



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:32 AM GMT

PDB ID : 3B7K
Title : Human Acyl-coenzyme A thioesterase 12
Authors : Lehtio, L.; Busam, R.D.; Arrowsmith, C.H.; Collins, R.; Dahlgren, L.G.; Edwards, A.M.; Flodin, S.; Flores, A.; Graslund, S.; Hammarstrom, M.; Hallberg, B.M.; Herman, M.D.; Johansson, A.; Johansson, I.; Kallas, A.; Karlberg, T.; Kotenyova, T.; Moche, M.; Nilsson, M.E.; Nordlund, P.; Nyman, T.; Persson, C.; Sagemark, J.; Sundstrom, M.; Svensson L.; Thorsell, A.G.; Tresaugues, L.; Van Den Berg, S.; Weigelt, J.; Welin, M.; Berglund, H.; Structural Genomics Consortium (SGC)
Deposited on : 2007-10-31
Resolution : 2.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

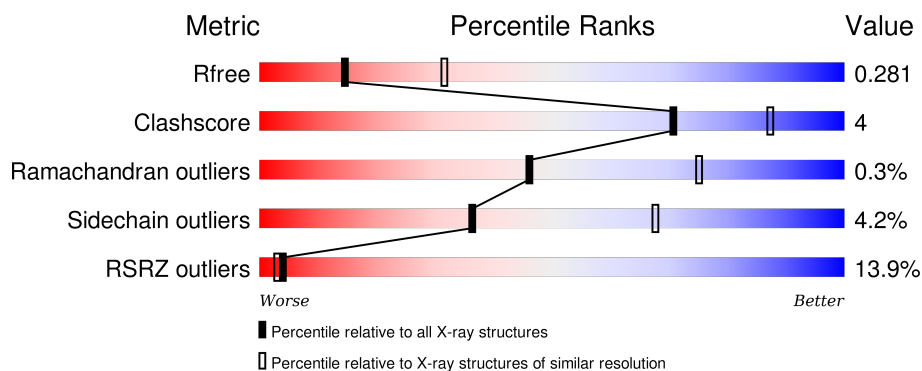
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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	333	<div> <div>8%</div> <div>70%</div> <div>10%</div> <div>20%</div> </div>
1	B	333	<div> <div>12%</div> <div>64%</div> <div>10%</div> <div>26%</div> </div>
1	C	333	<div> <div>13%</div> <div>66%</div> <div>10%</div> <div>23%</div> </div>

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
2	COA	B	317	X	-	-	-

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6061 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 Acyl-coenzyme A thioesterase 12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	267	Total	C	N	O	S	0	0	0
			2050	1291	362	384	13			
1	B	247	Total	C	N	O	S	0	0	0
			1901	1201	338	350	12			
1	C	255	Total	C	N	O	S	0	0	0
			1966	1243	349	361	13			

There are 69 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-16	MET	-	EXPRESSION TAG	UNP Q8WYK0
A	-15	HIS	-	EXPRESSION TAG	UNP Q8WYK0
A	-14	HIS	-	EXPRESSION TAG	UNP Q8WYK0
A	-13	HIS	-	EXPRESSION TAG	UNP Q8WYK0
A	-12	HIS	-	EXPRESSION TAG	UNP Q8WYK0
A	-11	HIS	-	EXPRESSION TAG	UNP Q8WYK0
A	-10	HIS	-	EXPRESSION TAG	UNP Q8WYK0
A	-9	SER	-	EXPRESSION TAG	UNP Q8WYK0
A	-8	SER	-	EXPRESSION TAG	UNP Q8WYK0
A	-7	GLY	-	EXPRESSION TAG	UNP Q8WYK0
A	-6	VAL	-	EXPRESSION TAG	UNP Q8WYK0
A	-5	ASP	-	EXPRESSION TAG	UNP Q8WYK0
A	-4	LEU	-	EXPRESSION TAG	UNP Q8WYK0
A	-3	GLY	-	EXPRESSION TAG	UNP Q8WYK0
A	-2	THR	-	EXPRESSION TAG	UNP Q8WYK0
A	-1	GLU	-	EXPRESSION TAG	UNP Q8WYK0
A	0	ASN	-	EXPRESSION TAG	UNP Q8WYK0
A	1	LEU	-	EXPRESSION TAG	UNP Q8WYK0
A	2	TYR	-	EXPRESSION TAG	UNP Q8WYK0
A	3	PHE	-	EXPRESSION TAG	UNP Q8WYK0
A	4	GLN	-	EXPRESSION TAG	UNP Q8WYK0
A	5	SER	-	EXPRESSION TAG	UNP Q8WYK0
A	6	MET	-	EXPRESSION TAG	UNP Q8WYK0

