	0
6	E	166	0	0	2	0
6	F	209	0	0	2	0
6	G	122	0	0	1	0
6	H	185	0	0	1	0
6	I	281	0	0	2	0
6	J	132	0	0	2	0
6	K	183	0	0	0	0
6	L	252	0	0	2	0
All	All	18077	0	15567	287	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 9.

The worst 5 of 287 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:F:113:LEU:HD11	3:F:188:ILE:HD12	1.36	1.05
3:I:82:ILE:HD11	3:I:117:ALA:HB2	1.44	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:GLN:HE21	1:A:26:GLN:H	1.08	0.97
3:F:115:VAL:HG22	3:F:188:ILE:HD11	1.47	0.94
1:D:45:ILE:HD11	1:D:96:PHE:HZ	1.32	0.93

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	116/126 (92%)	109 (94%)	7 (6%)	0	100	100
1	D	117/126 (93%)	111 (95%)	6 (5%)	0	100	100
1	G	118/126 (94%)	115 (98%)	3 (2%)	0	100	100
1	J	118/126 (94%)	114 (97%)	4 (3%)	0	100	100
2	B	150/157 (96%)	147 (98%)	3 (2%)	0	100	100
2	E	149/157 (95%)	145 (97%)	4 (3%)	0	100	100
2	H	154/157 (98%)	150 (97%)	4 (3%)	0	100	100
2	K	150/157 (96%)	146 (97%)	4 (3%)	0	100	100
3	C	215/243 (88%)	206 (96%)	8 (4%)	1 (0%)	34	22
3	F	214/243 (88%)	205 (96%)	7 (3%)	2 (1%)	21	10
3	I	215/243 (88%)	206 (96%)	8 (4%)	1 (0%)	34	22
3	L	214/243 (88%)	205 (96%)	8 (4%)	1 (0%)	34	22
All	All	1930/2104 (92%)	1859 (96%)	66 (3%)	5 (0%)	46	36

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	131	CYS

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Mol	Chain	Res	Type
3	F	131	CYS
3	I	131	CYS
3	L	131	CYS
3	F	238	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	100/108 (93%)	98 (98%)	2 (2%)	63	59
1	D	101/108 (94%)	101 (100%)	0	100	100
1	G	102/108 (94%)	102 (100%)	0	100	100
1	J	102/108 (94%)	102 (100%)	0	100	100
2	B	130/134 (97%)	127 (98%)	3 (2%)	58	53
2	E	129/134 (96%)	126 (98%)	3 (2%)	58	53
2	H	133/134 (99%)	129 (97%)	4 (3%)	48	42
2	K	130/134 (97%)	127 (98%)	3 (2%)	58	53
3	C	190/214 (89%)	190 (100%)	0	100	100
3	F	189/214 (88%)	186 (98%)	3 (2%)	70	67
3	I	190/214 (89%)	189 (100%)	1 (0%)	92	92
3	L	189/214 (88%)	188 (100%)	1 (0%)	92	92
All	All	1685/1824 (92%)	1665 (99%)	20 (1%)	78	76

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	37	LEU
3	F	188	ILE
2	K	48	HIS
2	E	85	TRP
3	F	35	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
3	F	175	GLN
1	G	84	ASN
2	K	100	GLN
1	G	14	HIS
2	H	61	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

16 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	$\# Z > 2$
4	FRU	B	3002	-	11,12,12	1.35	2 (18%)	10,18,18	1.75	2 (20%)
4	FRU	B	3008	-	11,12,12	2.31	4 (36%)	10,18,18	5.34	3 (30%)
4	FRU	C	3001	-	11,12,12	1.60	2 (18%)	10,18,18	1.84	2 (20%)
5	TAR	C	3401	-	3,9,9	0.87	0	6,12,12	1.16	1 (16%)
5	TAR	C	3501	-	3,9,9	0.84	0	6,12,12	1.23	1 (16%)
5	TAR	F	4401	-	3,9,9	0.83	0	6,12,12	1.17	1 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	TAR	F	4501	-	3,9,9	0.73	0	6,12,12	1.29	1 (16%)
4	FRU	H	3004	-	11,12,12	1.42	2 (18%)	10,18,18	1.80	2 (20%)
4	FRU	H	3006	-	11,12,12	1.33	1 (9%)	10,18,18	2.00	2 (20%)
4	FRU	H	3007	-	11,12,12	1.69	2 (18%)	10,18,18	1.79	2 (20%)
5	TAR	I	5401	-	3,9,9	1.01	0	6,12,12	1.13	0
5	TAR	I	5501	-	3,9,9	0.84	0	6,12,12	1.21	1 (16%)
4	FRU	K	3003	-	11,12,12	1.41	2 (18%)	10,18,18	1.85	2 (20%)
4	FRU	K	3005	-	11,12,12	1.59	2 (18%)	10,18,18	1.92	4 (40%)
5	TAR	L	6401	-	3,9,9	0.94	0	6,12,12	1.14	1 (16%)
5	TAR	L	6501	-	3,9,9	0.95	0	6,12,12	1.22	1 (16%)