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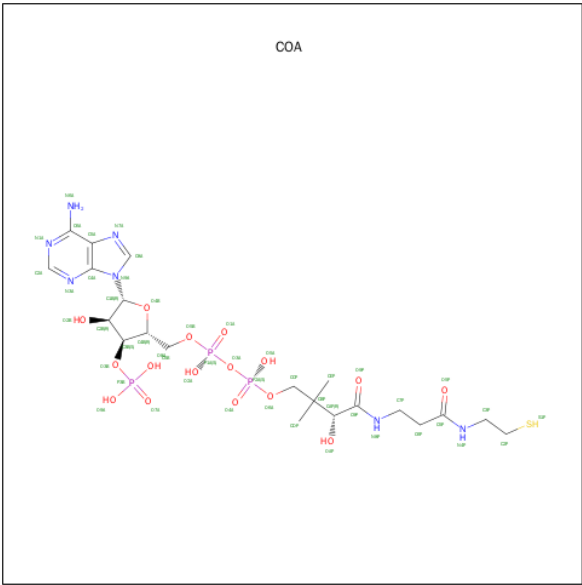
Chain	Residue	Modelled	Actual	Comment	Reference
B	-16	MET	-	EXPRESSION TAG	UNP Q8WYK0
B	-15	HIS	-	EXPRESSION TAG	UNP Q8WYK0
B	-14	HIS	-	EXPRESSION TAG	UNP Q8WYK0
B	-13	HIS	-	EXPRESSION TAG	UNP Q8WYK0
B	-12	HIS	-	EXPRESSION TAG	UNP Q8WYK0
B	-11	HIS	-	EXPRESSION TAG	UNP Q8WYK0
B	-10	HIS	-	EXPRESSION TAG	UNP Q8WYK0
B	-9	SER	-	EXPRESSION TAG	UNP Q8WYK0
B	-8	SER	-	EXPRESSION TAG	UNP Q8WYK0
B	-7	GLY	-	EXPRESSION TAG	UNP Q8WYK0
B	-6	VAL	-	EXPRESSION TAG	UNP Q8WYK0
B	-5	ASP	-	EXPRESSION TAG	UNP Q8WYK0
B	-4	LEU	-	EXPRESSION TAG	UNP Q8WYK0
B	-3	GLY	-	EXPRESSION TAG	UNP Q8WYK0
B	-2	THR	-	EXPRESSION TAG	UNP Q8WYK0
B	-1	GLU	-	EXPRESSION TAG	UNP Q8WYK0
B	0	ASN	-	EXPRESSION TAG	UNP Q8WYK0
B	1	LEU	-	EXPRESSION TAG	UNP Q8WYK0
B	2	TYR	-	EXPRESSION TAG	UNP Q8WYK0
B	3	PHE	-	EXPRESSION TAG	UNP Q8WYK0
B	4	GLN	-	EXPRESSION TAG	UNP Q8WYK0
B	5	SER	-	EXPRESSION TAG	UNP Q8WYK0
B	6	MET	-	EXPRESSION TAG	UNP Q8WYK0
C	-16	MET	-	EXPRESSION TAG	UNP Q8WYK0
C	-15	HIS	-	EXPRESSION TAG	UNP Q8WYK0
C	-14	HIS	-	EXPRESSION TAG	UNP Q8WYK0
C	-13	HIS	-	EXPRESSION TAG	UNP Q8WYK0
C	-12	HIS	-	EXPRESSION TAG	UNP Q8WYK0
C	-11	HIS	-	EXPRESSION TAG	UNP Q8WYK0
C	-10	HIS	-	EXPRESSION TAG	UNP Q8WYK0
C	-9	SER	-	EXPRESSION TAG	UNP Q8WYK0
C	-8	SER	-	EXPRESSION TAG	UNP Q8WYK0
C	-7	GLY	-	EXPRESSION TAG	UNP Q8WYK0
C	-6	VAL	-	EXPRESSION TAG	UNP Q8WYK0
C	-5	ASP	-	EXPRESSION TAG	UNP Q8WYK0
C	-4	LEU	-	EXPRESSION TAG	UNP Q8WYK0
C	-3	GLY	-	EXPRESSION TAG	UNP Q8WYK0
C	-2	THR	-	EXPRESSION TAG	UNP Q8WYK0
C	-1	GLU	-	EXPRESSION TAG	UNP Q8WYK0
C	0	ASN	-	EXPRESSION TAG	UNP Q8WYK0
C	1	LEU	-	EXPRESSION TAG	UNP Q8WYK0
C	2	TYR	-	EXPRESSION TAG	UNP Q8WYK0

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Chain	Residue	Modelled	Actual	Comment	Reference
C	3	PHE	-	EXPRESSION TAG	UNP Q8WYK0
C	4	GLN	-	EXPRESSION TAG	UNP Q8WYK0
C	5	SER	-	EXPRESSION TAG	UNP Q8WYK0
C	6	MET	-	EXPRESSION TAG	UNP Q8WYK0

- Molecule 2 is COENZYME A (three-letter code: COA) (formula: C₂₁H₃₆N₇O₁₆P₃S).

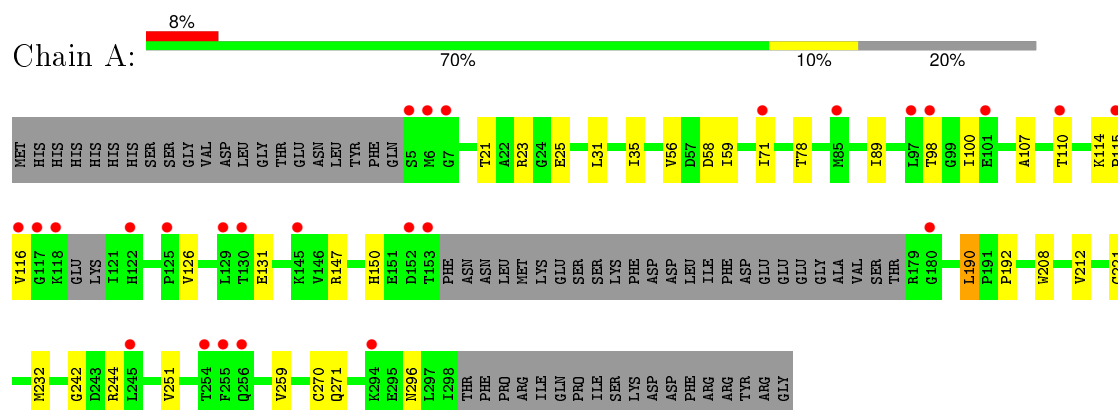


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	B	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	C	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		