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
4	FRU	B	3002	-	-	0/5/24/24	0/1/1/1
4	FRU	B	3008	-	-	0/5/24/24	0/1/1/1
4	FRU	C	3001	-	-	0/5/24/24	0/1/1/1
5	TAR	C	3401	-	2/2/4/4	0/4/12/12	0/0/0/0
5	TAR	C	3501	-	2/2/4/4	0/4/12/12	0/0/0/0
5	TAR	F	4401	-	2/2/4/4	0/4/12/12	0/0/0/0
5	TAR	F	4501	-	2/2/4/4	0/4/12/12	0/0/0/0
4	FRU	H	3004	-	-	0/5/24/24	0/1/1/1
4	FRU	H	3006	-	-	0/5/24/24	0/1/1/1
4	FRU	H	3007	-	-	0/5/24/24	0/1/1/1
5	TAR	I	5401	-	2/2/4/4	0/4/12/12	0/0/0/0
5	TAR	I	5501	-	2/2/4/4	0/4/12/12	0/0/0/0
4	FRU	K	3003	-	-	0/5/24/24	0/1/1/1
4	FRU	K	3005	-	-	0/5/24/24	0/1/1/1
5	TAR	L	6401	-	2/2/4/4	0/4/12/12	0/0/0/0
5	TAR	L	6501	-	2/2/4/4	0/4/12/12	0/0/0/0

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	3008	FRU	C4-C5	-3.34	1.44	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	K	3003	FRU	O5-C5	2.33	1.49	1.43
4	C	3001	FRU	O5-C5	2.36	1.49	1.43
4	H	3004	FRU	O5-C5	2.40	1.49	1.43
4	B	3008	FRU	O5-C5	2.42	1.49	1.43

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	3008	FRU	O2-C2-O5	-16.01	76.33	109.37
4	B	3008	FRU	O3-C3-C4	-2.75	103.42	113.29
4	H	3007	FRU	C6-C5-C4	-2.61	108.91	115.08
4	K	3003	FRU	C6-C5-C4	-2.56	109.02	115.08
5	F	4501	TAR	C4-C3-C2	-2.54	108.14	113.35

5 of 16 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	F	4501	TAR	C2
5	F	4501	TAR	C3
5	C	3501	TAR	C2
5	C	3501	TAR	C3
5	C	3401	TAR	C2

There are no torsion outliers.

There are no ring outliers.

12 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	3002	FRU	1	0
4	B	3008	FRU	1	0
4	C	3001	FRU	1	0
5	C	3401	TAR	1	0
5	F	4401	TAR	1	0
4	H	3004	FRU	1	0
4	H	3006	FRU	4	0
4	H	3007	FRU	1	0
5	I	5401	TAR	1	0
4	K	3003	FRU	2	0
4	K	3005	FRU	2	0
5	L	6401	TAR	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	118/126 (93%)	-0.17	3 (2%) 61 65	8, 14, 28, 34	0
1	D	119/126 (94%)	-0.19	2 (1%) 73 76	8, 13, 29, 36	0
1	G	120/126 (95%)	-0.14	4 (3%) 50 55	9, 15, 29, 43	0
1	J	120/126 (95%)	-0.30	2 (1%) 73 76	7, 12, 29, 38	0
2	B	152/157 (96%)	-0.44	1 (0%) 89 90	7, 11, 24, 33	0
2	E	151/157 (96%)	-0.34	6 (3%) 42 46	6, 12, 31, 41	0
2	H	156/157 (99%)	-0.34	4 (2%) 59 64	7, 11, 23, 60	0
2	K	152/157 (96%)	-0.33	7 (4%) 36 40	5, 11, 29, 37	0
3	C	217/243 (89%)	-0.21	3 (1%) 78 80	7, 14, 25, 46	0
3	F	216/243 (88%)	0.02	5 (2%) 64 67	7, 16, 30, 43	0
3	I	217/243 (89%)	-0.32	3 (1%) 78 80	8, 12, 21, 42	0
3	L	216/243 (88%)	-0.25	4 (1%) 70 73	7, 11, 23, 34	0
All	All	1954/2104 (92%)	-0.25	44 (2%) 64 67	5, 13, 27, 60	0

The worst 5 of 44 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	239	VAL	9.3
2	H	157	LYS	8.5
2	H	156	ALA	6.9
2	H	2	SER	5.4
2	H	3	SER	4.9

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

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

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
4	FRU	H	3004	12/12	0.73	0.30	46.02	29,37,41,42	0
4	FRU	H	3006	12/12	0.64	0.40	14.32	39,45,48,49	0
4	FRU	H	3007	12/12	0.61	0.38	14.09	35,38,40,40	0
4	FRU	B	3008	12/12	0.66	0.34	11.34	32,37,40,41	0
4	FRU	C	3001	12/12	0.78	0.26	10.27	32,36,37,41	0
4	FRU	K	3005	12/12	0.70	0.30	10.09	29,34,36,39	0
4	FRU	B	3002	12/12	0.72	0.32	9.56	29,37,40,40	0
4	FRU	K	3003	12/12	0.62	0.34	5.71	43,45,49,50	0
5	TAR	I	5401	10/10	0.97	0.11	0.18	13,16,19,21	0
5	TAR	L	6401	10/10	0.98	0.11	-0.07	13,15,19,19	0
5	TAR	C	3401	10/10	0.97	0.10	-0.72	14,17,19,22	0
5	TAR	F	4401	10/10	0.98	0.10	-0.85	13,16,18,20	0
5	TAR	F	4501	10/10	0.94	0.17	-	18,23,27,29	0
5	TAR	I	5501	10/10	0.93	0.23	-	20,24,28,30	0
5	TAR	C	3501	10/10	0.94	0.19	-	16,22,29,29	0
5	TAR	L	6501	10/10	0.95	0.16	-	15,21,26,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.