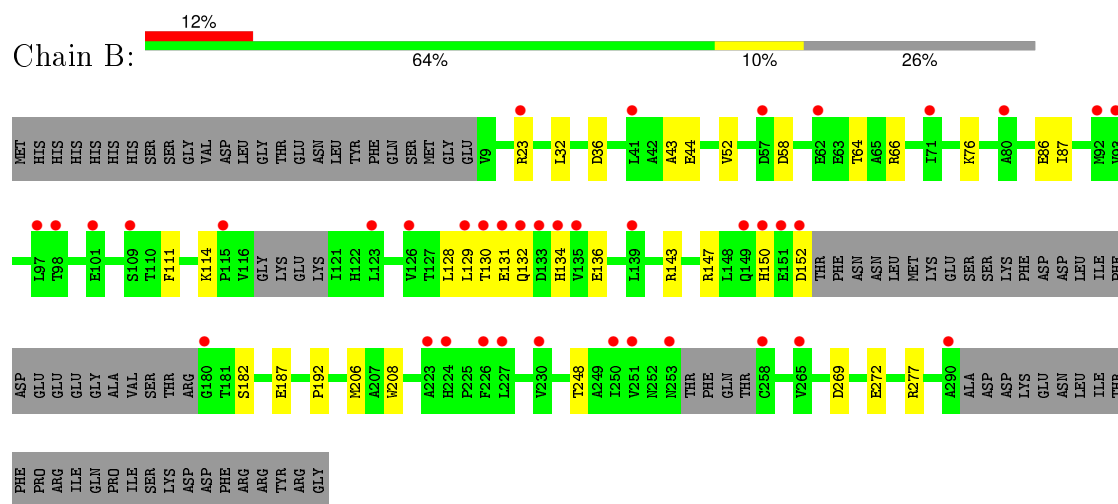
3 Residue-property plots

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.

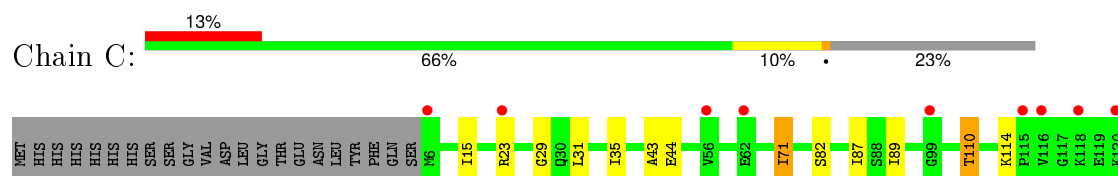
• Molecule 1: Acyl-coenzyme A thioesterase 12

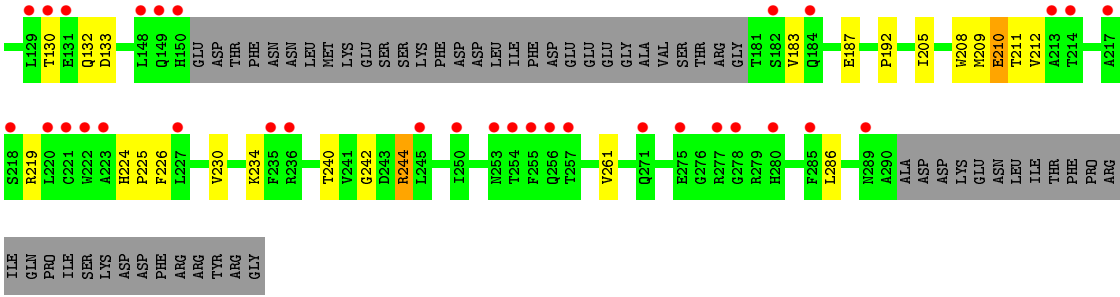


• Molecule 1: Acyl-coenzyme A thioesterase 12



• Molecule 1: Acyl-coenzyme A thioesterase 12





ILE
GLN
PRO
ILE
SER
LYS
ASP
ASP
PHE
ARG
ARG
TVR
ARG
GLY

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	82.70Å 126.05Å 185.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.89 – 2.70 19.74 – 2.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.89-2.70) 99.6 (19.74-2.70)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.01 (at 2.71Å)	Xtriage
Refinement program	REFMAC 5.3.0040	Depositor
R, R_{free}	0.234 , 0.285 0.231 , 0.281	Depositor DCC
R_{free} test set	1339 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	52.7	Xtriage
Anisotropy	0.155	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 58.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 26805 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6061	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.56% 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: COA

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	0.43	0/2086	0.58	0/2825
1	B	0.40	0/1935	0.52	0/2621
1	C	0.38	0/2003	0.52	0/2713
All	All	0.40	0/6024	0.54	0/8159

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	2050	0	2046	20	0
1	B	1901	0	1906	16	0
1	C	1966	0	1979	20	0
2	A	48	0	32	2	0
2	B	48	0	32	1	0
2	C	48	0	32	3	0
All	All	6061	0	6027	53	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 4.

All (53) 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:A:147:ARG:HA	1:A:232:MET:HE1	1.52	0.89
1:A:147:ARG:HA	1:A:232:MET:CE	2.10	0.82
1:C:242:GLY:O	1:C:244:ARG:NH1	2.19	0.75
1:C:31:LEU:HD13	1:C:71:ILE:HD12	1.69	0.74
1:A:35:ILE:HG23	1:A:89:ILE:HG21	1.74	0.69
1:A:192:PRO:HG3	1:C:192:PRO:HB3	1.76	0.67
1:A:242:GLY:O	1:A:244:ARG:NH1	2.28	0.67
1:A:21:THR:HG23	1:A:23:ARG:H	1.62	0.65
1:B:187:GLU:HG2	1:B:208:TRP:CE2	2.32	0.64
1:B:52:VAL:HB	2:B:317:COA:HN4	1.63	0.63
1:C:187:GLU:HG2	1:C:208:TRP:CE2	2.35	0.61
1:B:36:ASP:OD1	1:B:111:PHE:HZ	1.82	0.61
1:B:23:ARG:O	1:B:66:ARG:NH2	2.34	0.60
1:A:208:TRP:O	1:A:212:VAL:HG23	2.02	0.58
1:A:190:LEU:HB3	1:A:192:PRO:HD2	1.91	0.53
1:C:205:ILE:O	1:C:209:MET:HB2	2.09	0.53
1:C:23:ARG:HH22	1:C:226:PHE:HB3	1.74	0.53
1:C:234:LYS:HD2	2:C:317:COA:H62A	1.74	0.52
1:A:110:THR:HG21	2:A:317:COA:H2A	1.95	0.49
1:B:152:ASP:OD1	1:B:152:ASP:N	2.44	0.49
1:C:130:THR:HG22	1:C:132:GLN:H	1.79	0.48
1:A:98:THR:HB	1:A:100:ILE:HG22	1.95	0.48
2:C:317:COA:H131	2:C:317:COA:N8P	2.28	0.48
1:A:244:ARG:NH2	1:C:44:GLU:OE1	2.44	0.48
1:C:35:ILE:HG23	1:C:89:ILE:HG21	1.95	0.48
1:A:59:ILE:HD12	1:A:107:ALA:HB1	1.96	0.48
1:B:44:GLU:OE1	1:C:244:ARG:NH2	2.46	0.47
1:A:192:PRO:HB3	1:B:192:PRO:HG3	1.97	0.46
1:B:32:LEU:HD13	1:B:206:MET:HB3	1.98	0.46
1:B:136:GLU:HG3	1:B:143:ARG:HH22	1.81	0.46
1:C:43:ALA:HB2	1:C:87:ILE:HD11	1.97	0.45
1:B:36:ASP:OD1	1:B:111:PHE:CZ	2.68	0.45
1:A:147:ARG:HA	1:A:232:MET:HE3	1.95	0.44
1:B:130:THR:HG22	1:B:132:GLN:H	1.82	0.44
1:B:277:ARG:O	1:B:277:ARG:HD2	2.17	0.44
1:A:23:ARG:HE	1:A:25:GLU:CD	2.21	0.44
1:A:251:VAL:HG13	1:A:259:VAL:HG23	1.99	0.44
1:A:56:VAL:HG12	1:A:59:ILE:HD11	2.00	0.44
1:C:208:TRP:O	1:C:212:VAL:HG23	2.18	0.43
1:C:15:ILE:HD11	1:C:71:ILE:HG13	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:183:VAL:HG22	1:C:219:ARG:NH1	2.34	0.42
1:B:269:ASP:HB2	1:B:272:GLU:CG	2.49	0.42
1:C:29:GLY:N	1:C:210:GLU:HG2	2.34	0.42
1:C:110:THR:HG21	2:C:317:COA:H2A	2.02	0.42
1:C:230:VAL:HG22	1:C:286:LEU:HD22	2.02	0.42
1:A:110:THR:HG21	2:A:317:COA:C2A	2.50	0.41
1:B:128:LEU:HD23	1:B:134:HIS:CD2	2.55	0.41
1:B:86:GLU:HG3	1:B:147:ARG:HH22	1.85	0.41
1:C:130:THR:O	1:C:133:ASP:HB2	2.20	0.41
1:B:43:ALA:HB2	1:B:87:ILE:HD11	2.02	0.41
1:C:224:HIS:HA	1:C:225:PRO:HD3	1.91	0.41
1:A:221:CYS:HA	1:A:296:ASN:O	2.21	0.41
1:A:114:LYS:HA	1:A:115:PRO:HD2	1.73	0.41

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	261/333 (78%)	247 (95%)	13 (5%)	1 (0%)	39	69
1	B	239/333 (72%)	228 (95%)	10 (4%)	1 (0%)	39	69
1	C	251/333 (75%)	237 (94%)	14 (6%)	0	100	100
All	All	751/999 (75%)	712 (95%)	37 (5%)	2 (0%)	46	75

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	150	HIS
1	A	150	HIS

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	222/284 (78%)	212 (96%)	10 (4%)	34	65
1	B	206/284 (72%)	198 (96%)	8 (4%)	39	70
1	C	213/284 (75%)	204 (96%)	9 (4%)	36	68
All	All	641/852 (75%)	614 (96%)	27 (4%)	36	68

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	LEU
1	A	58	ASP
1	A	71	ILE
1	A	78	THR
1	A	116	VAL
1	A	126	VAL
1	A	131	GLU
1	A	190	LEU
1	A	270	CYS
1	A	271	GLN
1	B	58	ASP
1	B	64	THR
1	B	76	LYS
1	B	114	LYS
1	B	129	LEU
1	B	131	GLU
1	B	182	SER
1	B	248	THR
1	C	71	ILE
1	C	82	SER
1	C	110	THR
1	C	114	LYS
1	C	210	GLU
1	C	211	THR
1	C	240	THR
1	C	244	ARG

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Mol	Chain	Res	Type
1	C	261	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	132	GLN
1	A	271	GLN
1	B	134	HIS
1	B	184	GLN
1	C	184	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

3 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
2	COA	A	317	-	40,50,50	1.67	3 (7%)	50,75,75	1.83	4 (8%)
2	COA	B	317	-	40,50,50	1.73	3 (7%)	50,75,75	1.86	2 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	COA	C	317	-	40,50,50	1.70	3 (7%)	50,75,75	2.05	5 (10%)

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	COA	A	317	-	-	0/44/64/64	0/3/3/3
2	COA	B	317	-	1/1/11/13	2/44/64/64	0/3/3/3
2	COA	C	317	-	-	0/44/64/64	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	317	COA	C2A-N1A	2.29	1.38	1.33
2	B	317	COA	C2A-N1A	2.45	1.38	1.33
2	C	317	COA	C2A-N1A	2.61	1.38	1.33
2	A	317	COA	C2A-N3A	3.49	1.38	1.32
2	B	317	COA	C2A-N3A	3.64	1.38	1.32
2	C	317	COA	C2A-N3A	3.70	1.38	1.32
2	A	317	COA	O9P-C9P	9.08	1.41	1.23
2	C	317	COA	O9P-C9P	9.10	1.41	1.23
2	B	317	COA	O9P-C9P	9.45	1.41	1.23

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	317	COA	N3A-C2A-N1A	-11.74	119.90	128.89
2	B	317	COA	N3A-C2A-N1A	-11.24	120.28	128.89
2	A	317	COA	N3A-C2A-N1A	-10.56	120.81	128.89
2	C	317	COA	P2A-O3A-P1A	-4.41	120.35	132.73
2	A	317	COA	P2A-O3A-P1A	-3.74	122.24	132.73
2	C	317	COA	C1B-N9A-C4A	-3.15	122.18	126.94
2	C	317	COA	C4B-O4B-C1B	-2.55	106.92	109.72
2	B	317	COA	O5A-P2A-O3A	2.03	114.32	105.09
2	A	317	COA	O4B-C1B-N9A	2.26	112.83	108.10
2	A	317	COA	O3B-P3B-O7A	2.35	112.98	107.11
2	C	317	COA	O4B-C1B-N9A	3.41	115.23	108.10

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	317	COA	CAP

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	317	COA	CAP-C9P-N8P-C7P
2	B	317	COA	C6P-C5P-N4P-C3P

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	317	COA	2	0
2	B	317	COA	1	0
2	C	317	COA	3	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	267/333 (80%)	0.67	26 (9%) 10 7	47, 54, 60, 66	0
1	B	247/333 (74%)	1.02	39 (15%) 3 2	47, 56, 63, 66	0
1	C	255/333 (76%)	0.85	42 (16%) 2 2	48, 56, 61, 67	0
All	All	769/999 (76%)	0.84	107 (13%) 4 3	47, 55, 61, 67	0

All (107) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	257	THR	6.5
1	A	153	THR	5.8
1	C	256	GLN	5.4
1	A	122	HIS	5.3
1	A	6	MET	5.2
1	C	149	GLN	5.1
1	C	130	THR	4.8
1	A	115	PRO	4.8
1	A	5	SER	4.5
1	B	151	GLU	4.4
1	C	255	PHE	4.4
1	C	6	MET	4.4
1	B	152	ASP	4.3
1	C	150	HIS	4.2
1	B	132	GLN	4.1
1	C	289	ASN	4.1
1	C	221	CYS	4.0
1	B	253	ASN	4.0
1	B	290	ALA	3.9
1	C	254	THR	3.9
1	A	256	GLN	3.9
1	B	115	PRO	3.8
1	B	135	VAL	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	97	LEU	3.6
1	B	23	ARG	3.6
1	B	62	GLU	3.5
1	A	117	GLY	3.5
1	C	131	GLU	3.4
1	A	130	THR	3.4
1	B	97	LEU	3.4
1	C	222	TRP	3.4
1	B	133	ASP	3.4
1	A	152	ASP	3.4
1	B	109	SER	3.4
1	A	255	PHE	3.3
1	B	251	VAL	3.3
1	A	245	LEU	3.2
1	C	116	VAL	3.2
1	B	129	LEU	3.1
1	B	224	HIS	3.1
1	B	92	MET	3.0
1	C	253	ASN	3.0
1	B	130	THR	3.0
1	C	148	LEU	2.9
1	C	99	GLY	2.9
1	B	131	GLU	2.8
1	A	98	THR	2.8
1	A	180	GLY	2.7
1	B	139	LEU	2.7
1	B	93	VAL	2.7
1	A	294	LYS	2.6
1	C	277	ARG	2.6
1	C	182	SER	2.6
1	C	120	LYS	2.6
1	C	250	ILE	2.6
1	B	101	GLU	2.6
1	C	245	LEU	2.6
1	C	275	GLU	2.6
1	A	85	MET	2.6
1	B	149	GLN	2.5
1	A	129	LEU	2.5
1	B	180	GLY	2.5
1	B	57	ASP	2.5
1	B	223	ALA	2.4
1	A	71	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	125	PRO	2.4
1	B	123	LEU	2.4
1	C	220	LEU	2.4
1	C	118	LYS	2.3
1	C	271	GLN	2.3
1	B	126	VAL	2.3
1	C	235	PHE	2.3
1	A	118	LYS	2.3
1	C	129	LEU	2.3
1	B	150	HIS	2.3
1	B	265	VAL	2.3
1	C	184	GLN	2.3
1	B	98	THR	2.2
1	B	41	LEU	2.2
1	C	115	PRO	2.2
1	C	213	ALA	2.2
1	A	110	THR	2.2
1	B	226	PHE	2.2
1	B	230	VAL	2.2
1	A	116	VAL	2.2
1	A	254	THR	2.2
1	C	62	GLU	2.2
1	C	56	VAL	2.2
1	C	236	ARG	2.1
1	A	101	GLU	2.1
1	C	223	ALA	2.1
1	C	23	ARG	2.1
1	A	7	GLY	2.1
1	C	227	LEU	2.1
1	C	278	GLY	2.1
1	C	217	ALA	2.1
1	C	214	THR	2.1
1	C	280	HIS	2.1
1	B	227	LEU	2.1
1	C	218	SER	2.1
1	B	134	HIS	2.1
1	B	71	ILE	2.0
1	C	285	PHE	2.0
1	B	250	ILE	2.0
1	A	145	LYS	2.0
1	B	80	ALA	2.0
1	B	258	CYS	2.0

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 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
2	COA	B	317	48/48	0.90	0.28	0.87	45,53,57,58	0
2	COA	A	317	48/48	0.94	0.23	0.37	31,41,44,46	0
2	COA	C	317	48/48	0.91	0.23	-0.06	44,55,59,59	0

6.5 Other polymers [i](#)

There are no such residues in this entry.